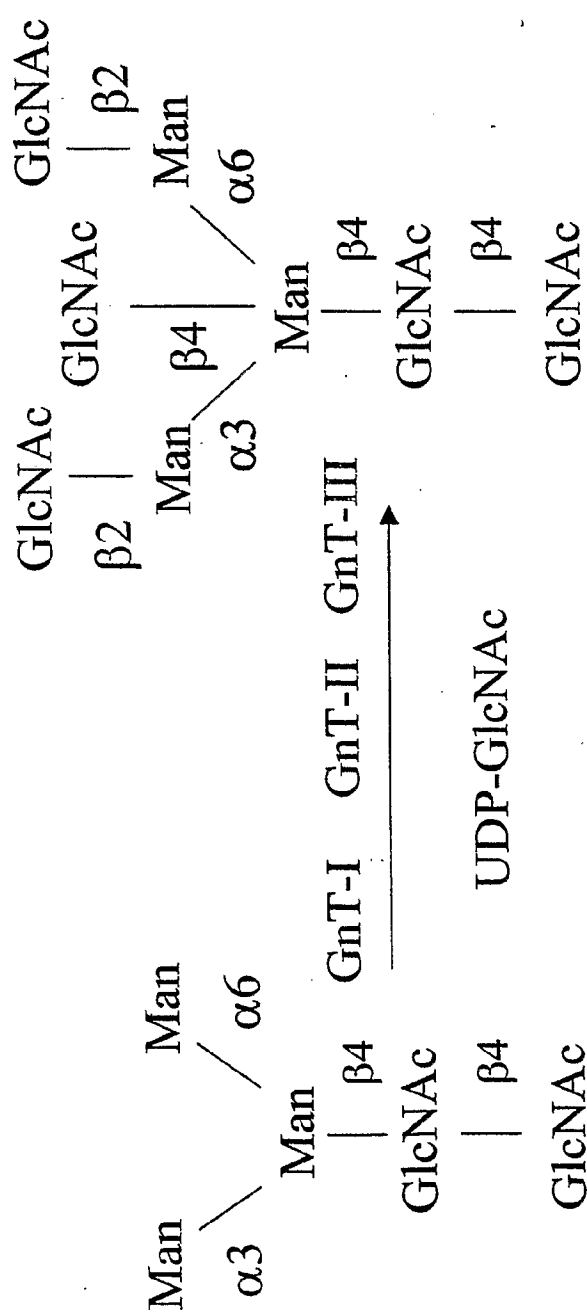


1/498



Trimannosyl core

Trimannosyl core with
Bisecting GlcNAc

FIG. 1

2/498

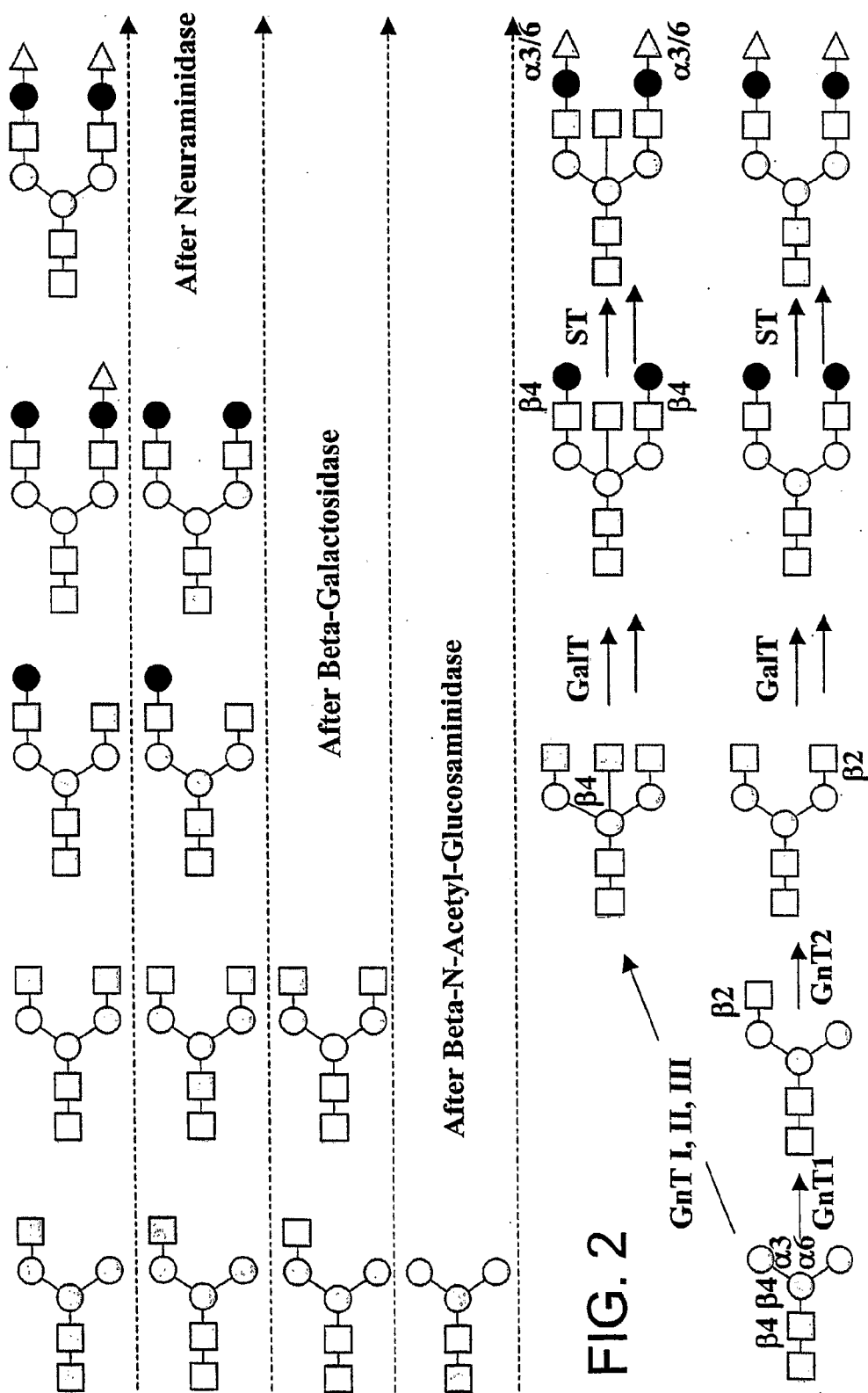


FIG. 2

3/498

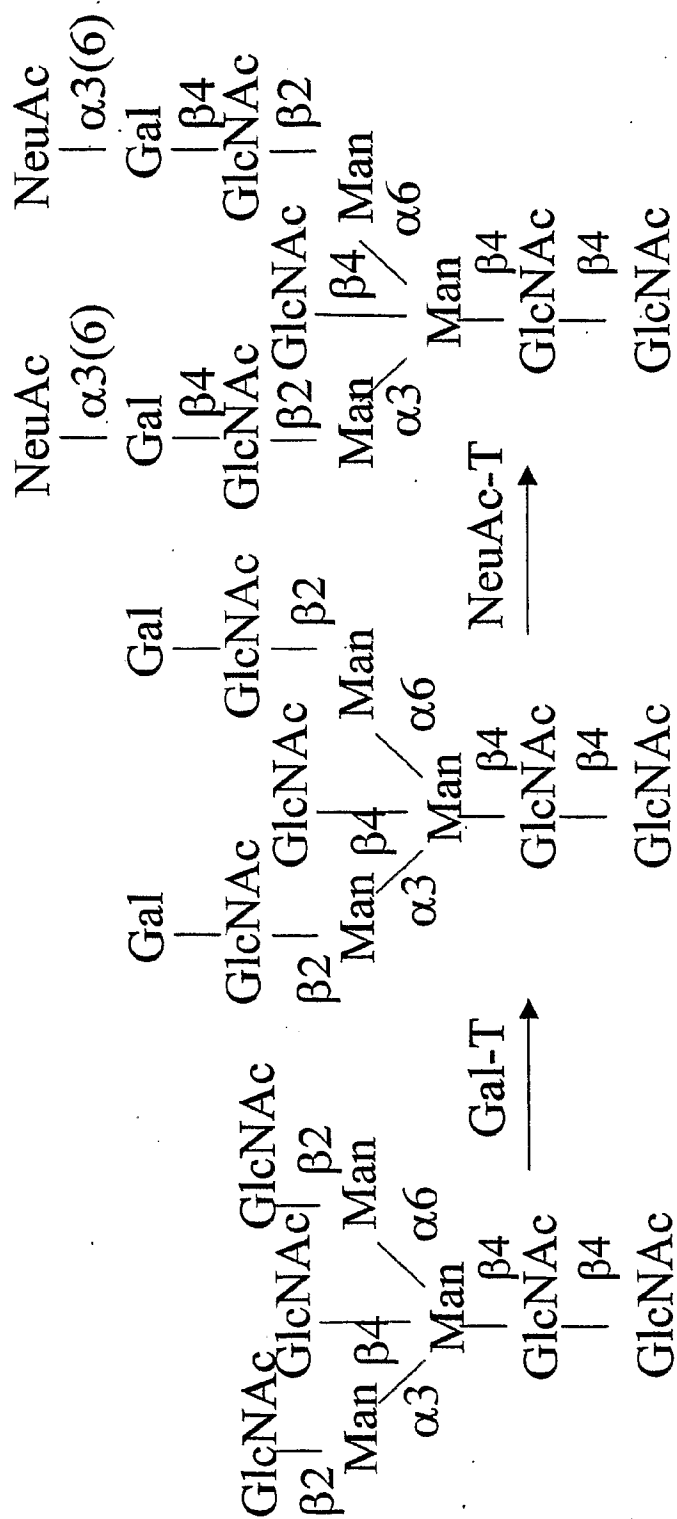


FIG. 3

4/498

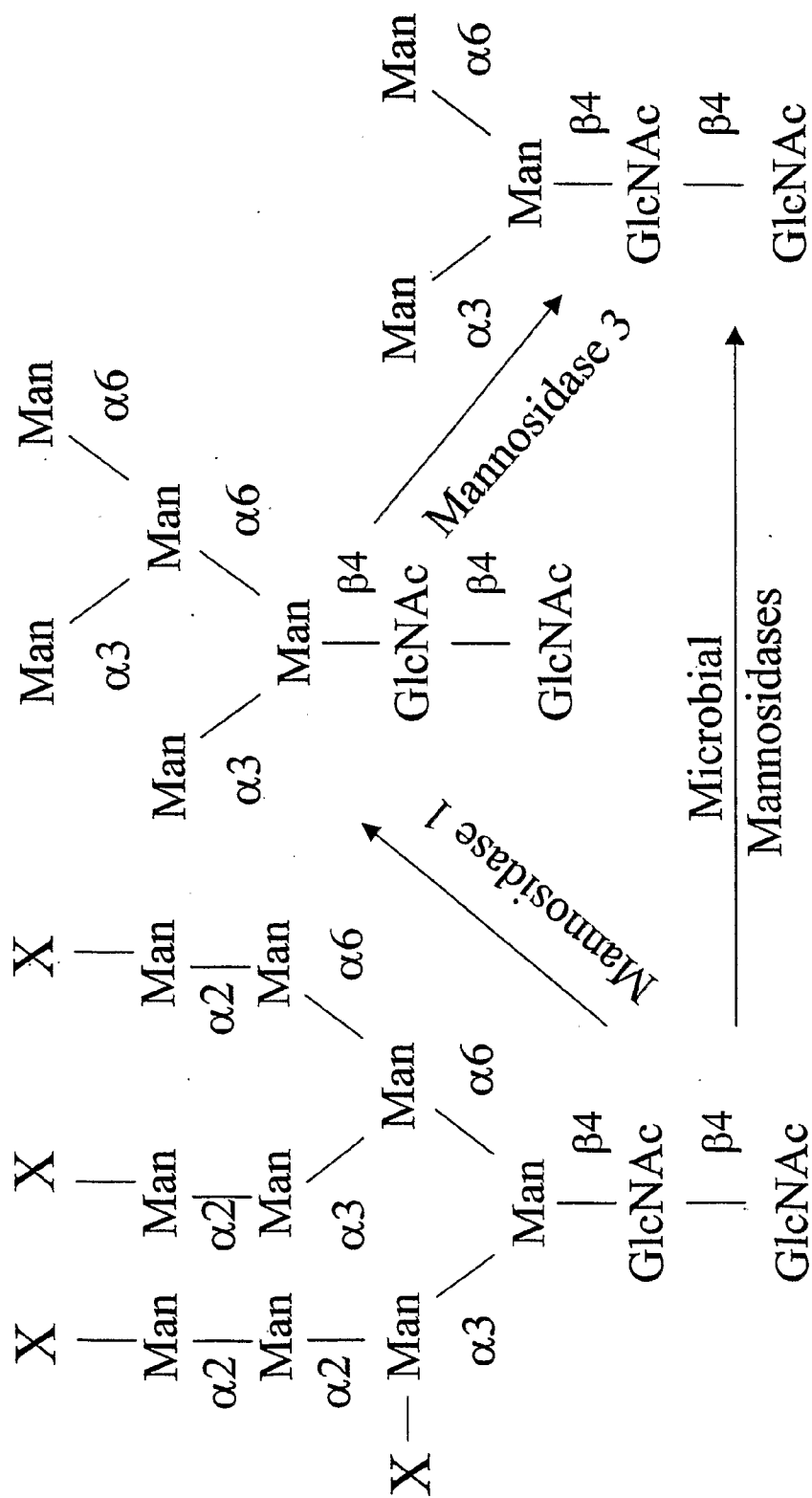


FIG. 4

5/498

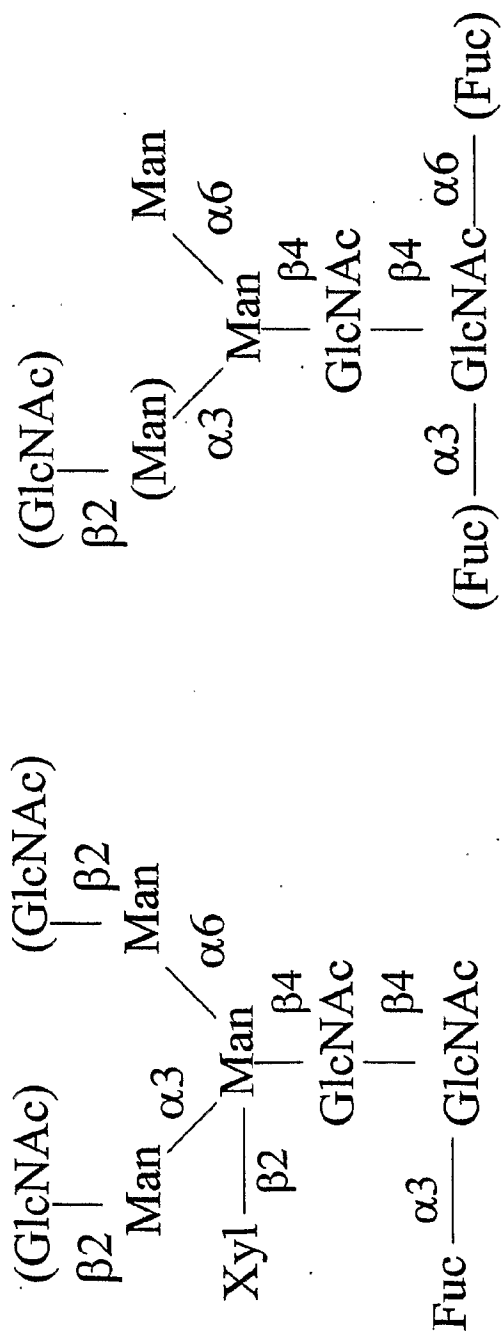


FIG. 5

FIG. 6

6/498

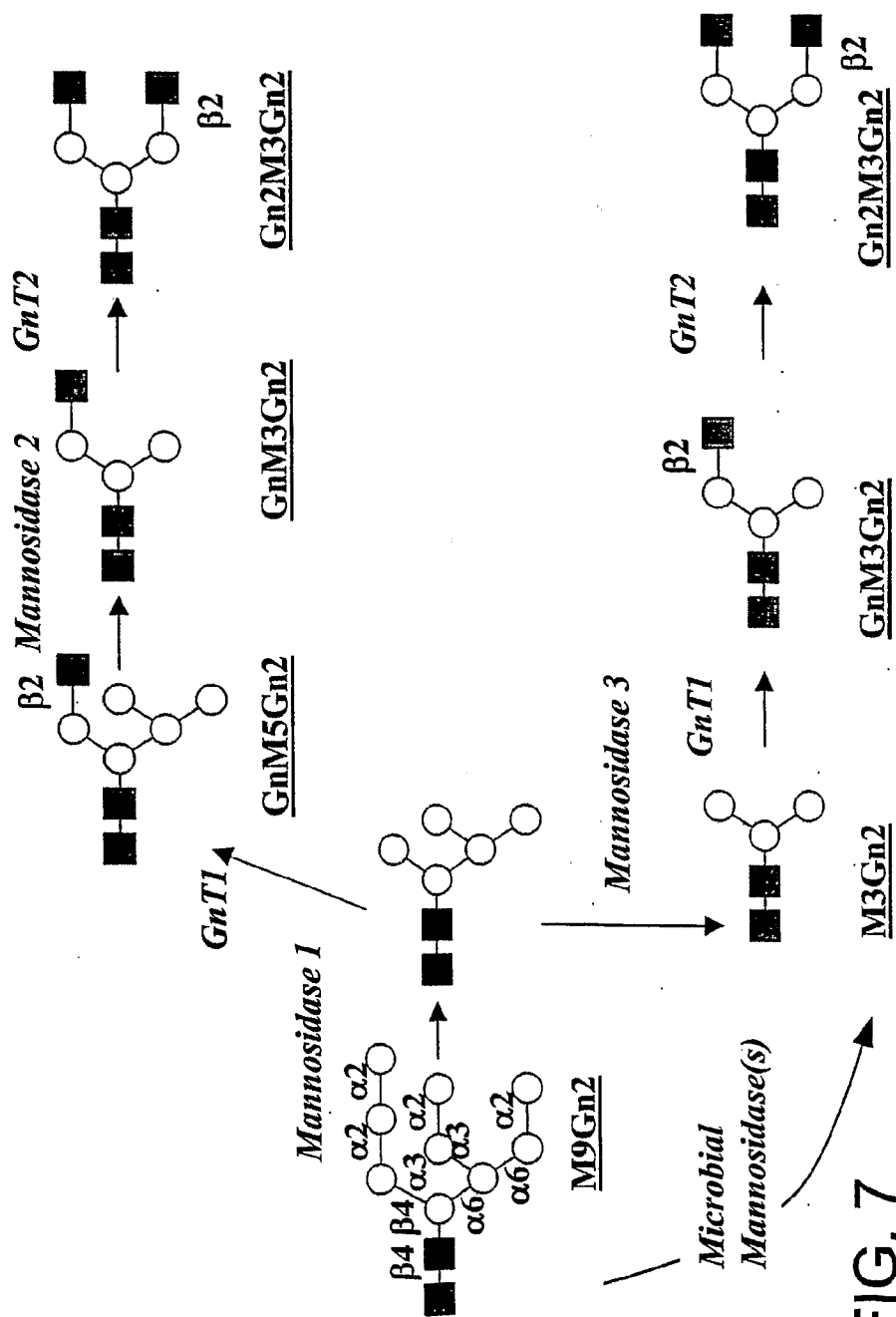


FIG. 7

7/498

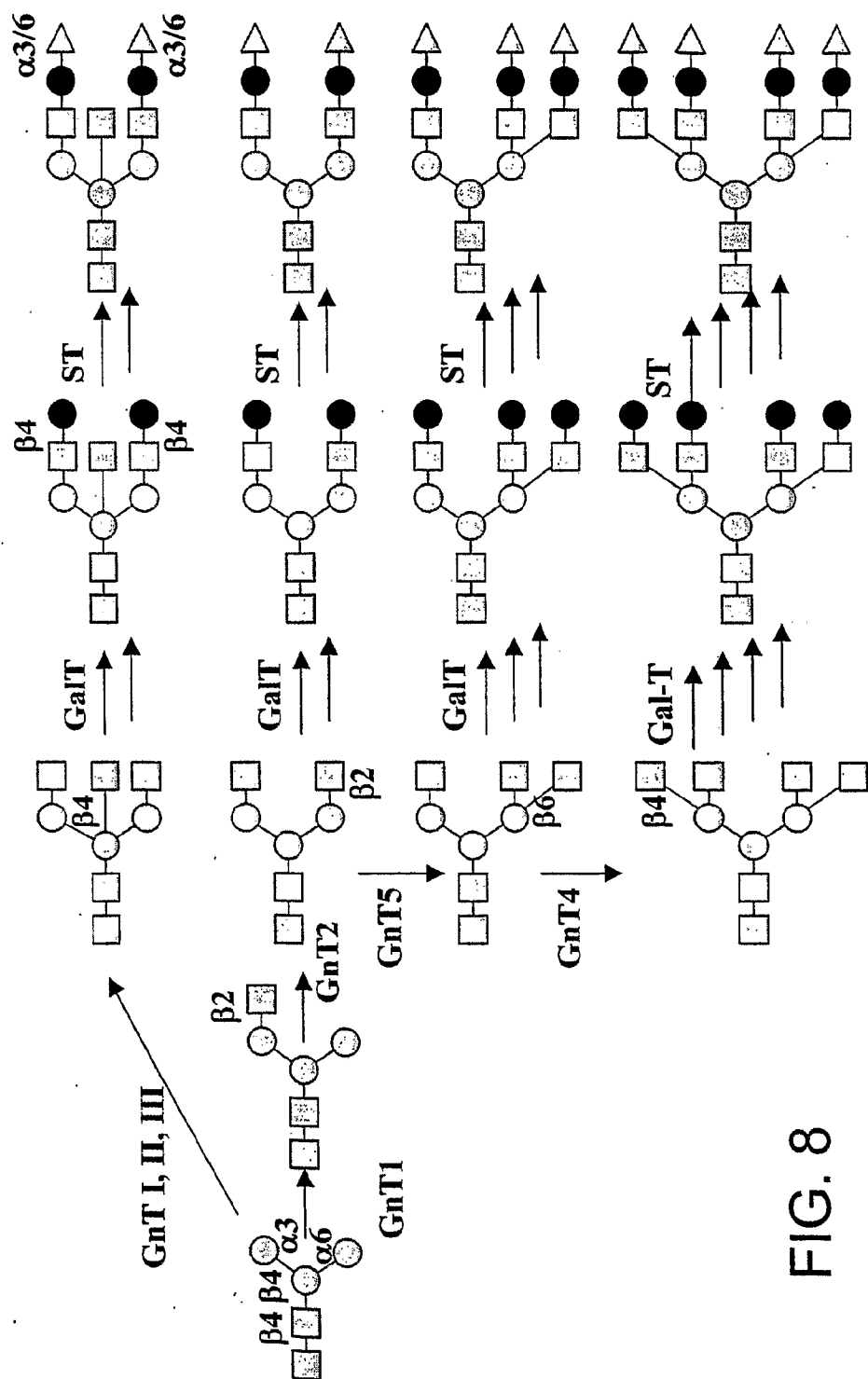


FIG. 8

8/498

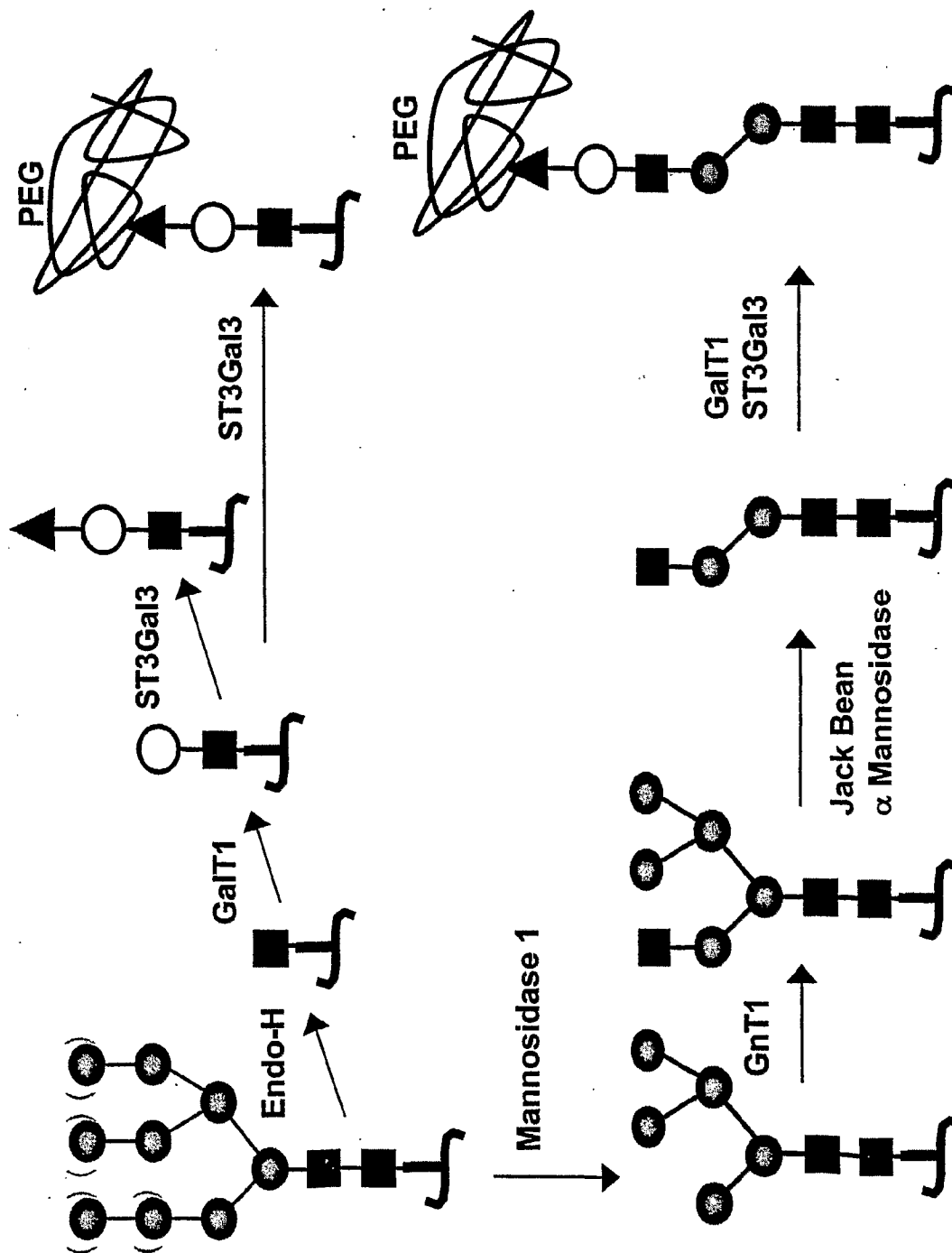


FIG. 9

9/498

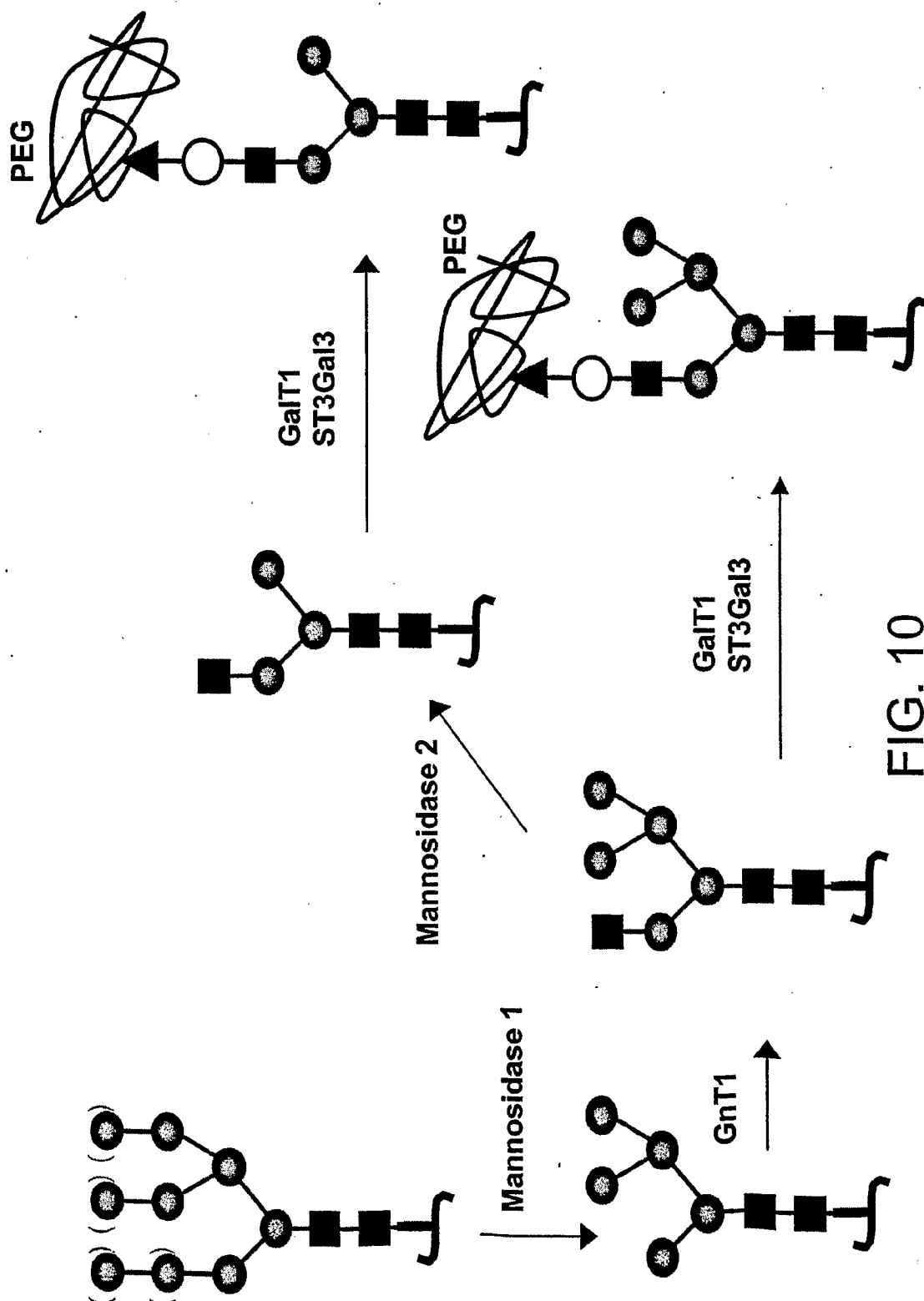


FIG. 10

10/498

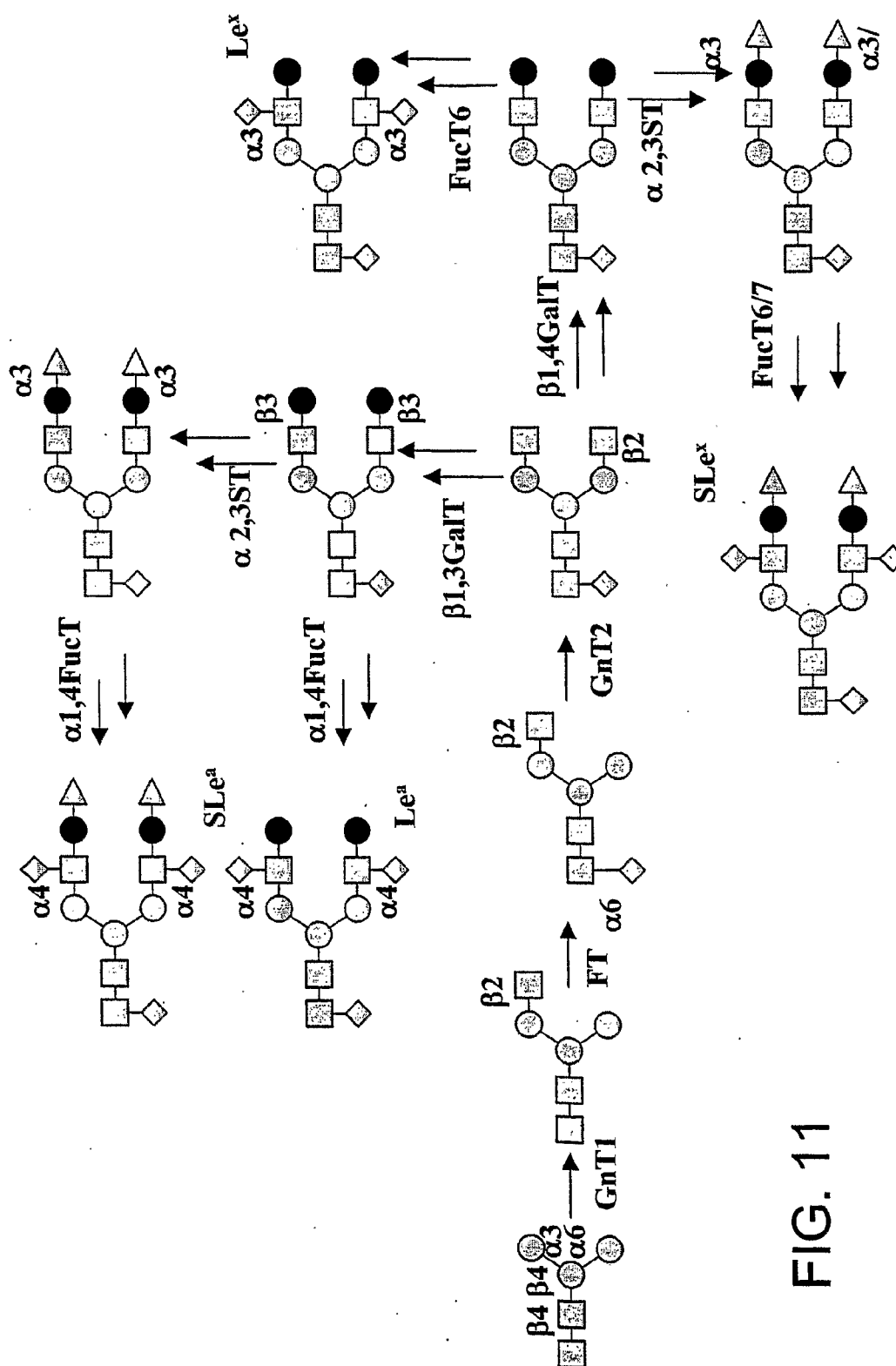


FIG. 11

11/498

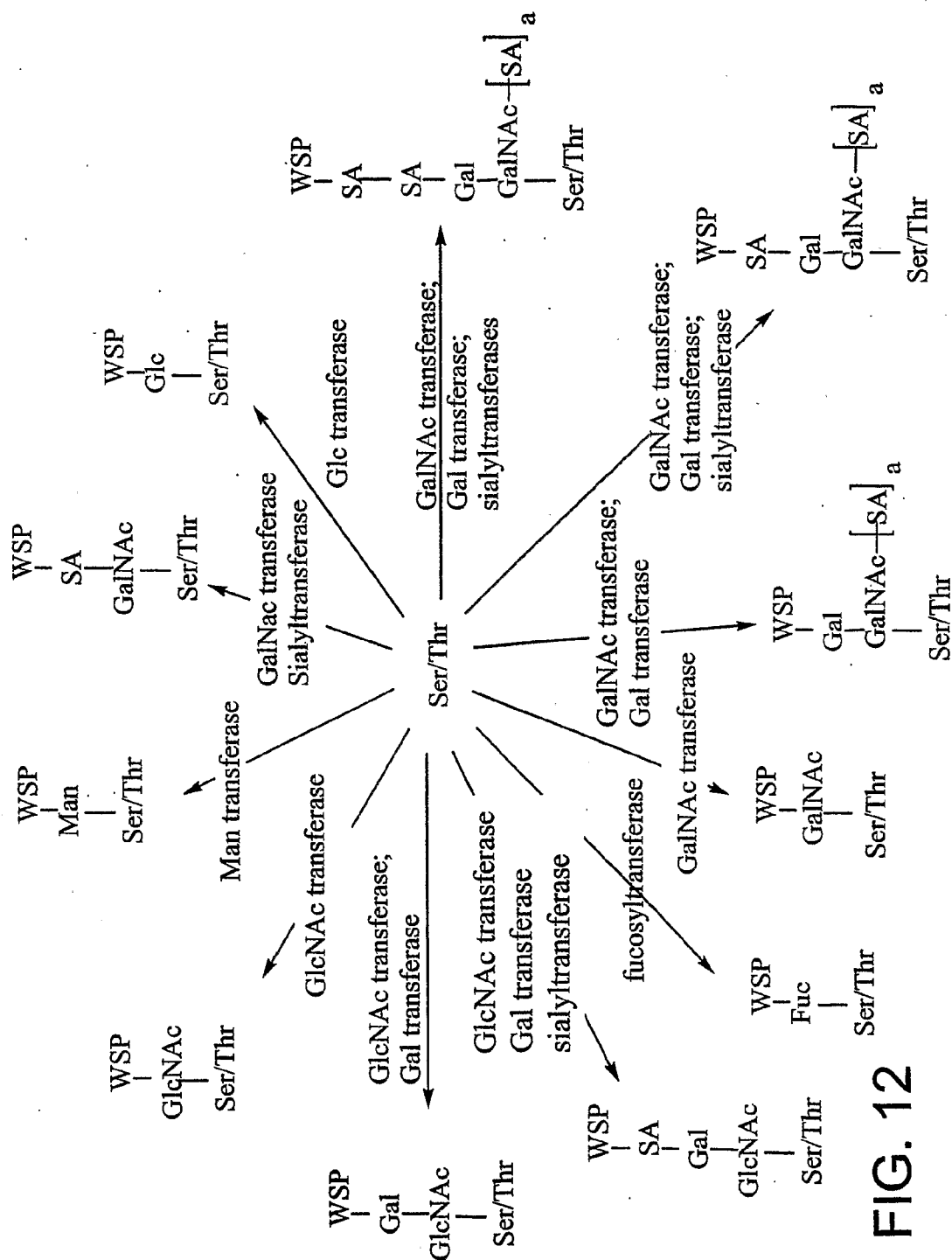


FIG. 12

12/498

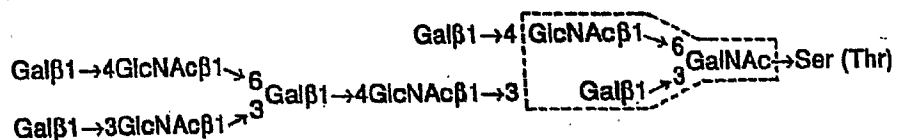
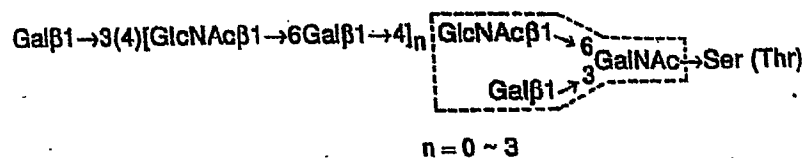
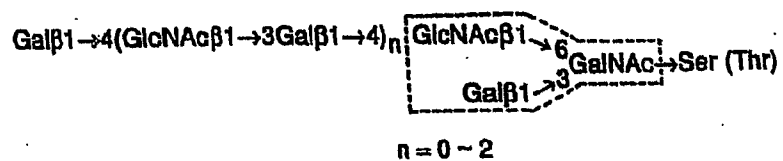
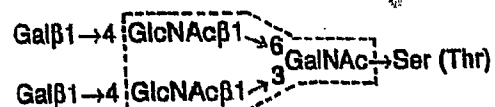
Core 1**Core 2****Core 3****Core 4**

FIG. 13

14/498

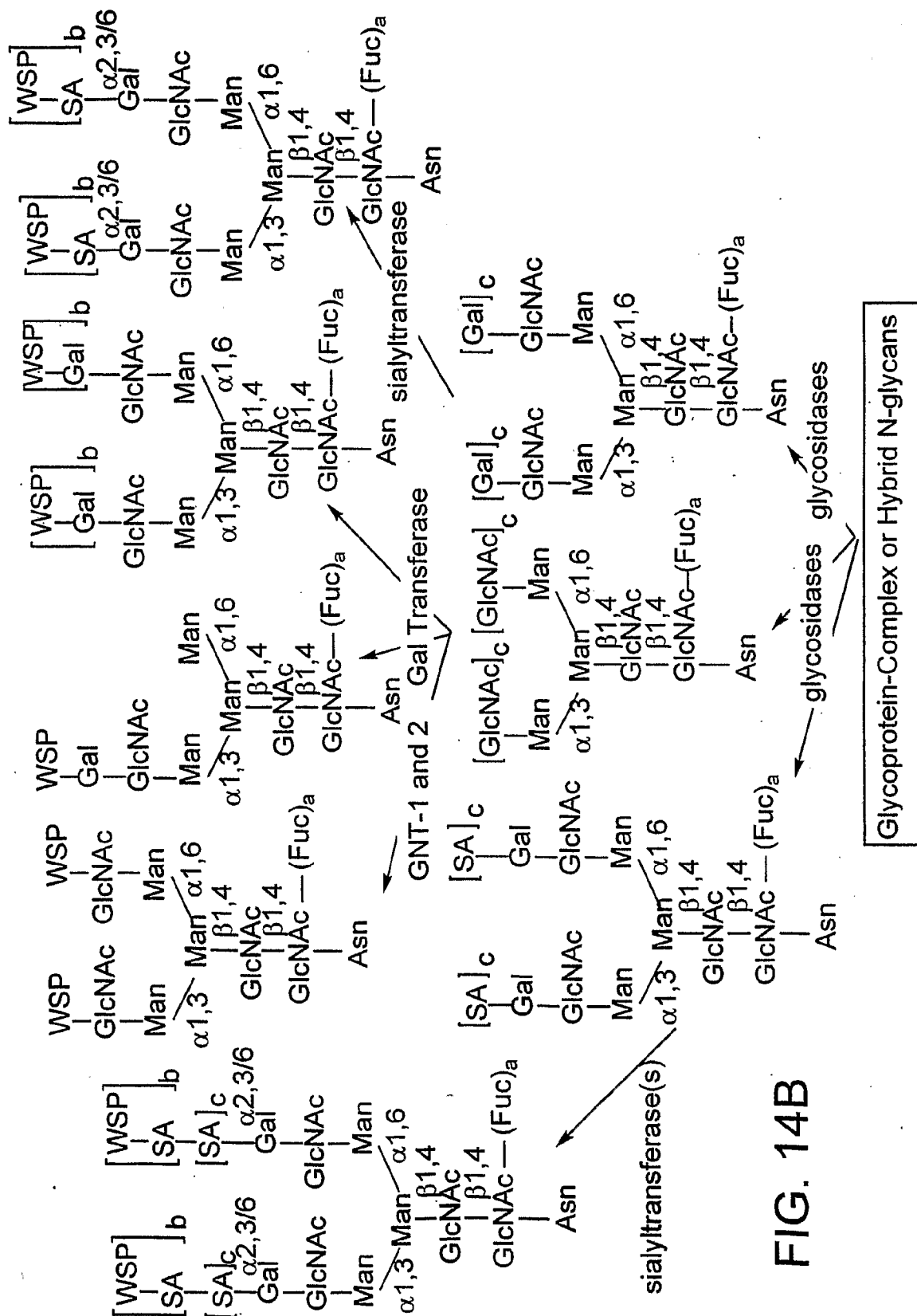


FIG. 14B

15/498

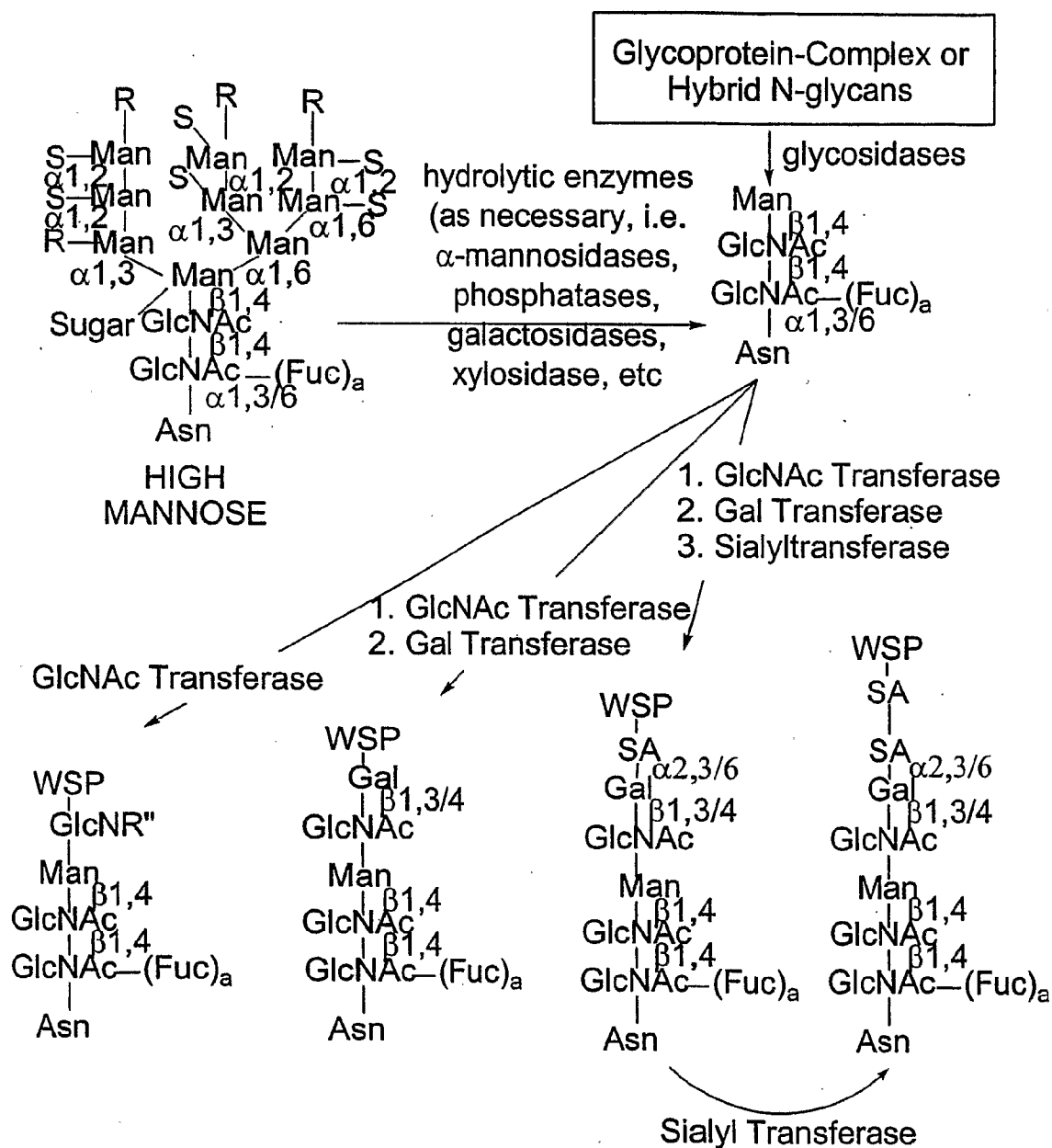


FIG. 15

16/498

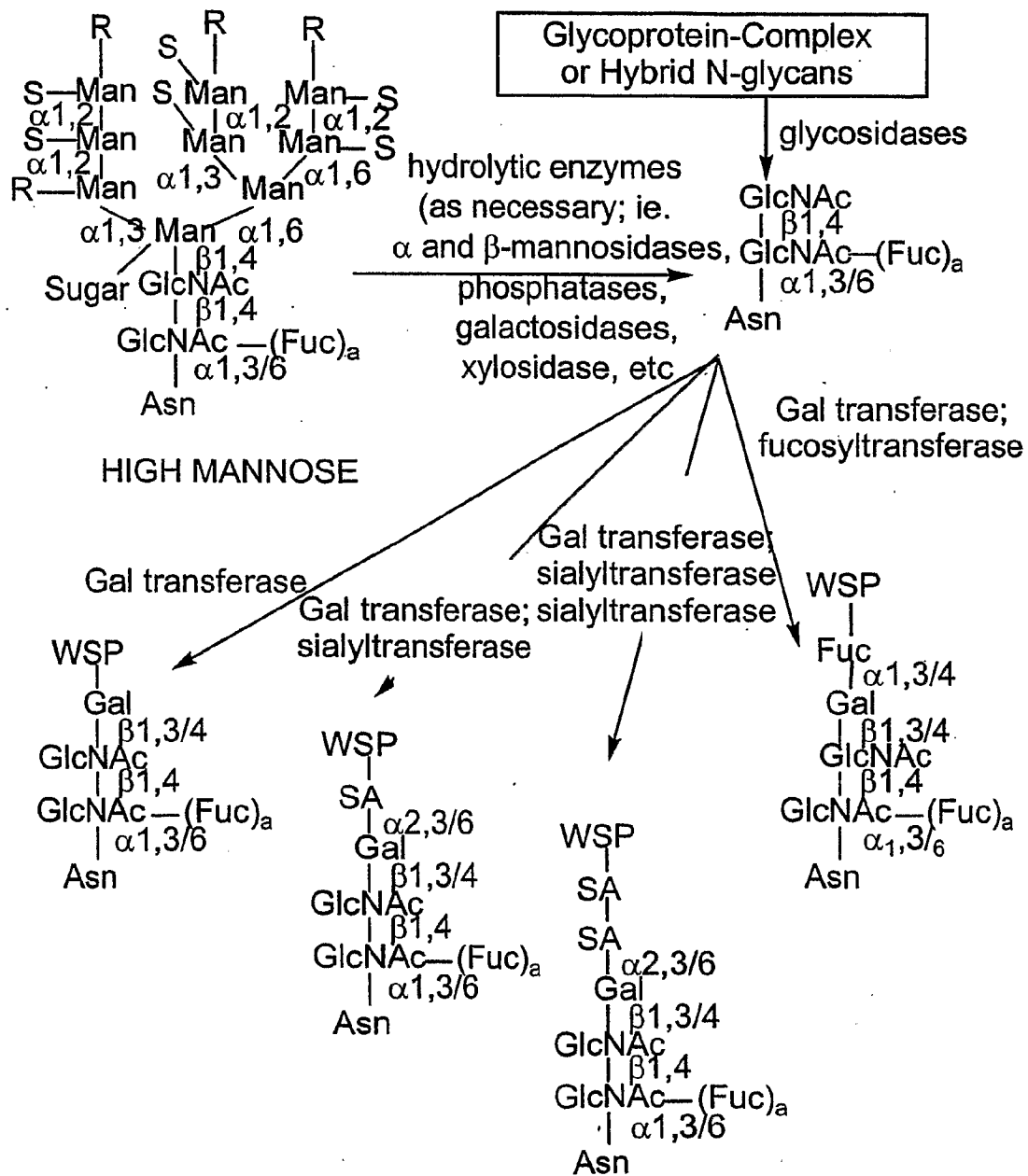


FIG. 16

17/498

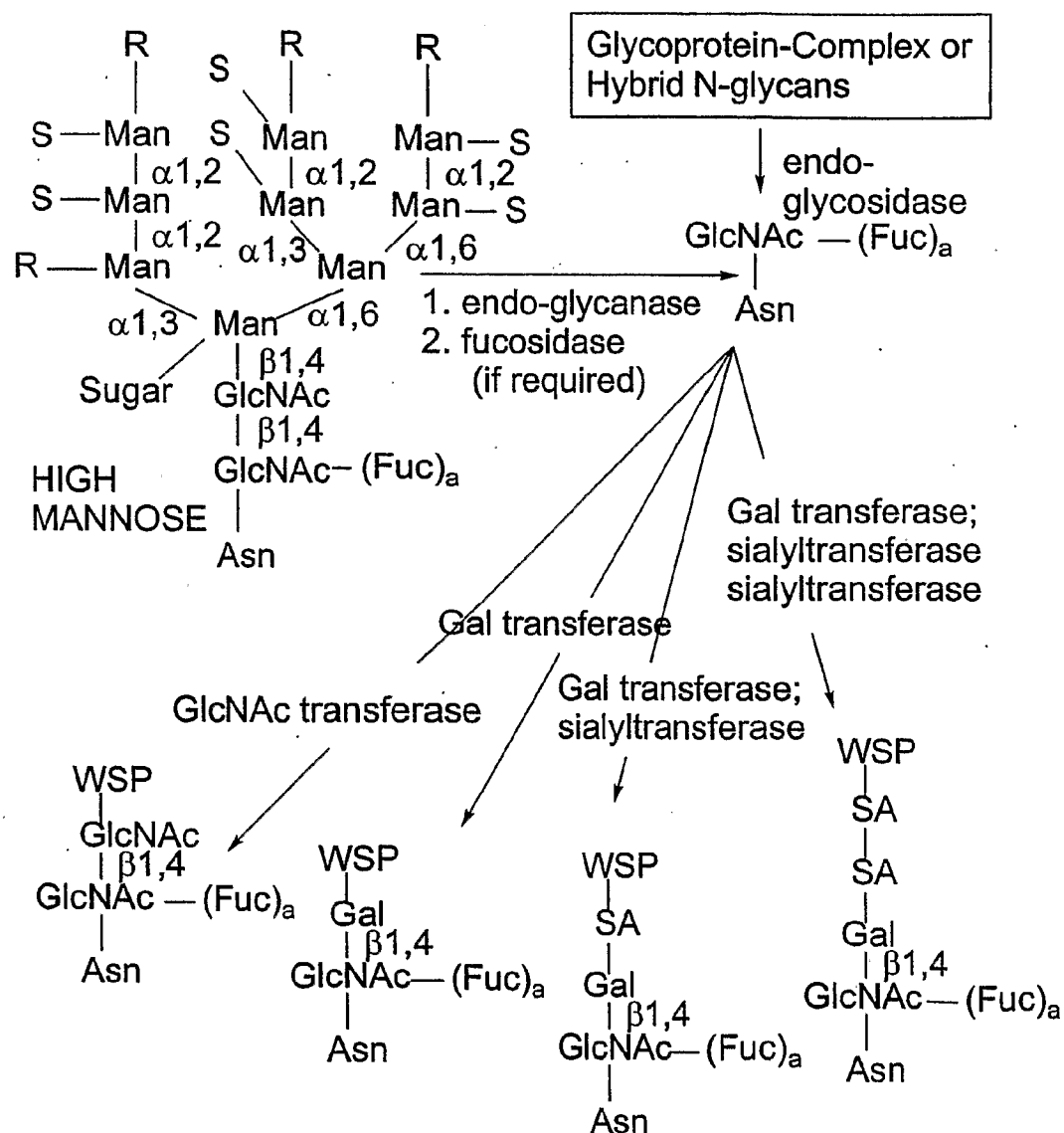
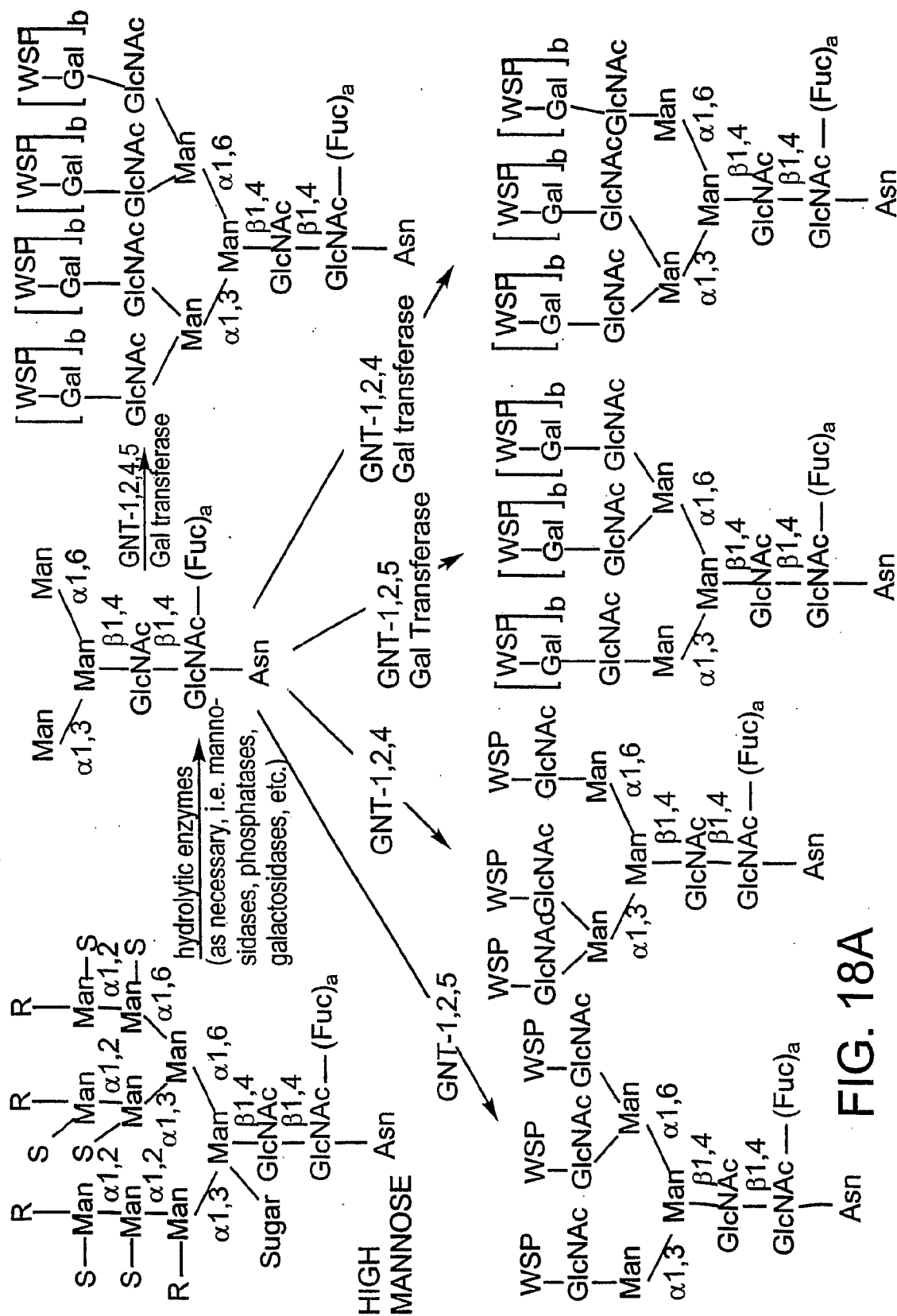


FIG. 17

18/498



19/498

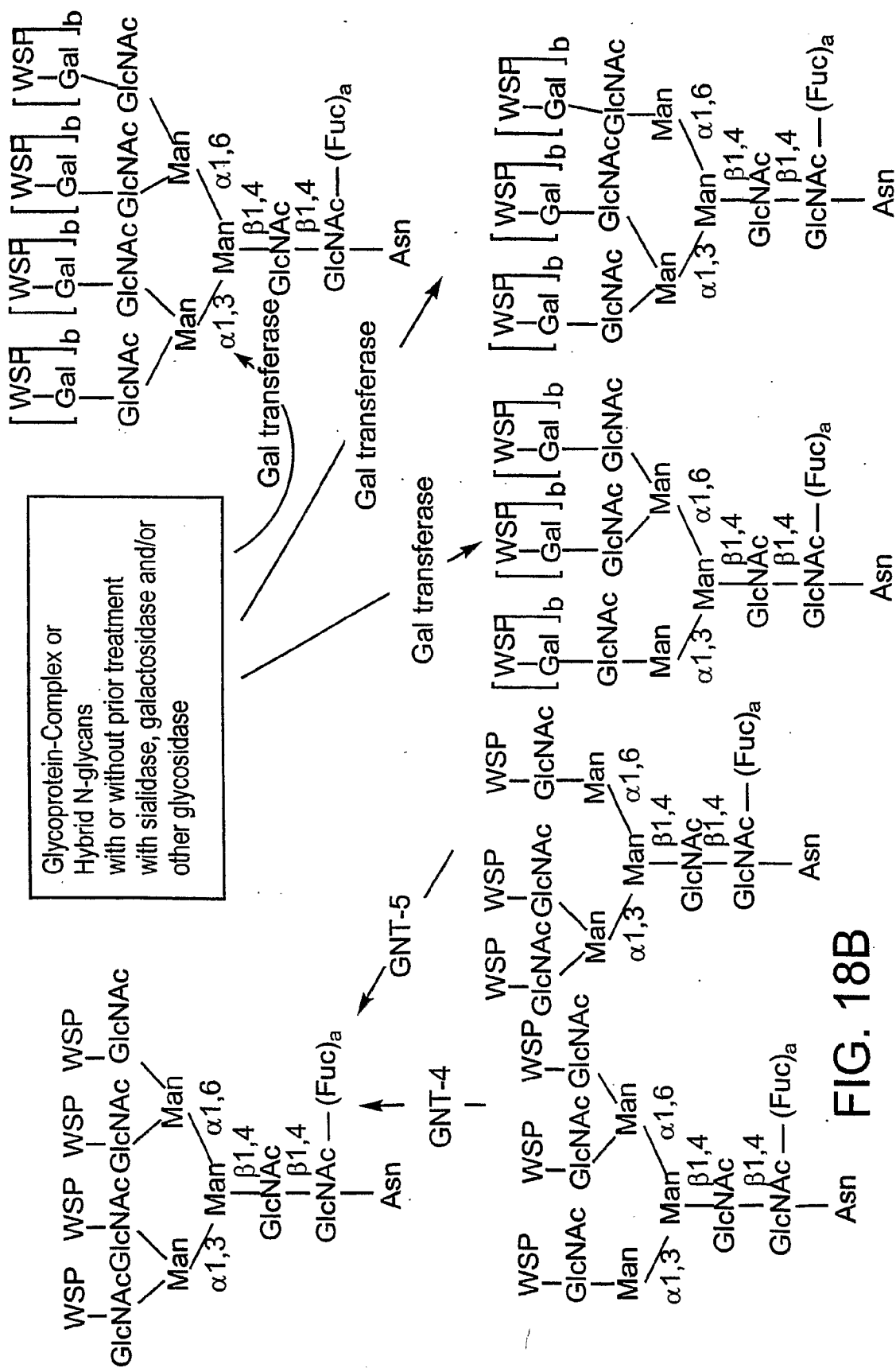
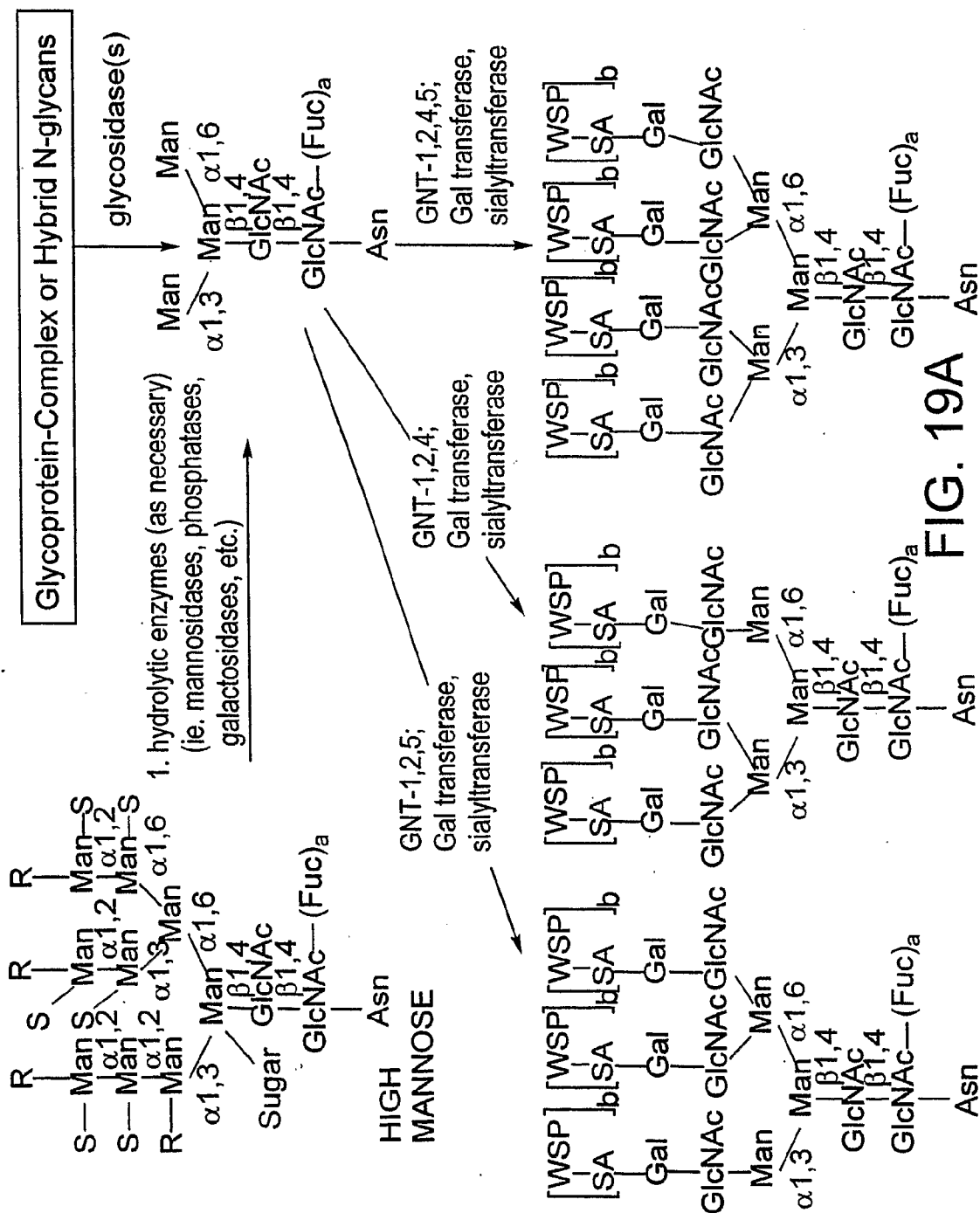


FIG. 18B

20/498



21/498

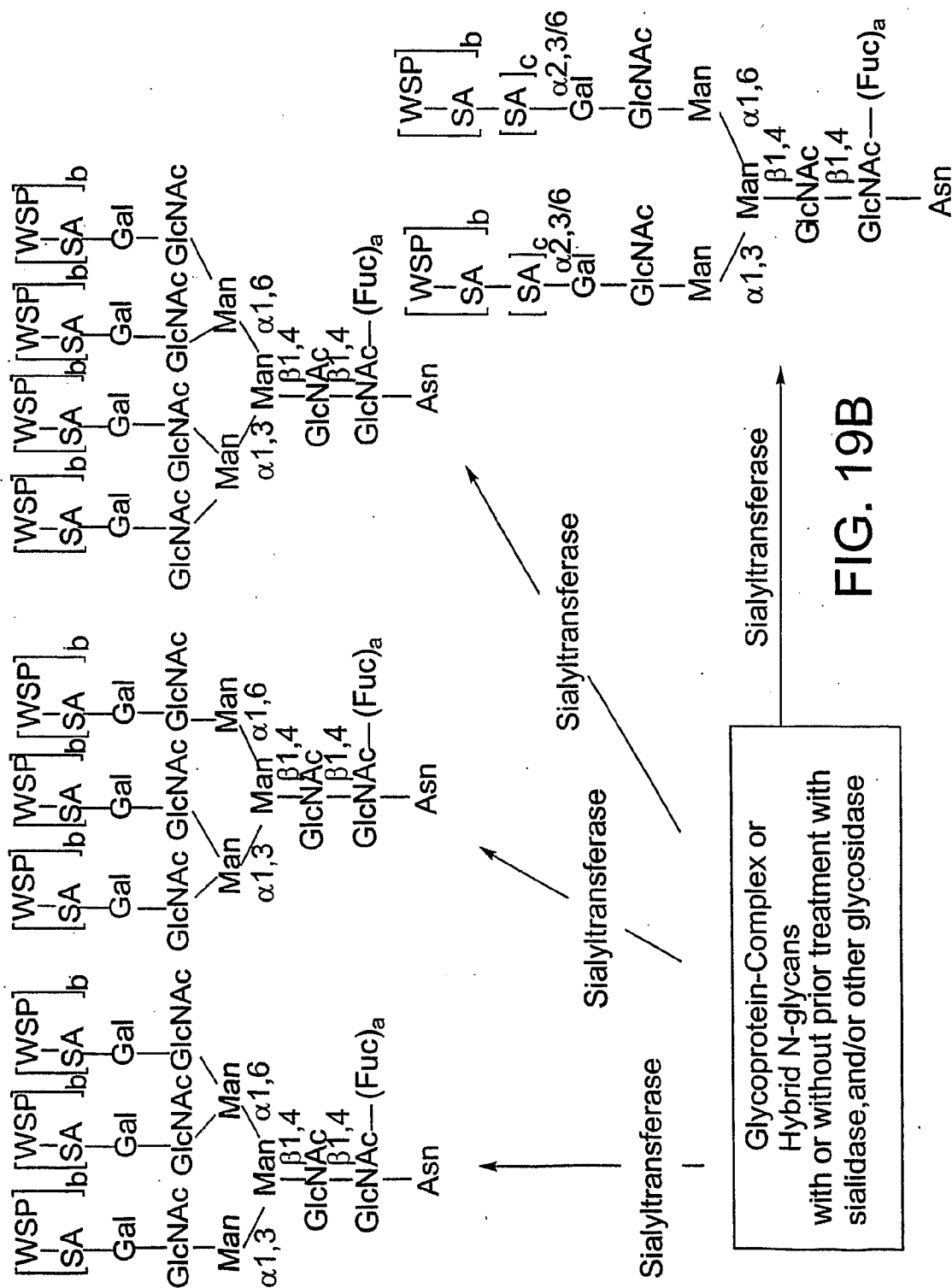


FIG. 19B

22/498

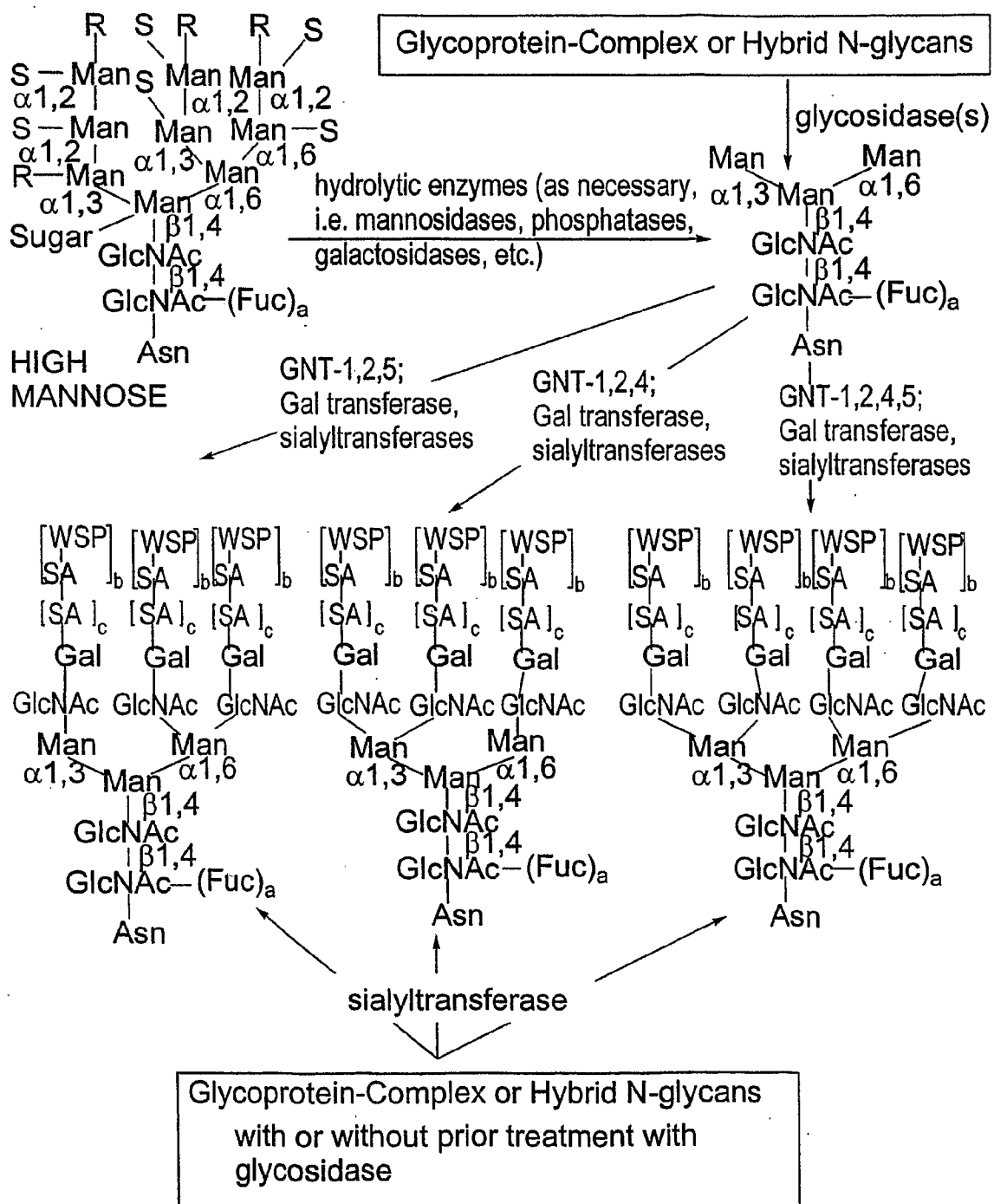


FIG. 20

23/498

O-LINKED OLIGOSACCHARIDES

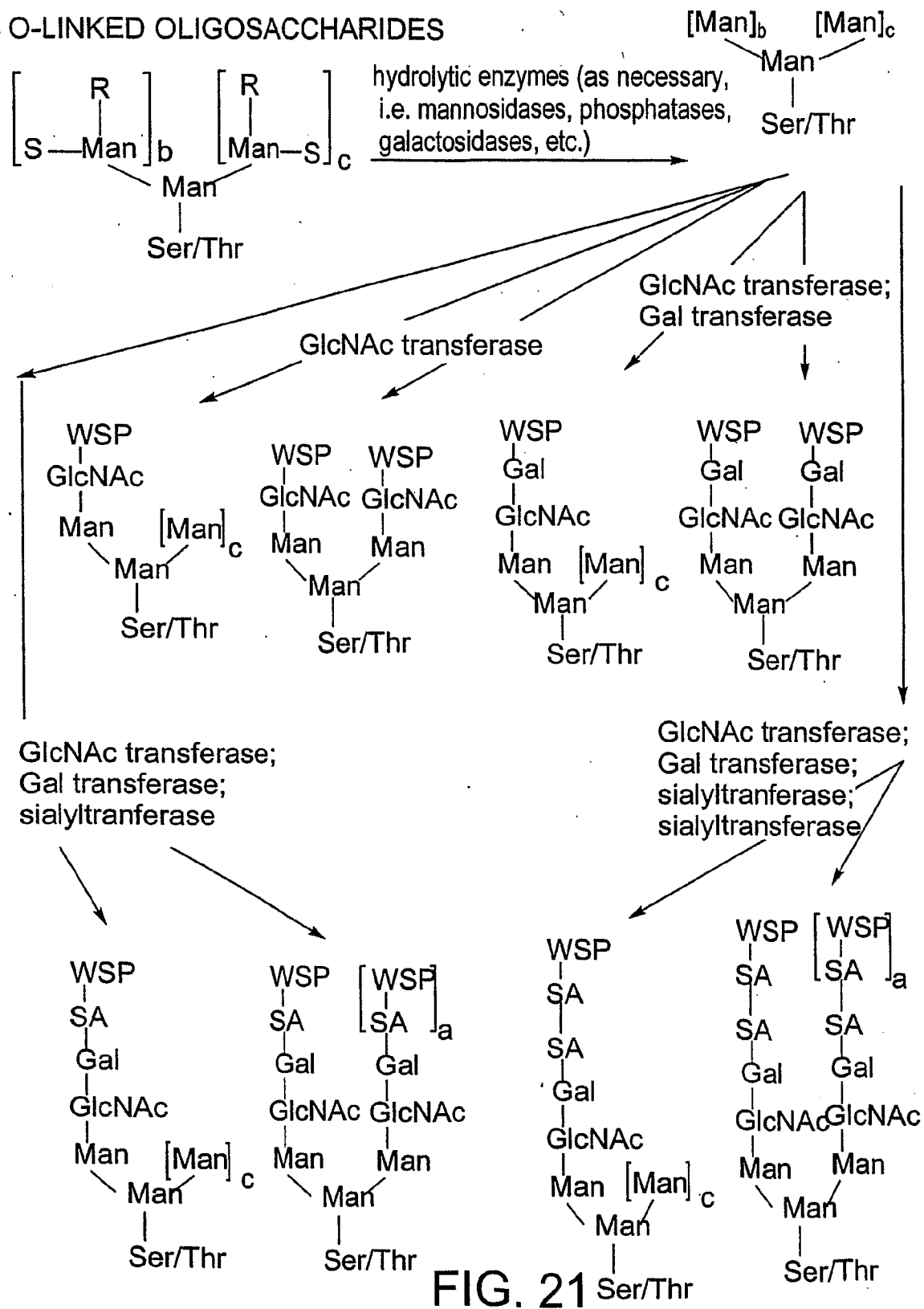
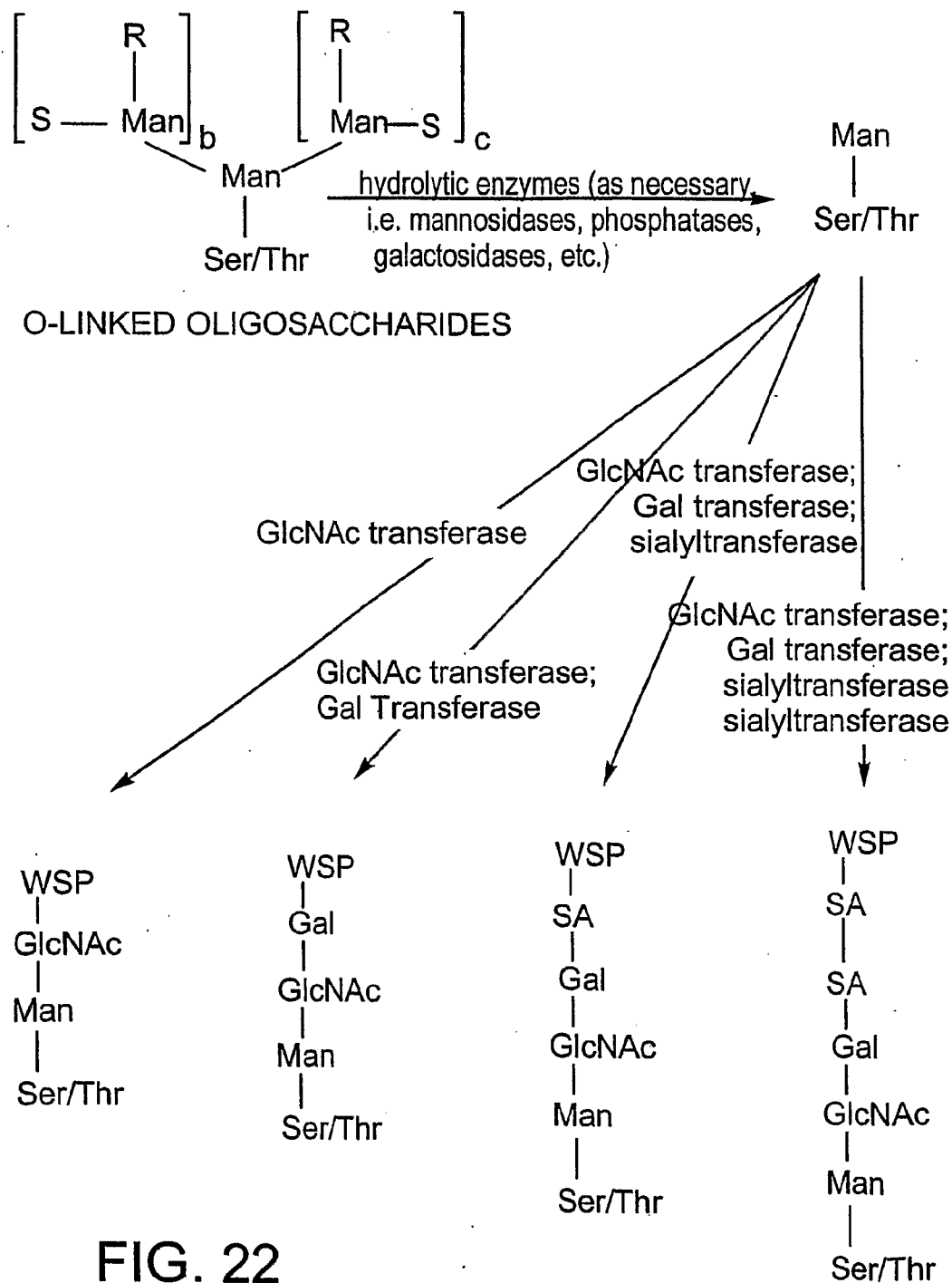
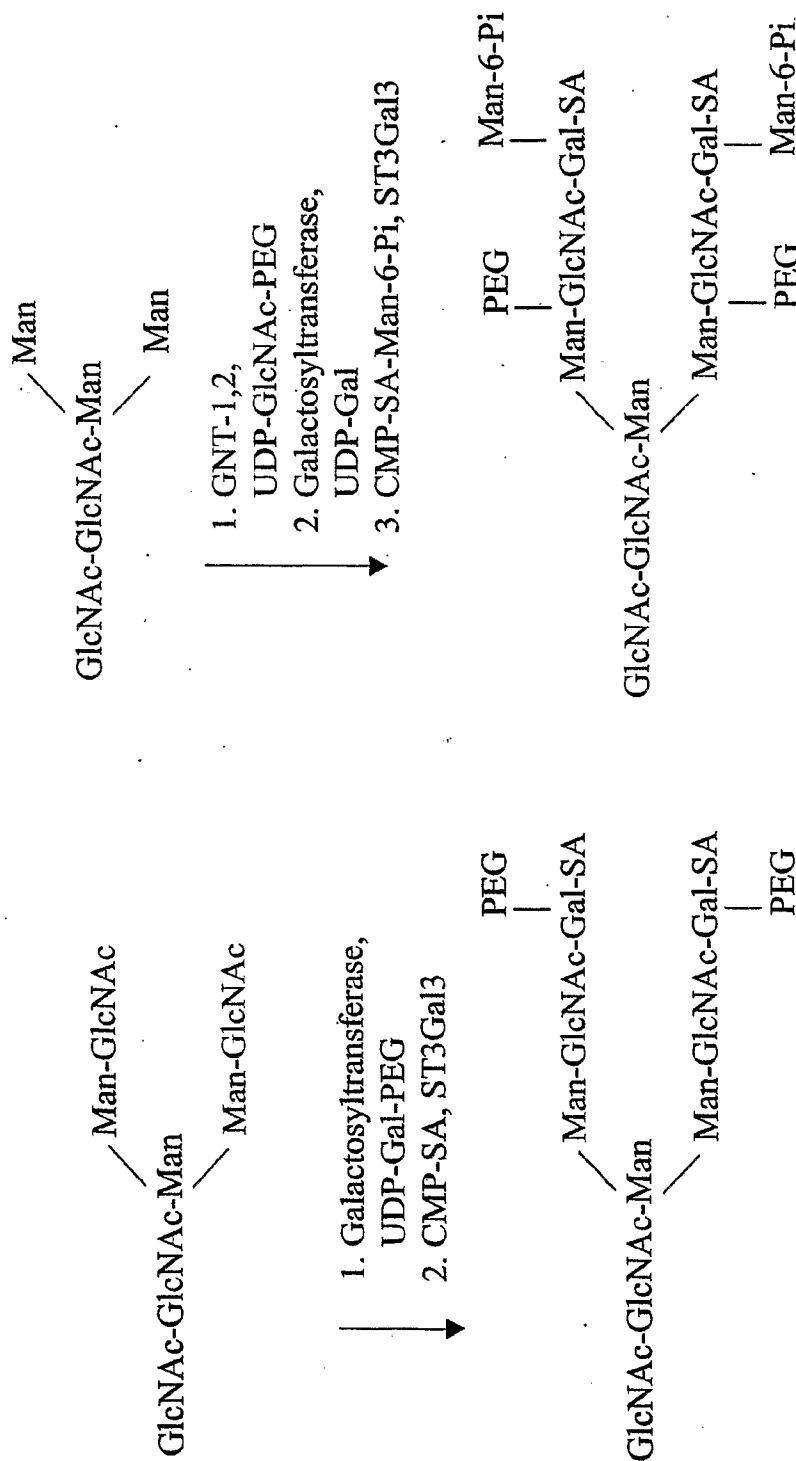


FIG. 21 Ser/Thr

24/498



25/498



26/498

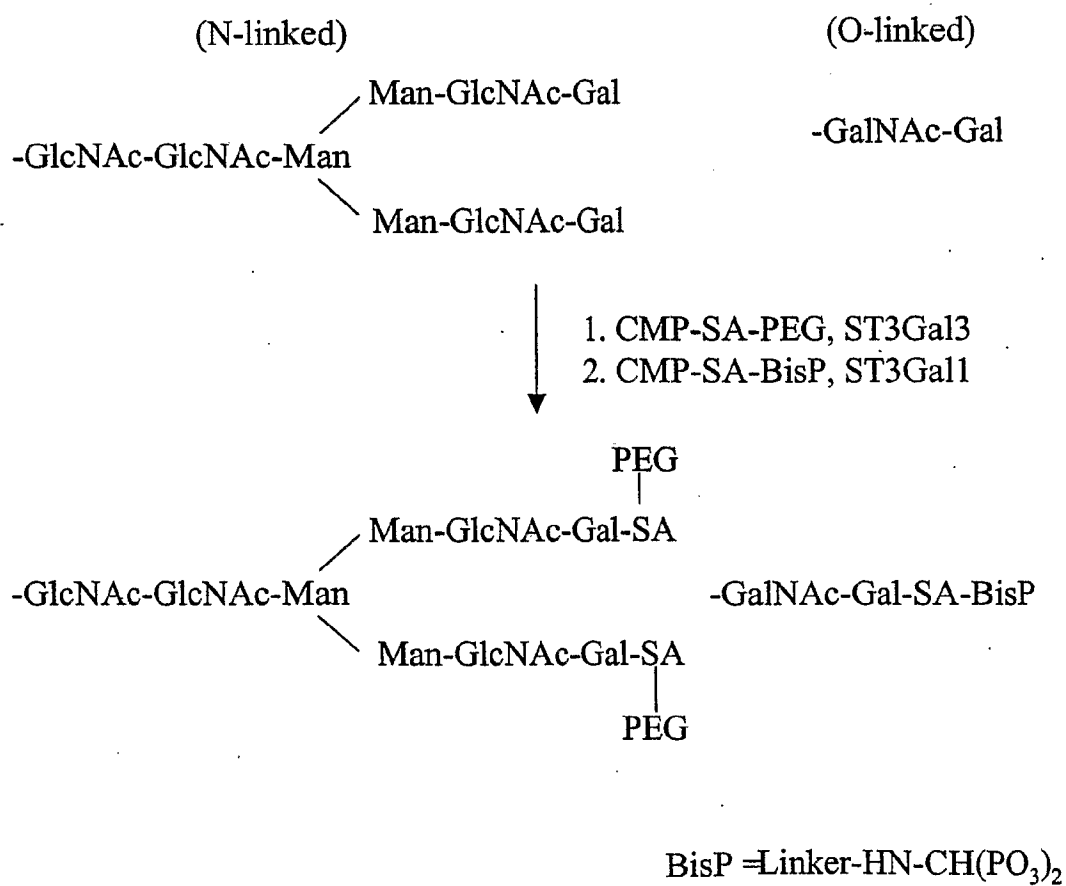


FIG. 23C

27/498

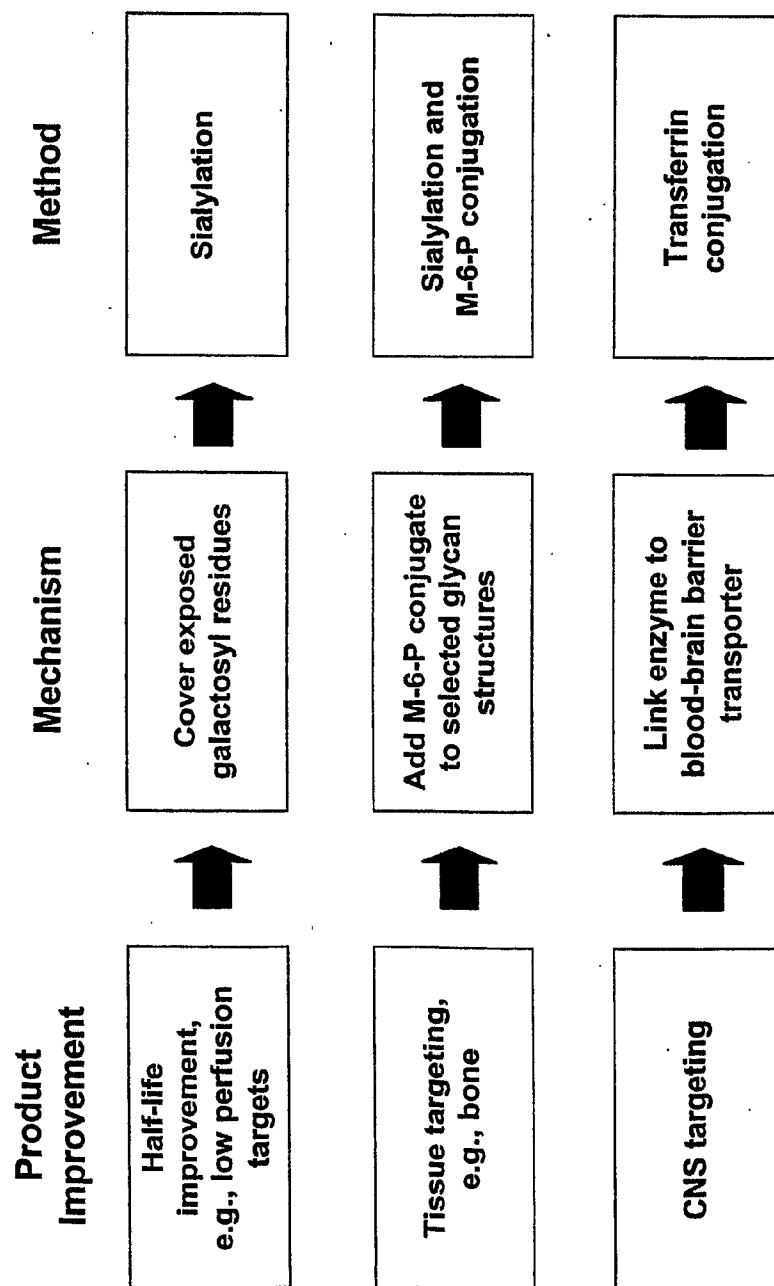


FIG. 24

28/498

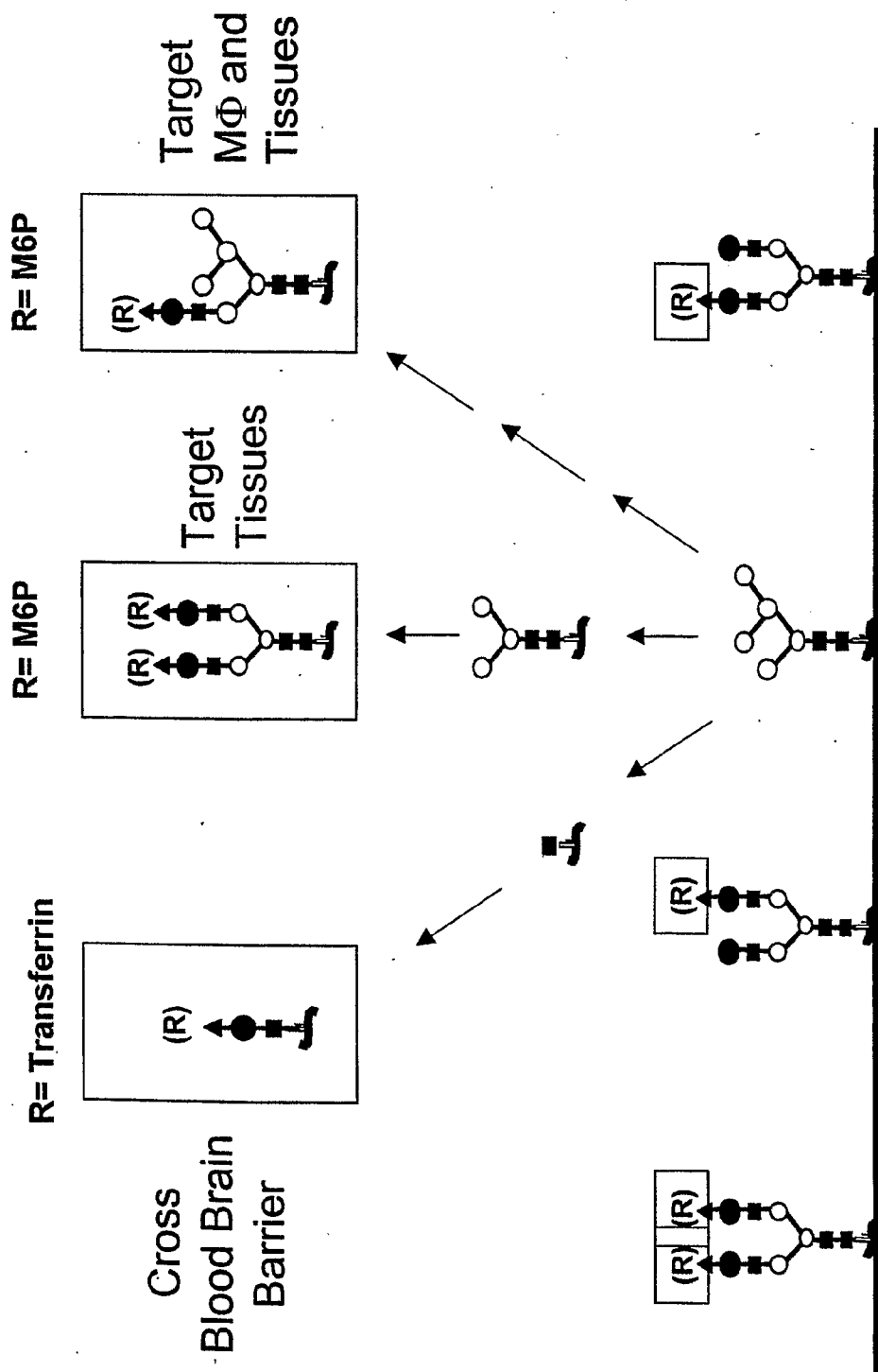


FIG. 25

29/498

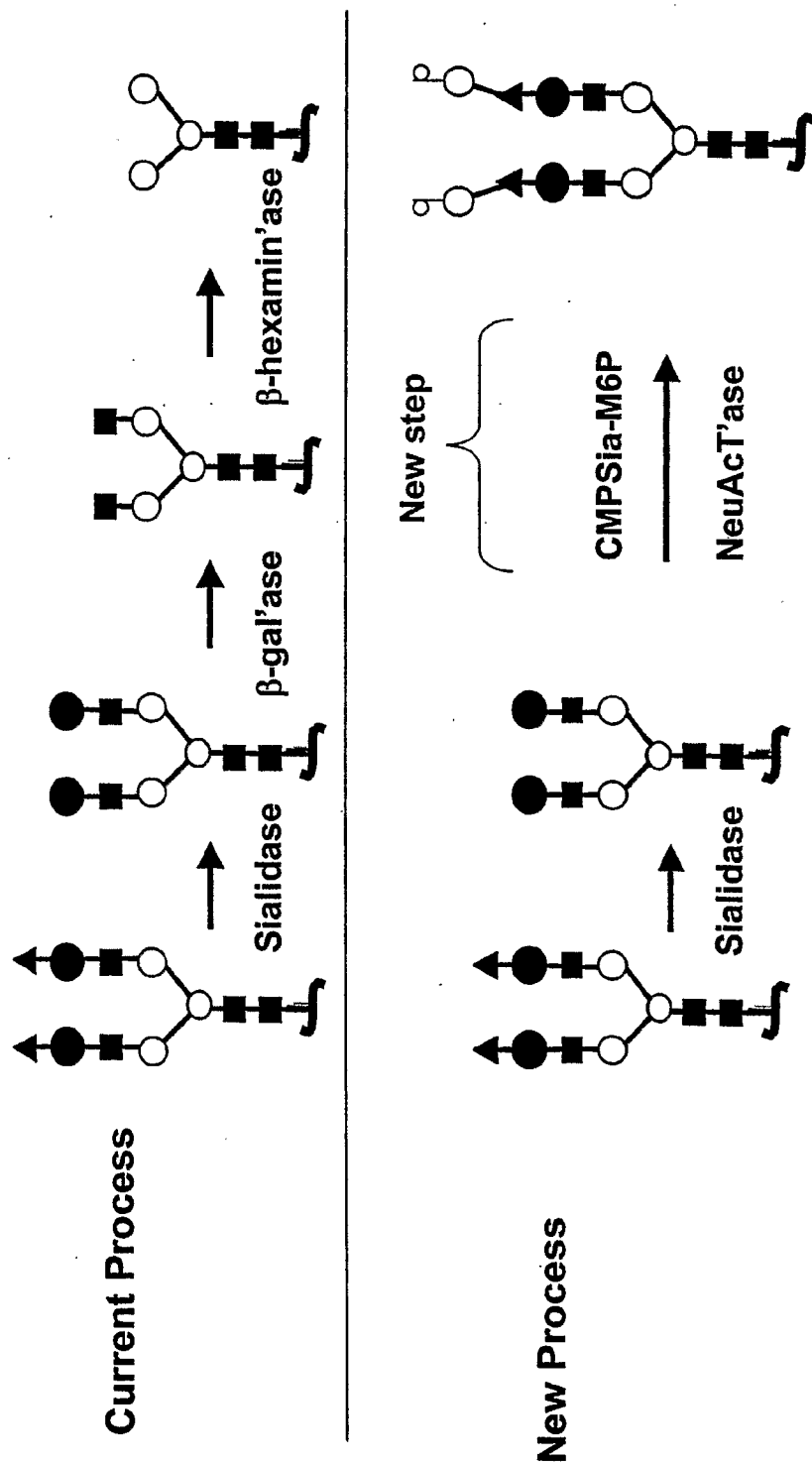


FIG. 26

30/498

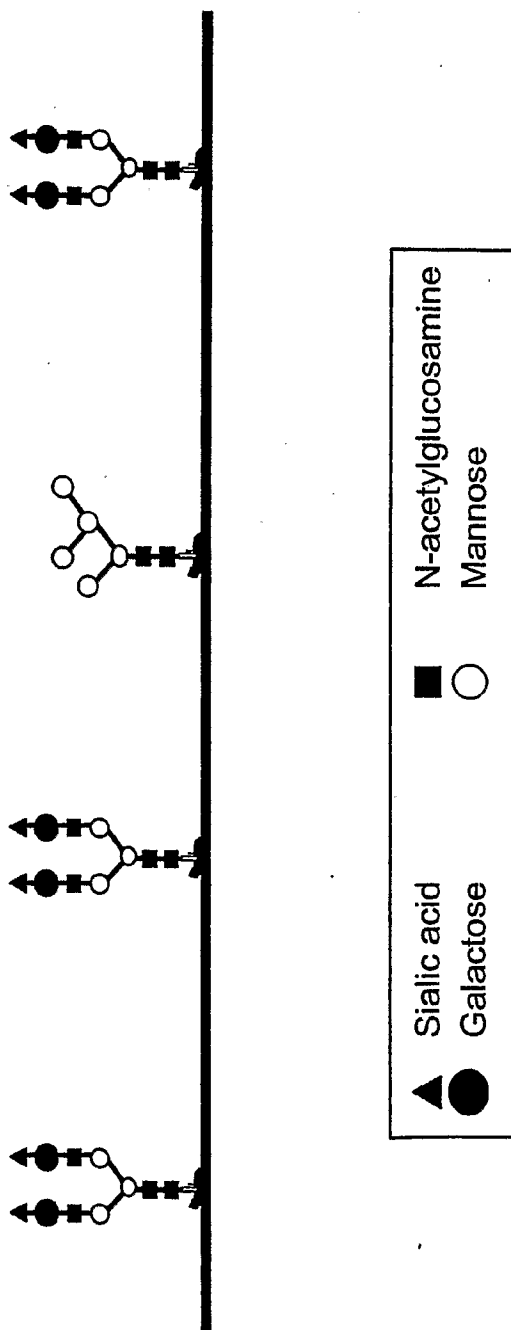


FIG. 27

31/498

| | |
|--|---|
| 12AP1/E5 -- Viventia Biotech | AI-201 -- AutoImmune |
| 1964 -- Aventis | AI-301 -- AutoImmune |
| 20K growth hormone -- AMUR | AIDS vaccine -- ANRS, CIBG, Hesed |
| 28P6/E6 -- Viventia Biotech | Biomed, Hollis-Eden, Rome, United |
| 3-Hydroxyphthaloyl-beta-lactoglobulin -- | Biomedical, American Home Products, |
| 4-IBB ligand gene therapy -- | Maxygen |
| 64-Cu MAb conjugate TETA-1A3 -- | airway receptor ligand -- IC Innovations |
| Mallinckrodt Institute of Radiology | AJvW 2 -- Ajinomoto |
| 64-Cu MAb conjugate TETA-cT84.66 | AK 30 NGF -- Alkermes |
| 64-Cu Trastuzumab TETA conjugate -- | Albuferon -- Human Genome Sciences |
| Genentech | albumin -- Biogen, DSM Anti-Infectives, |
| A 200 -- Amgen | Genzyme Transgenics, PPL Therapeutics, |
| A10255 -- Eli Lilly | TranXenoGen, Welfide Corp. |
| A1PDX -- Hedral Therapeutics | aldesleukin -- Chiron |
| A6 -- Angstrom | alefacept -- Biogen |
| aaAT-III -- Genzyme | Alemtuzumab |
| Abciximab -- Centocor | Allergy therapy -- ALK-Abello/Maxygen, |
| ABI.001 -- Atlantic BioPharmaceuticals | ALK-Abello/RP Scherer |
| ABT-828 -- Abbott | allergy vaccines -- Allergy Therapeutics |
| Accutin | Alnidofibatide -- Aventis Pasteur |
| Actinohivin | Alnorine -- SRC VB VECTOR |
| activin -- Biotech Australia, Human | ALP 242 -- Gruenenthal |
| Therapeutics, Curis | Alpha antitrypsin -- Arriva/Hyland |
| AD 439 -- Tanox | Immuno/ProMetic/Protease Sciences |
| AD 519 -- Tanox | Alpha-1 antitrypsin -- Cutter, Bayer, PPL |
| Adalimumab -- Cambridge Antibody Tech. | Therapeutics, Profile, ZymoGenetics, |
| Adenocarcinoma vaccine -- Biomira -- NIS | Arriva |
| Adenosine deaminase -- Enzond | Alpha-1 protease inhibitor -- Genzyme |
| Adenosine A2B receptor antagonists -- | Transgenics, Welfide Corp. |
| Adenosine Therapeutics | Alpha-galactose fusion protein -- |
| ADP-001 -- Axis Genetics | Immunomedics |
| AF 13948 -- Affymax | Alpha-galactosidase A -- Research |
| Afelimomab -- Knoll | Corporation Technologies, Genzyme |
| AFP-SCAN -- Immunomedics | Alpha-glucosidase -- Genzyme, Novazyme |
| AG 2195 -- Corixa | Alpha-lactalbumin |
| agalsidase alfa -- Transkaryotic Therapies | Alpha-L-iduronidase -- Transkaryotic |
| agalsidase beta -- Genzyme | Therapies, BioMarin |
| AGENT-- Antisoma | alteplase -- Genentech |
| AI 300 -- AutoImmune | alvircept sudotox -- NIH |
| AI-101 -- Teva | ALX-0600, a GLP-2 agonist -- NPS Allelix |
| AI-102 -- Teva | Corp. |

FIG. 28A

32/498

| | |
|--|---|
| ALX1-11 --sNPS Pharmaceuticals | Anti-alphav β 3 integrin MAb -- Applied |
| Alzheimer's disease gene therapy | Molecular Evolution |
| AM-133 -- AMRAD | Anti-angiogenesis monoclonal antibodies -- |
| Amb a 1 immunostim conj. -- Dynavax | KS Biomedix/Schering AG |
| AMD 3100 -- AnorMED -- NIS | Anti-B4 MAb-DC1 conjugate -- ImmunoGen |
| AMD 3465 -- AnorMED -- NIS | Anti-B7 antibody PRIMATIZED -- IDEC |
| AMD 3465 -- AnorMED -- NIS | Anti-B7-1 MAb 16-10A1 |
| AMD Fab -- Genentech | Anti-B7-1 MAb 1G10 |
| Amediplase -- Menarini, Novartis | Anti-B7-2 MAb GL-1 |
| AM-F9 | Anti-B7-2-gelonin immunotoxin -- |
| Amoebiasis vaccine | Antibacterials/antifungals -- |
| Amphiregulin -- Octagene | Diversa/IntraBiotics |
| anakinra -- Amgen | Anti-beta-amyloid monoclonal antibodies -- |
| analgesic -- Nobex | Cambridge Antibody Tech., Wyeth-Ayerst |
| ancestim -- Amgen | Anti-BLyS antibodies -- Cambridge |
| AnergiX.RA -- Corixa, Organon | Antibody Tech. /Human Genome Sciences |
| Angiocidin -- InKine | Antibody-drug conjugates -- Seattle |
| angiogenesis inhibitors -- ILEX | Genetics/Eos |
| AngioMab -- Antisoma | Anti-C5 MAb BB5-1 -- Alexion |
| Angiopoietins -- Regeneron/Procter & | Anti-C5 MAb N19-8 -- Alexion |
| Gamble | Anti-C8 MAb |
| angiostatin -- EntreMed | anticancer cytokines -- BioPulse |
| Angiostatin/endostatin gene therapy -- | anticancer matrix -- Telios Integra |
| Genetix Pharmaceuticals | Anticancer monoclonal antibodies -- ARIUS, |
| angiotensin-II, topical -- Maret | Immunex |
| Anthrax -- EluSys Therapeutics/US Army | anticancer peptides -- Maxygen, Micrologix |
| Medical Research Institute | Anticancer prodrug Tech. -- Alexion |
| Anthrax vaccine | Antibody Technologies |
| Anti platelet-derived growth factor D human | anticancer Troy-Bodies -- Affite -- Affitech |
| monoclonal antibodies -- CuraGen | anticancer vaccine -- NIH |
| Anti-17-1A MAb 3622W94 -- | anticancers -- Epimmune |
| GlaxoSmithKline | Anti-CCR5/CXCR4 sheep MAb -- KS |
| Anti-2C4 MAb -- Genentech | Biomedix Holdings |
| anti-4-1BB monoclonal antibodies -- Bristol- | Anti-CD11a MAb KBA -- |
| Myers Squibb | Anti-CD11a MAb M17 |
| Anti-Adhesion Platform Tech. -- Cytovax | Anti-CD11a MAb TA-3 -- |
| Anti-adipocyte MAb -- Cambridge Antibody | Anti-CD11a MAb WT.1 -- |
| Tech./ObeSys | Anti-CD11b MAb -- Pharmacia |
| antiallergics -- Maxygen | Anti-CD11b MAb LM2 |
| antiallergy vaccine -- Acambis | Anti-CD154 MAb -- Biogen |
| Anti-alpha-4-integrin MAb | Anti-CD16-anti-CD30 MAb -- Biotest |

FIG. 28B

33/498

| | |
|---|---|
| Anti-CD18 MAb -- Pharmacia | Anti-CD4 MAb -- Centocor, IDEC |
| Anti-CD19 MAb B43 -- | Pharmaceuticals, Xenova Group |
| Anti-CD19 MAb -liposomal sodium butyrate conjugate -- | Anti-CD4 MAb 16H5 |
| Anti-CD147 | Anti-CD4 MAb 4162W94 -- GlaxoSmithKline |
| Anti-CD19 MAb-saporin conjugate -- | Anti-CD4 MAb B-F5 -- Diaclone |
| Anti-CD19-dsFv-PE38-immunotoxin -- | Anti-CD4 MAb GK1-5 |
| Anti-CD2 MAb 12-15 -- | Anti-CD4 MAb KT6 |
| Anti-CD2 MAb B-E2 -- Diaclone | Anti-CD4 MAb OX38 |
| Anti-CD2 MAb OX34 -- | Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb |
| Anti-CD2 MAb OX54 -- | Anti-CD4 MAb RIB 5-2 |
| Anti-CD2 MAb OX55 -- | Anti-CD4 MAb W3/25 |
| Anti-CD2 MAb RM2-1 | Anti-CD4 MAb YTA 3.1.2 |
| Anti-CD2 MAb RM2-2 | Anti-CD4 MAb YTS 177-9 |
| Anti-CD2 MAb RM2-4 | Anti-CD40 ligand MAb 5c8 -- Biogen |
| Anti-CD20 MAb BCA B20 | Anti-CD40 MAb |
| Anti-CD20-anti-Fc alpha RI bispecific MAb -- Medarex, Tenovus | Anti-CD40 MAb 5D12 -- Tanox |
| Anti-CD22 MAb-saporin-6 complex -- | Anti-CD44 MAb A3D8 |
| Anti-CD3 immunotoxin -- | Anti-CD44 MAb GKWA3 |
| Anti-CD3 MAb 145-2C11 -- Pharming | Anti-CD44 MAb IM7 |
| Anti-CD3 MAb CD4IgG conjugate -- Genentech | Anti-CD44 MAb KM81 |
| Anti-CD3 MAb humanised -- Protein Design, RW Johnson | Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University |
| Anti-CD3 MAb WT32 | Anti-CD45 MAb BC8-I-131 |
| Anti-CD3 MAb-ricin-chain-A conjugate -- | Anti-CD45RB MAb |
| Anti-CD3 MAb-xanthine-oxidase conjugate -- | Anti-CD48 MAb HuLy-m3 |
| Anti-CD30 MAb BerH2 -- Medac | Anti-CD48 MAb WM-63 |
| Anti-CD30 MAb-saporin conjugate | Anti-CD5 MAb -- Becton Dickinson |
| Anti-CD30-scFv-ETA'-immunotoxin | Anti-CD5 MAb OX19 |
| Anti-CD38 MAb AT13/5 | Anti-CD6 MAb |
| Anti-CD38 MAb-saporin conjugate | Anti-CD7 MAb-PAP conjugate |
| Anti-CD3-anti-CD19 bispecific MAb | Anti-CD7 MAb-ricin-chain-A conjugate |
| Anti-CD3-anti-EGFR MAb | Anti-CD8 MAb -- Amerimmune, Cytodyn, Becton Dickinson |
| Anti-CD3-anti-interleukin-2-receptor MAb | Anti-CD8 MAb 2-43 |
| Anti-CD3-anti-MOV18 MAb -- Centocor | Anti-CD8 MAb OX8 |
| Anti-CD3-anti-SCLC bispecific MAb | Anti-CD80 MAb P16C10 -- IDEC |
| Anti-CD4 idiotype vaccine | Anti-CD80 MAb P7C10 -- ID Vaccine |
| | Anti-CD8-idarubicin conjugate |
| | Anti-CEA MAb CE-25 |
| | Anti-CEA MAb MN 14 -- Immunomedics |

FIG. 28C

34/498

| | |
|--|--|
| Anti-CEA MAb MN14-PE40 conjugate -- Immunomedics | Anti-heparanase human monoclonal antibodies -- Oxford Glycosciences/Medarex |
| Anti-CEA MAb T84.66-interleukin-2 conjugate | Anti-hepatitis C virus human monoclonal antibodies -- XTL Biopharmaceuticals |
| Anti-CEA sheep MAb -- KS Biomedix Holdings | Anti-HER-2 antibody gene therapy |
| Anti-cell surface monoclonal antibodies -- Cambridge Antibody Tech. /Pharmacia | Anti-herpes antibody -- Epicyte |
| Anti-c-erbB2-anti-CD3 bifunctional MAb -- Otsuka | Anti-HIV antibody -- Epicyte |
| Anti-CMV MAb -- Scotgen | anti-HIV catalytic antibody -- Hesed Biomed |
| Anti-complement | anti-HIV fusion protein -- Idun |
| Anti-CTLA-4 MAb | anti-HIV proteins -- Cangene |
| Anti-EGFR catalytic antibody -- Hesed Biomed | Anti-HM1-24 MAb -- Chugai |
| anti-EGFR immunotoxin -- IVAX | Anti-hR3 MAb |
| Anti-EGFR MAb -- Abgenix | Anti-Human-Carcinoma-Antigen MAb -- Epicyte |
| Anti-EGFR MAb 528 | Anti-ICAM-1 MAb -- Boehringer Ingelheim |
| Anti-EGFR MAb KSB 107 -- KS Biomedix | Anti-ICAM-1 MAb 1A-29 -- Pharmacia |
| Anti-EGFR MAb-DM1 conjugate -- ImmunoGen | Anti-ICAM-1 MAb HA58 |
| Anti-EGFR MAb-LA1 -- | Anti-ICAM-1 MAb YN1/1.7.4 |
| Anti-EGFR sheep MAb -- KS Biomedix | Anti-ICAM-3 MAb ICM3 -- ICOS |
| Anti-FAP MAb F19-I-131 | Anti-idiotype breast cancer vaccine 11D10 |
| Anti-Fas IgM MAb CH11 | Anti-idiotype breast cancer vaccine ACA14C5 -- |
| Anti-Fas MAb Jo2 | Anti-idiotype cancer vaccine -- ImClone Systems/Merck KGaA ImClone, Viventia Biotech |
| Anti-Fas MAb RK-8 | Anti-idiotype cancer vaccine 1A7 -- Titan |
| Anti-Flt-1 monoclonal antibodies -- ImClone | Anti-idiotype cancer vaccine 3H1 -- Titan |
| Anti-fungal peptides -- State University of New York | Anti-idiotype cancer vaccine TriAb -- Titan |
| antifungal tripeptides -- BTG | Anti-idiotype Chlamydia trachomatis vaccine |
| Anti-ganglioside GD2 antibody-interleukin-2 fusion protein -- Lexigen | Anti-idiotype colorectal cancer vaccine -- Novartis |
| Anti-GM2 MAb -- Kyowa | Anti-idiotype colorectal cancer vaccine -- Onyvax |
| Anti-GM-CSF receptor monoclonal antibodies -- AMRAD | Anti-idiotype melanoma vaccine -- IDEC Pharmaceuticals |
| Anti-gp130 MAb -- Tosoh | Anti-idiotype ovarian cancer vaccine ACA 125 |
| Anti-HCA monoclonal antibodies -- AltaRex/Epigen | Anti-idiotype ovarian cancer vaccine AR54 - AltaRex |
| Anti-hCG antibodies -- Abgenix/AVI BioPharma | |

FIG. 28D

35/498

| | |
|---|--|
| Anti-idiotypic ovarian cancer vaccine CA-125 – AltaRex, Biomira | Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University |
| Anti-IgE catalytic antibody -- Hersed Biomed | Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital |
| Anti-IgE MAb E26 -- Genentech | Anti-MHC monoclonal antibodies |
| Anti-IGF-1 MAb | Anti-MIF antibody humanised – IDEC, Cytokine PharmaSciences |
| anti-inflammatory -- GeneMax | Anti-MRSA/VRSA sheep MAb -- KS Biomedix Holdings |
| anti-inflammatory peptide -- BTG | Anti-mu MAb -- Novartis |
| anti-integrin peptides -- Burnha | Anti-MUC-1 MAb |
| Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management | Anti-MUC 18 |
| Anti-interferon-gamma MAb -- Protein Design Labs | Anti-Nogo-A MAb IN1 |
| Anti-interferon-gamma polyclonal antibody - Advanced Biotherapy | Anti-nuclear autoantibodies -- Procyon |
| Anti-interleukin-10 MAb – | Anti-ovarian cancer monoclonal antibodies - Dompe |
| Anti-interleukin-12 MAb – | Anti-p185 monoclonal antibodies |
| Anti-interleukin-1-beta polyclonal antibody -- R&D Systems | Anti-p43 MAb |
| Anti-interleukin-2 receptor MAb 2A3 | Antiparasitic vaccines |
| Anti-interleukin-2 receptor MAb 33B3-1 -- Immunotech | Anti-PDGF/bFGF sheep MAb -- KS Biomedix |
| Anti-interleukin-2 receptor MAb ART-18 | Anti-properdin monoclonal antibodies -- Abgenix/Gliatech |
| Anti-interleukin-2 receptor MAb LO-Tact-1 | Anti-PSMA (prostate specific membrane antigen) |
| Anti-interleukin-2 receptor MAb Mikbeta1 | Anti-PSMA MAb J591 -- BZL Biologics |
| Anti-interleukin-2 receptor MAb NDS61 | Anti-Rev MAb gene therapy – |
| Anti-interleukin-4 MAb 11B11 | Anti-RSV antibodies – Epicyte, Intracell |
| Anti-interleukin-5 MAb -- Wallace Laboratories | Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune |
| Anti-interleukin-6 MAb – Centocor, Diaclone, Pharmadigm | Anti-RSV MAb, inhalation -- Alkermes/MedImmune |
| Anti-interleukin-8 MAb -- Abgenix | Anti-RT gene therapy |
| Anti-interleukin-8 MAb – Xenotech | Antisense K-ras RNA gene therapy |
| Anti-JL1 MAb | Anti-SF-25 MAb |
| Anti-Klebsiella sheep MAb -- KS Biomedix Holdings | Anti-sperm antibody -- Epicyte |
| Anti-Laminin receptor MAb-liposomal doxorubicin conjugate | Anti-Tac(Fv)-PE38 conjugate |
| Anti-LCG MAb -- Cytoclonal | Anti-TAPA/CD81 MAb AMP1 |
| Anti-lipopolysaccharide MAb -- VitaResc | Anti-tat gene therapy |

FIG. 28E

36/498

| | |
|--|---|
| Anti-TCR-alphabeta MAb H57-597 | AOP-RANTES -- Senetek |
| Anti-TCR-alphabeta MAb R73 | Apan-CH -- Praecis Pharmaceuticals |
| Anti-tenascin MAb BC-4-I-131 | APC-8024 -- Demegen |
| Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme | ApoA-1 -- Milano, Pharmacia |
| Anti-TGF-beta MAb 2G7 -- Genentech | Apogen -- Alexion |
| Antithrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad | apolipoprotein A1 -- Avanir |
| Anti-Thy1 MAb | Apolipoprotein E -- Bio-Tech. General |
| Anti-Thy1.1 MAb | Applaggin -- Biogen |
| Anti-tissue factor/factor VIIA sheep MAb -- KS Biomedix | aprotinin -- ProdiGene |
| Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharacia, Serono | APT-070C -- AdProTech |
| Anti-TNF sheep MAb -- KS Biomedix Holdings | AR 177 -- Aronex Pharmaceuticals |
| Anti-TNFalpha MAb -- Genzyme | AR 209 -- Aronex Pharmaceuticals, Antigenics |
| Anti-TNFalpha MAb B-C7 -- Diaclone | AR545C |
| Anti-tooth decay MAb -- Planet BioTech. | ARGENT gene delivery systems -- ARIAD |
| Anti-TRAIL receptor-1 MAb -- Takeda | Arresten |
| Antitumour RNases -- NIH | ART-123 -- Asahi Kasei |
| Anti-VCAM MAb 2A2 -- Alexion | arylsulfatase B -- BioMarin |
| Anti-VCAM MAb 3F4 -- Alexion | Arylsulfatase B, Recombinant human -- BioMarin |
| Anti-VCAM-1 MAb | AS 1051 -- Ajinomoto |
| Anti-VEC MAb -- ImClone | ASI-BCL -- Intracell |
| Anti-VEGF MAb -- Genentech | Asparaginase - Merck |
| Anti-VEGF MAb 2C3 | ATL-101 -- Alizyme |
| Anti-VEGF sheep MAb -- KS Biomedix Holdings | Atrial natriuretic peptide -- Pharis |
| Anti-VLA-4 MAb HP1/2 -- Biogen | Aurintricarboxylic acid-high molecular weight |
| Anti-VLA-4 MAb PS/2 | Autoimmune disorders -- GPC Biotech/MorphoSys |
| Anti-VLA-4 MAb R1-2 | Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme |
| Anti-VLA-4 MAb TA-2 | Tra |
| Anti-VAP-1 human MAb | Autoimmune disorders/cancer -- Abgenix/Chiron, CuraGen |
| Anti-VRE sheep MAb -- KS Biomedix Holdings | Autotaxin |
| ANUP -- TranXenoGen | Avicidin -- NeoRx |
| ANUP-1 -- Pharis | axogenesis factor-1 -- Boston Life Sciences |
| | Axokine -- Regeneron |
| | B cell lymphoma vaccine -- Biomira |
| | B7-1 gene therapy -- |
| | BABS proteins -- Chiron |

FIG. 28F

37/498

| | |
|--|---|
| BAM-002 -- Novelos Therapeutics | BMP 2 -- Genetics Institute/Medtronic- |
| Basiliximab (anti CD25 MAb) -- Novartis | Sofamor Danek, Genetics Institute/ |
| Bay-16-9996 -- Bayer | Collagenesis, Genetics |
| Bay-39-9437 -- Bayer | Institute/Yamanouch |
| Bay-50-4798 -- Bayer | BMP 2 gene therapy |
| BB-10153 -- British Biotech | BMP 52 -- Aventis Pasteur, Biopharm |
| BBT-001 -- Bolder BioTech. | BMP-2 -- Genetics Institute |
| BBT-002 -- Bolder BioTech. | BMS 182248 -- Bristol-Myers Squibb |
| BBT-003 -- Bolder BioTech. | BMS 202448 -- Bristol-Myers Squibb |
| BBT-004 -- Bolder BioTech. | bone growth factors -- IsoTis |
| BBT-005 -- Bolder BioTech. | BPC-15 -- Pfizer |
| BBT-006 -- Bolder BioTech. | brain natriuretic peptide -- |
| BBT-007 -- Bolder BioTech. | Breast cancer -- Oxford |
| BCH-2763 -- Shire | GlycoSciences/Medarex |
| BCSF -- Millenium Biologix | Breast cancer vaccine -- Therion Biologics, |
| BDNF -- Regeneron -- Amgen | Oregon |
| Becaplermin -- Johnson & Johnson, Chiron | BSSL -- PPL Therapeutics |
| Bectumomab -- Immunomedics | BST-2001 -- BioStratum |
| Beriplast -- Aventis | BST-3002 -- BioStratum |
| Beta-adrenergic receptor gene therapy -- | BTI 322 -- |
| University of Arkansas | butyrylcholinesterase -- Shire |
| bFGF -- Scios | C 6822 -- COR Therapeutics |
| BI 51013 -- Behringwerke AG | C1 esterase inhibitor -- Pharming |
| BIBH 1 -- Boehringer Ingelheim | C3d adjuvant -- AdProTech |
| BIM-23190 -- Beaufour-Ipsen | CAB-2.1 -- Millennium |
| birch pollen immunotherapy -- Pharmacia | calcitonin -- Inhale Therapeutics Systems, |
| bispecific fusion proteins -- NIH | Aventis, Genetronics, TranXenoGen, |
| Bispecific MAb 2B1 -- Chiron | Unigene, Rhone Poulenc Rohrer |
| Bitistatin | calcitonin -- oral -- Nobex, Emisphere, |
| BIWA 4 -- Boehringer Ingelheim | Pharmaceutical Discovery |
| blood substitute -- Northfield, Baxter Intl. | Calcitonin gene-related peptide -- Asahi |
| BLP-25 -- Biomira | Kasei -- Unigene |
| BLS-0597 -- Boston Life Sciences | calcitonin, human -- Suntory |
| BLyS -- Human Genome Sciences | calcitonin, nasal -- Novartis, Unigene |
| BLyS radiolabelled -- Human Genome | calcitonin, Panoderm -- Elan |
| Sciences | calcitonin, Peptitrol -- Shire |
| BM 06021 -- Boehringer Mannheim | calcitonin, salmon -- Therapicon |
| BM-202 -- BioMarin | calin -- Biopharm |
| BM-301 -- BioMarin | Calphobindin I |
| BM-301 -- BioMarin | calphobindin I -- Kowa |
| BM-302 -- BioMarin | calreticulin -- NYU |

FIG. 28G

38/498

| | |
|--|---|
| Campath-1G | CD4 fusion toxin -- Senetek |
| Campath-1M | CD4 IgG -- Genentech |
| cancer therapy -- Cangene | CD4 receptor antagonists -- |
| cancer vaccine -- Aixlie, Aventis Pasteur, | Pharmacoepia/Progenics |
| Center of Molecular Immunology ,YM | CD4 soluble -- Progenics |
| BioSciences, Cytos, Genzyme, | CD4, soluble -- Genzyme Transgenics |
| Transgenics, GlobelImmune, Igeneon, | CD40 ligand -- Immunex |
| ImClone, Virogenetics, InterCell, Iomai, | CD4-ricin chain A -- Genentech |
| Jenner Biotherapies, Memorial Sloan- | CD59 gene therapy -- Alexion |
| Kettering Cancer Center, Sydney Kimmel | CD8 TIL cell therapy -- Aventis Pasteur |
| Cancer Center, Novavax, Protein | CD8, soluble -- Avidex |
| Sciences, Argonex, SIGA | CD95 ligand -- Roche |
| Cancer vaccine ALVAC-CEA B7.1 -- | CDP 571 -- Celltech |
| Aventis Pasteur/Therion Biologics | CDP 850 -- Celltech |
| Cancer vaccine CEA-TRICOM -- Aventis | CDP-860 (PEG-PDGF MAb) -- Celltech |
| Pasteur/Therion Biologics | CDP 870 -- Celltech |
| Cancer vaccine gene therapy -- Cantab | CDS-1 -- Ernest Orlando |
| Pharmaceuticals | Cedelizumab -- Ortho-McNeil |
| Cancer vaccine HER-2/neu -- Corixa | Cetermin -- Insmad |
| Cancer vaccine THERATOPE -- Biomira | CETP vaccine -- Avant |
| cancer vaccine, PolyMASC -- Valentis | Cetrorelix |
| Candida vaccine -- Corixa, Inhibitex | Cetuximab |
| Canstatin -- ILEX | CGH 400 -- Novartis |
| CAP-18 -- Panorama | CGP 42934 -- Novartis |
| Cardiovascular gene therapy -- Collateral | CGP 51901 -- Tanox |
| Therapeutics | CGRP -- Unigene |
| carperitide -- Suntory | CGS 27913 -- Novartis |
| Casocidin-1 -- Pharis | CGS 32359 -- Novartis |
| CAT 152 -- Cambridge Antibody Tech. | Chagas disease vaccine -- Corixa |
| CAT 192 -- Cambridge Antibody Tech. | chemokines -- Immune Response |
| CAT 213 -- Cambridge Antibody Tech. | CHH 380 -- Novartis |
| Catalase-- Enzon | chitinase -- Genzyme, ICOS |
| Cat-PAD -- Circassia | Chlamydia pneumoniae vaccine -- Antex |
| CB 0006 -- Celltech | Biologics |
| CCK(27-32)-- Akzo Nobel | Chlamydia trachomatis vaccine -- Antex |
| CCR2-64I -- NIH | Biologics |
| CD, Procept -- Paligent | Chlamydia vaccine -- GlaxoSmithKline |
| CD154 gene therapy | Cholera vaccine CVD 103-HgR -- Swiss |
| CD39 -- Immunex | Serum and Vaccine Institute Berne |
| CD39-L2 -- Hyseq | Cholera vaccine CVD 112 -- Swiss Serum |
| CD39-L4 -- Hyseq | and Vaccine Institute Berne |

FIG. 28H

39/498

| | |
|--|--|
| Cholera vaccine inactivated oral -- SBL Vaccin | CRL 1605 -- CytRx |
| Chrysalin -- Chrysalis BioTech. | CS-560 -- Sankyo |
| CI-782 -- Hitachi Kase | CSF -- ZymoGenetics |
| Ciliary neurotrophic factor -- Fidia, Roche | CSF-G -- Hangzhou, Dong-A, Hanmi |
| CIM project -- Active Biotech | CSF-GM -- Cangene, Hunan, LG Chem |
| CL 329753 -- Wyeth-Ayerst | CSF-M -- Zarix |
| CL22, Cobra -- ML Laboratories | CT 1579 -- Merck Frosst |
| Clenoliximab -- IDEC | CT 1786 -- Merck Frosst |
| Clostridium difficile antibodies -- Epicyte | CT-112 [^] -- BTG |
| clotting factors -- Octagene | CTB-134L -- Xenova |
| CMB 401 -- Celltech | CTC-111 -- Kaketsuken |
| CNTF -- Sigma-Tau | CTGF -- FibroGen |
| Cocaine abuse vaccine -- Cantab, ImmuLogic, Scripps | CTLA4-Ig -- Bristol-Myers Squibb |
| coccidiomycosis vaccine -- Arizo | CTLA4-Ig gene therapy -- |
| collagen -- Type I -- Pharming | CTP-37 -- AVI BioPharma |
| Collagen formation inhibitors -- FibroGen | C-type natriuretic peptide -- Suntory |
| Collagen/hydroxyapatite/bone growth factor -- Aventis Pasteur, Biopharm, Orquest | CVS 995 -- Corvas Intl. |
| collagenase -- BioSpecifics | CX 397 -- Nikko Kyodo |
| Colorectal cancer vaccine -- Wistar Institute | CY 1747 -- Epimmune |
| Component B, Recombinant -- Serono | CY 1748 -- Epimmune |
| Connective tissue growth factor inhibitors -- FibroGen/Taisho | Cyanovirin-N |
| Contortrostatin | Cystic fibrosis therapy -- CBR/IVAX |
| contraceptive vaccine -- Zonagen | CYT 351 |
| Contraceptive vaccine hCG | cytokine Traps -- Regeneron |
| Contraceptive vaccine male reversible -- IMMUCON | cytokines -- Enzon, Cytoclonal |
| Contraceptive vaccine zona pellucida -- Zonagen | Cytomegalovirus glycoprotein vaccine -- Chiron, Aquila Biopharmaceuticals, Aventis Pasteur, Virogenetics |
| Copper-64 labelled MAb TETA-1A3 -- NCI | Cytomegalovirus vaccine live -- Aventis Pasteur |
| Coralyne | Cytosine deaminase gene therapy -- GlaxoSmithKline |
| Corsevin M | DA-3003 -- Dong-A |
| C-peptide analogues -- Schwarz | DAB389interleukin-6 -- Senetek |
| CPI-1500 -- Consensus | DAB389interleukin-7 |
| CRF -- Neurobiological Tech. | DAC:GLP-2 -- ConjuChem, Inc. |
| cRGDfV pentapeptide -- | Daclizumab (anti-IL2R MAb) -- Protein Design Labs |
| CRL 1095 -- CytRx | DAMP [^] -- Incyte Genomics |
| CRL 1336 -- CytRx | Daniplestim -- Pharmacia |
| | darbepoetin alfa -- Amgen |

FIG. 28I

40/498

| | |
|---|--|
| DBI-3019 -- Diabetogen | dural graft matrix -- Integra |
| DCC -- Genzyme | Duteplase -- Baxter Intl. |
| DDF -- Hyseq | DWP-401 -- Daewoong |
| decorin -- Integra, Telios | DWP-404 -- Daewoong |
| defensins -- Large Scale Biology | DWP-408 -- Daewoong |
| DEGR-VIIa | Dx 88 (Epi-KAL2) -- Dyax |
| Delimmunised antibody 3B6/22 AGEN | Dx 890 (elastin inhibitors) -- Dyax |
| Deimmunised anti-cancer antibodies -- Biovation/Viragen | E coli O157 vaccine -- NIH |
| Dendroamide A | E21-R -- BresaGen |
| Dengue vaccine -- Bavarian Nordic, Merck | Eastern equine encephalitis virus vaccine -- |
| denileukin diftitox -- Ligand | Echicetin -- |
| DES-1101 -- Desmos | Echinhibin 1 -- |
| desirudin -- Novartis | Echistatin -- Merck |
| desmopressin -- Unigene | Echitamine -- |
| Desmoteplase -- Merck, Schering AG | Ecromeximab -- Kyowa Hakko |
| Destabilase | EC-SOD -- PPL Therapeutics |
| Diabetes gene therapy -- DeveloGen, Pfizer | Eculizumab (5G1.1) -- Alexion |
| Diabetes therapy -- Crucell | EDF -- Ajinomoto |
| Diabetes type 1 vaccine -- Diamyd Therapeutics | EDN derivative -- NIH |
| DiaCIM -- YM BioSciences | EDNA -- NIH |
| dialytic oligopeptides -- Research Corp | Edobacomab -- XOMA |
| Diamyd -- Diamyd Therapeutics | Edrecolomab -- Centocor |
| DiaPep227 -- Pepgen | EF 5077 |
| DiavaX -- Corixa | Efalizumab -- Genentech |
| Digoxin MAb -- Glaxo | EGF fusion toxin -- Seragen, Ligand |
| Diphtheria tetanus pertussis-hepatitis B vaccine -- GlaxoSmithKline | EGF-P64k vaccine -- Center of Molecular Immunology |
| DIR therapy -- Solis Therapeutics -- | EL 246 -- LigoCyte |
| DNase -- Genentech | elastase inhibitor -- Synergen |
| Dornase alfa -- Genentech | elcatonin -- Therapicon |
| Dornase alfa, inhalation -- Genentech | EMD 72000 -- Merck KGaA |
| Doxorubicin-anti-CEA MAb conjugate -- Immunomedics | Emdogain -- BIORA |
| DP-107 -- Trimeris | emfilermin -- AMRAD |
| drotrecogin alfa -- Eli Lilly | Emoctakin -- Novartis |
| DTctGMCSF | enamel matrix protein -- BIORA |
| DTP-polio vaccine -- Aventis Pasteur | Endo III -- NYU |
| DU 257-KM231 antibody conjugate -- Kyowa | endostatin -- EntreMed, Pharis |
| | Enhancins -- Micrologix |
| | Enlimomab -- Isis Pharm. |
| | Enoxaparin sodium -- Pharmuka |

FIG. 28J

41/498

| | |
|---|---|
| enzyme linked antibody nutrient depletion therapy -- KS Biomedix Holdings | Factor IX gene therapy -- Cell Genesys |
| Eosinophil-derived neutralizing agent -- EP-51216 -- Asta Medica | Factor VII -- Novo Nordisk, Bayer, Baxter Intl. |
| EP-51389 -- Asta Medica | Factor VIIa -- PPL Therapeutics, ZymoGenetics |
| EPH family ligands -- Regeneron | Factor VIII -- Bayer Genentech, Beaufour-Ipsen, CLB, Inex, Octagen, Pharmacia, Pharming |
| Epidermal growth factor -- Hitachi Kasei, Johnson & Johnson | Factor VIII -- PEGylated -- Bayer |
| Epidermal growth factor fusion toxin -- Senetek | Factor VIII fragments -- Pharmacia |
| Epidermal growth factor-genistein -- EPI-HNE-4 -- Dyax | Factor VIII gene therapy -- Targeted Genetics |
| EPI-KAL2 -- Dyax | Factor VIII sucrose formulation -- Bayer, Genentech |
| Epoetin-alfa -- Amgen, Dragon Pharmaceuticals, Nanjing Huaxin | Factor VIII-2 -- Bayer |
| Epratuzumab -- Immunomedics | Factor VIII-3 -- Bayer |
| Epstein-Barr virus vaccine -- Aviron/SmithKline Beecham, Bioresearch | Factor Xa inhibitors -- Merck, Novo Nordisk, Mochida |
| Eptacog alfa -- Novo Nordisk | Factor XIII -- ZymoGenetics |
| Eptifibatide -- COR Therapeutics | Factors VIII and IX gene therapy -- Genetics Institute/Targeted Genetics |
| erb-38 -- | Famoxin -- Genset |
| Erlizumab -- Genentech | Fas (delta) TM protein -- LXR BioTech. |
| erythropoietin -- Alkermes, ProLease, Dong-A, Elanex, Genetics Institute, LG Chem, Protein Sciences, Serono, Snow Brand, SRC VB VECTOR, Transkaryotic Therapies | Fas TR -- Human Genome Sciences |
| Erythropoietin Beta -- Hoffman La Roche | Felvizumab -- Scotgen |
| Erythropoietin/Epoetin alfa -- Chugai | FFR-VIIa -- Novo Nordisk |
| Escherichia coli vaccine -- North American Vaccine, SBL Vaccin, Swiss Serum and Vaccine Institute Berne | FG-001 -- F-Gene |
| etanercept -- Immunex | FG-002 -- F-Gene |
| examorelin -- Mediolanum | FG-004 -- F-Gene |
| Exendin 4 -- Amylin | FG-005 -- F-Gene |
| exonuclease VII | FGF + fibrin -- Repair |
| F 105 -- Centocor | Fibrimage -- Bio-Tech. General |
| F-992 -- Fornix | fibrin-binding peptides -- ISIS Innovation |
| Factor IX -- Alpha Therapeutics, Welfide Corp., CSL, enetics Institute/AHP, Pharmacia, PPL Therapeutics | fibrinogen -- PPL Therapeutics, Pharming |
| | fibroblast growth factor -- Chiron, NYU, Ramot, ZymoGenetics |
| | fibrolase conjugate -- Schering AG |
| | Filgrastim -- Amgen |
| | filgrastim -- PDA modified -- Xencor |
| | FLT-3 ligand -- Immunex |
| | FN18 CRM9 -- |

FIG. 28K

42/498

| | |
|--|---|
| follistatin -- Biotech Australia, Human Therapeutics | Glucocerebrosidase -- Genzyme |
| follitropin alfa -- Alkermes, ProLease, PowderJect, Serono, Akzo Nobel | glutamate decarboxylase -- Genzyme Transgenics |
| Follitropin Beta -- Bayer, Organon | Glycoprotein S3 -- Kureha |
| FP 59 | GM-CSF -- Immuhex |
| FSH -- Ferring | GM-CSF tumour vaccine -- PowderJect |
| FSH + LH -- Ferring | GnRH immunotherapeutic -- Protherics |
| F-spondin -- CeNeS | Goserelin (LhRH antagonist) -- AstraZeneca |
| fusion protein delivery system -- UAB Research Foundation | gp75 antigen -- ImClone |
| fusion toxins -- Boston Life Sciences | gp96 -- Antigenics |
| G 5598 -- Genentech | GPI 0100 -- Galenica |
| GA-II -- Transkaryotic Therapies | GR 4991W93 -- GlaxoSmithKline |
| Gamma-interferon analogues -- SRC VB VECTOR | Granulocyte colony-stimulating factor -- Dong-A |
| Ganirelix -- Roche | Granulocyte colony-stimulating factor conjugate |
| gastric lipase -- Meristem | grass allergy therapy -- Dynavax |
| Gavilimomab -- | GRF1-44 -- ICN |
| G-CSF -- Amgen, SRC VB VECTOR | Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo |
| GDF-1 -- CeNeS | growth factor peptides -- Biotherapeutics |
| GDF-5 -- Biopharm | growth hormone -- LG Chem |
| GDNF (glial derived neurotrophic factor) -- Amgen | growth hormone, Recombinant human -- Serono |
| gelsolin -- Biogen | GT 4086 -- Gliatech |
| Gemtuzumab ozogamicin -- Celltech | GW 353430 -- GlaxoSmithKline |
| Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies | GW-278884 -- GlaxoSmithKline |
| Glanzmann thrombasthenia gene therapy -- | H 11 -- Viventia Biotech |
| Glatiramer acetate -- Yeda | H5N1 influenza A virus vaccine -- Protein Sciences |
| glial growth factor 2 -- CeNeS | haemoglobin -- Biopure |
| GLP-1 -- Amylin, Suntory, TheraTech, Watson | haemoglobin 3011, Recombinant -- Baxter Healthcare |
| GLP-1 peptide analogues -- Zealand Pharmaceuticals | haemoglobin crosfumaril -- Baxter Intl. |
| GLP-2 -- Novo Nordisk, Ontario, Inc., Suntory Limited | haemoglobin stabilized -- Ajinomoto |
| glucagon -- Eli Lilly, ZymoGenetics | haemoglobin, recombinant -- Apex |
| Glucagon-like peptide-1 7-36 amide -- Suntory | HAF -- Immune Response |
| Glucogen-like peptide -- Amylin | Hantavirus vaccine |
| | HB 19 |
| | HBNF -- Regeneron |
| | HCC-1 -- Pharis |

FIG. 28L

43/498

| | |
|--|--|
| hCG -- Milkhaus | Herpes simplex glycoprotein DNA vaccine -- |
| hCG vaccine -- Zonagen | Merck, Wyeth-Lederle Vaccines-Malvern, |
| HE-317 -- Hollis-Eden Pharmaceuticals | Genentech, GlaxoSmithKline, Chiron, |
| Heat shock protein cancer and influenza | Takeda |
| vaccines -- StressGen | Herpes simplex vaccine -- Cantab |
| Helicobacter pylori vaccine -- Acambis, | Pharmaceuticals, CEL-SCI, Henderson |
| AstraZeneca/CSL, Chiron, Provalis | Morley |
| Helistat-G -- GalaGen | Herpes simplex vaccine live -- ImClone |
| Hemolink -- Hemosol | Systems/Wyeth-Lederle, Aventis Pasteur |
| hepapoietin -- Snow Brand | HGF derivatives -- Dompe |
| heparanase -- InSight | hIAPP vaccine -- Crucell |
| heparinase I -- Ibex | Hib-hepatitis B vaccine -- Aventis Pasteur |
| heparinase III -- Ibex | HIC 1 |
| Hepatitis A vaccine -- American Biogenetic | HIP-- Altachem |
| Sciences | Hirudins -- Biopharma, Cangene, Dongkook, |
| Hepatitis A vaccine inactivated | Japan Energy Corporation, Pharmacia |
| Hepatitis A vaccine Nothav -- Chiron | Corporation, SIR International, Sanofi- |
| Hepatitis A-hepatitis B vaccine -- | Synthelabo, Sotragene, Rhein Biotech |
| GlaxoSmithKline | HIV edible vaccine -- ProdiGene |
| hepatitis B therapy -- Tripep | HIV gp120 vaccine -- Chiron, Ajinomoto, |
| Hepatitis B vaccine -- Amgen, Chiron SpA, | GlaxoSmithKline, ID Vaccine, Progenics, |
| Meiji Milk, NIS, Prodeva, PowderJect, | VaxGen |
| Rhein Biotech | HIV gp120 vaccine gene therapy -- |
| Hepatitis B vaccine recombinant -- Evans | HIV gp160 DNA vaccine -- PowderJect, |
| Vaccines, Epitec Combiotech, Genentech, | Aventis Pasteur, Oncogen, Hyland |
| MedImmune, Merck Sharp & Dohme, | Immuno, Protein Sciences |
| Rhein Biotech, Shantha Biotechnics, | HIV gp41 vaccine -- Panacos |
| Vector, Yeda | HIV HGP-30W vaccine -- CEL-SCI |
| Hepatitis B vaccine recombinant TGP 943 -- | HIV immune globulin -- Abbott, Chiron |
| Takeda | HIV peptides -- American Home Products |
| Hepatitis C vaccine -- Bavarian Nordic, | HIV vaccine -- Applied bioTech., Axis |
| Chiron, Innogenetics Acambis, | Genetics, Biogen, Bristol-Myers Squibb, |
| Hepatitis D vaccine -- Chiron Vaccines | Genentech, Korea Green Cross, NIS, |
| Hepatitis E vaccine recombinant -- | Oncogen, Protein Sciences Corporation, |
| Genelabs/GlaxoSmithKline, Novavax | Terumo, Tonen Corporation, Wyeth- |
| hepatocyte growth factor -- Panorama, | Ayerst, Wyeth-Lederle Vaccines-Malvern, |
| Sosei | Advanced BioScience Laboratories, |
| hepatocyte growth factor kringle fragments - | Bavarian Nordic, Bavarian Nordic/Statens |
| - EntreMed | Serum Institute, GeneCure, Immune |
| Her-2/Neu peptides -- Corixa | Response, Progenics, Therion Biologics, |
| | United Biomedical, Chiron |

FIG. 28M

44/498

| | |
|--|--|
| HIV vaccine vCP1433 -- Aventis Pasteur | Human monoclonal antibodies -- |
| HIV vaccine vCP1452 -- Aventis Pasteur | Medarex/Northwest Biotherapeutics, |
| HIV vaccine vCP205 -- Aventis Pasteur | Medarex/Seattle Genetics |
| HL-9 -- American BioScience | human netrin-1 -- Exelixis |
| HM-9239 -- Cytran | human papillomavirus antibodies -- Epicyte |
| HML-103 -- Hemosol | Human papillomavirus vaccine -- Biotech |
| HML-104 -- Hemosol | Australia, IDEC, StressGen |
| HML-105 -- Hemosol | Human papillomavirus vaccine MEDI 501 -- |
| HML-109 -- Hemosol | MedImmune/GlaxoSmithKline |
| HML-110 -- Hemosol | Human papillomavirus vaccine MEDI |
| HML-121 -- Hemosol | 503/MEDI 504 -- |
| hNLP -- Pharis | MedImmune/GlaxoSmithKline |
| Hookworm vaccine | Human papillomavirus vaccine TA-CIN -- |
| host-vector vaccines -- Henogen | Cantab Pharmaceuticals |
| HPM 1 -- Chugai | Human papillomavirus vaccine TA-HPV -- |
| HPV vaccine -- MediGene | Cantab Pharmaceuticals |
| HSA -- Meristem | Human papillomavirus vaccine TH-GW -- |
| HSF -- StressGen | Cantab/GlaxoSmithKline |
| HSP carriers --Weizmann, Yeda, Peptor | human polyclonal antibodies -- Biosite/Eos |
| HSPPC-70 -- Antigenics | BioTech./ Medarex |
| HSPPC-96, pathogen-derived -- Antigenics | human type II anti factor VIII monoclonal |
| HSV 863 -- Novartis | antibodies -- ThromboGenics |
| HTLV-I DNA vaccine | humanised anti glycoprotein Ib murine |
| HTLV-I vaccine | monoclonal antibodies -- ThromboGenics |
| HTLV-II vaccine -- Access | HumaRAD -- Intracell |
| HU 901 -- Tanox | HuMax EGFR -- Genmab |
| Hu23F2G -- ICOS | HuMax-CD4 -- Medarex |
| HuHMFG1 | HuMax-IL15 -- Genmab |
| HumaLYM -- Intracell | HYB 190 -- Hybridon |
| Human krebs statika -- Yamanouchi | HYB 676 -- Hybridon |
| human monoclonal antibodies -- | I-125 MAb A33 -- Celltech |
| Abgenix/Biogen, Abgenix/ Corixa, | Ibritumomab tiuxetan -- IDEC |
| Abgenix/Immunex, Abgenix/Lexicon, | IBT-9401 -- Ibex |
| Abgenix/ Pfizer, Athersys/Medarex, | IBT-9402 -- Ibex |
| Biogen/MorphoSys, CAT/Searle, | IC 14 -- ICOS |
| Centocor/Medarex, Corixa/Kirin Brewery, | Idarubicin anti-Ly-2.1 -- |
| Corixa/Medarex, Eos BioTech./Medarex, | IDEC 114 -- IDEC |
| Eos/Xenerex, Exelixis/Protein Design | IDEC 131 -- IDEC |
| Labs, ImmunoGen/ Raven, Medarex/ | IDEC 152 -- IDEC |
| B.Twelve, MorphoSys/ImmunoGen, XTL | IDM 1 -- IDM |
| Biopharmaceuticals/Dyax, | IDPS -- Hollis-Eden Pharmaceuticals |

FIG. 28N

45/498

| | |
|--|---|
| iduronate-2-sulfatase -- Transkaryotic Therapies | insulin -- AutoImmune, Altea, Biobras, BioSante, Bio-Tech. General, Chong Kun Dang, Emisphere, Flamel, Provalis, Rhein Biotech, TranXenoGen |
| IGF/IBP-2-13 -- Pharis | insulin (bovine) -- Novartis |
| IGN-101 -- Igeneon | insulin analogue -- Eli Lilly |
| IK HIR02 -- Iketon | Insulin Aspart -- Novo Nordisk |
| IL-11 -- Genetics Institute/AHP | insulin detemir -- Novo Nordisk |
| IL-13-PE38 -- NeoPharm | insulin glargine -- Aventis |
| IL-17 receptor -- Immunex | insulin inhaled -- Inhale Therapeutics Systems, Alkermes |
| IL-18BP -- Yeda | insulin oral -- Inovax |
| IL-1Hy1 -- Hyseq | insulin, AeroDose -- AeroGen |
| IL-1 β -- Celltech | insulin, AERx -- Aradigm |
| IL-1 β adjuvant -- Celltech | insulin, BEODAS -- Elan |
| IL-2 -- Chiron | insulin, Biphax -- Helix |
| IL-2 + IL-12 -- Hoffman La-Roche | insulin, buccal -- GenereX |
| IL-6/sIL-6R fusion -- Hadasit | insulin, I2R -- Flemington |
| IL-6R derivative -- Tosoh | insulin, intranasal -- Bentley |
| IL-7-Dap 389 fusion toxin -- Ligand | insulin, oral -- Nobex, Unigene |
| IL-21 -- Novo Nordisk, ZymoGenetics | insulin, Orasome -- Endorex |
| IM-862 -- Cytran | insulin, ProMaxx -- Epic |
| IMC-1C11 -- ImClone | insulin, Quadrant -- Elan |
| imiglucerase -- Genzyme | insulin, recombinant -- Aventis |
| Immune globulin intravenous (human) -- Hoffman La Roche | insulin, Spiros -- Elan |
| immune privilege factor -- Proneuron | insulin, Transfersome -- IDEA |
| Immunocal -- Immunotec | insulin, Zymo, recombinant -- Novo Nordisk |
| Immunogene therapy -- Briana Bio-Tech | insulinotropin -- Scios |
| Immunoliposomal 5-fluorodeoxyuridine-dipalmitate -- | Insulysin gene therapy -- |
| immunosuppressant vaccine -- Aixlie | integrin antagonists -- Merck |
| immunotoxin -- Antisoma, NIH | interferon (Alpha2) -- SRC VB VECTOR, Viragen, Dong-A, Hoffman La-Roche, Genentech |
| ImmuRAIT-Re-188 -- Immunomedics | interferon -- BioMedicines, Human Genome Sciences |
| imreg-1 -- Imreg | interferon (Alfa-n3) -- Interferon Sciences Intl. |
| infertility -- Johnson & Johnson, E-TRANS | interferon (Alpha), Biphax -- Helix |
| Infliximab -- Centocor | |
| Influenza virus vaccine -- Aventis Pasteur, Protein Sciences | |
| inhibin -- Biotech Australia, Human Therapeutics | |
| Inhibitory G protein gene therapy | |
| INKP-2001 -- InKine | |
| Inolimomab -- Diaclone | |

FIG. 280

46/498

| | |
|---|---|
| interferon (Alpha)—Amgen, BioNative, | IL-2/ diphtheria toxin -- Ligand |
| Novartis, Genzyme Transgenics, | Interleukin-3 -- Cangene |
| Hayashibara, Inhale Therapeutics | Interleukin-4 -- Immunology Ventures, |
| Systems, Medusa, Flamel, Dong-A, | Sanofi Winthrop, Schering-Plough, |
| GeneTrol, Nastech, Shantha, | Immunex/ Sanofi Winthrop, Bayer, Ono |
| Wassermann, LG Chem, Sumitomo, | interleukin-4 + TNF-Alpha -- NIH |
| Aventis, Behring EGIS, Pepgen, Servier, | interleukin-4 agonist -- Bayer |
| Rhein Biotech, | interleukin-4 fusion toxin -- Ligand |
| interferon (Alpha2A) | Interleukin-4 receptor -- Immunex, Immun |
| interferon (Alpha2B) -- Enzon, Schering- | Interleukin-6 -- Ajinomoto, Cangene, Yeda, |
| Plough, Biogen, IDEA | Genetics Institute, Novartis |
| interferon (Alpha-N1) -- GlaxoSmithKline | interleukin-6 fusion protein |
| interferon (beta) -- Rentschler, GeneTrol, | interleukin-6 fusion toxin -- Ligand, Serono |
| Meristem, Rhein Biotech, Toray, Yeda, | interleukin-7 -- IC Innovations |
| Daiichi, Mochida | interleukin-7 receptor -- Immunex |
| interferon (Beta1A) -- Serono, Biogen | interleukin-8 antagonists -- Kyowa |
| interferon (beta1A),inhale -- Biogen | Hakko/Millennium/Pfizer |
| interferon (β1b)-- Chiron | interleukin-9 antagonists -- Genaera |
| interferon (tau)-- Pepgen | Interleukin-10 -- DNAX, Schering-Plough |
| Interferon alfacon-1 -- Amgen | Interleukin-10 gene therapy -- |
| Interferon alpha-2a vaccine | interleukin-12 -- Genetics Institute, Hoffman |
| Interferon Beta 1b -- Schering/Chiron, | La-Roche |
| InterMune | interleukin-13 -- Sanofi |
| Interferon Gamma -- Boehringer Ingelheim, | interleukin-13 antagonists -- AMRAD |
| Sheffield, Rentschler, Hayashibara | Interleukin-13-PE38QQR |
| interferon receptor , Type I -- Serono | interleukin-15 -- Immunex |
| interferon(Gamma1B) -- Genentech | interleukin-16 -- Research Corp |
| Interferon-alpha-2b + ribavirin -- Biogen, | interleukin-18 -- GlaxoSmithKline |
| ICN | Interleukin-18 binding protein -- Serono |
| Interferon-alpha-2b gene therapy -- | Ior-P3 -- Center of Molecular Immunology |
| Schering-Plough | IP-10 -- NIH |
| Interferon-con1 gene therapy -- | IPF -- Metabolex |
| interleukin-1 antagonists -- Dompe | IR-501 -- Immune Response |
| Interleukin-1 receptor antagonist -- Abbott | ISIS 9125 -- Isis Pharmaceuticals |
| Bioresearch, Pharmacia | ISURF No. 1554 -- Millennium |
| Interleukin-1 receptor type I -- Immunex | ISURF No. 1866 -- Iowa State Univer. |
| interleukin-1 receptor Type II -- Immunex | ITF-1697 -- Italfarmaco |
| Interleukin-1 trap -- Regeneron | IxC 162 -- Ixion |
| Interleukin-1-alpha -- Immunex/Roche | J 695 -- Cambridge Antibody Tech., |
| interleukin-2 -- SRC VB VECTOR, | Genetics Inst., Knoll |
| Ajinomoto, Biomira, Chiron | Jagged + FGF -- Repair |

FIG. 28P

47/498

| | |
|--|---|
| JKC-362 -- Phoenix Pharmaceuticals | leptin, 2nd-generation -- Amgen |
| JTP-2942 -- Japan Tobacco | leridistim -- Pharmacia |
| Juman monoclonal antibodies -- Medarex/Raven | leuprolide, ProMaxx -- Epic |
| K02 -- Axys Pharmaceuticals | leuprorelin, oral -- Unigene |
| Keliximab -- IDEC | LeuTech -- Papatin |
| Keyhole limpet haemocyanin | LEX 032 -- SuperGen |
| KGF -- Amgen | LiDEPT -- Novartis |
| KM 871 -- Kyowa | Lintuzumab (anti-CD33 MAb) -- Protein Design Labs |
| KPI 135 -- Scios | lipase -- Altus Biologics |
| KPI-022 -- Scios | lipid A vaccine -- EntreMed |
| Kringle 5 | lipid-linked anchor Tech. -- ICRT, ID Biomedical |
| KSB 304 | liposome-CD4 Tech. -- Sheffield |
| KSB-201 -- KS Biomedix | Listeria monocytogenes vaccine |
| L 696418 -- Merck | LMB 1 |
| L 703801 -- Merck | LMB 7 |
| L1 -- Acorda | LMB 9 -- Battelle Memorial Institute, NIH |
| L-761191 -- Merck | LM-CD45 -- Cantab Pharmaceuticals |
| lactoferrin -- Meristem, Pharming, Agennix | lovastatin -- Merck |
| lactoferrin cardio -- Pharming | LSA-3 |
| LAG-3 -- Serono | LT- β receptor -- Biogen |
| LAIT -- GEMMA | lung cancer vaccine -- Corixa |
| LAK cell cytotoxin -- Arizona | lusupultide -- Scios |
| lamellarins -- PharmaMar/University of Malaga | L-Vax -- AVAX |
| laminin A peptides -- NIH | LY 355455 -- Eli Lilly |
| lanotepase -- Genetics Institute | LY 366405 -- Eli Lilly |
| laronidase -- BioMarin | LY-355101 -- Eli Lilly |
| Lassa fever vaccine | Lyme disease DNA vaccine -- Vical/Aventis Pasteur |
| LCAT -- NIH | Lyme disease vaccine -- Aquila |
| LDP 01 -- Millennium | Biopharmaceuticals, Aventis, Pasteur, Symbicom, GlaxoSmithKline, Hyland |
| LDP 02 -- Millennium | Immuno, MedImmune |
| Lecithinized superoxide dismutase -- Seikagaku | Lymphocytic choriomeningitis virus vaccine |
| LeIF adjuvant -- Corixa | lymphoma vaccine -- Biomira, Genitope |
| leishmaniasis vaccine -- Corixa | LYP18 |
| lenercept -- Hoffman La-Roche | lys plasminogen, recombinant |
| Lenograstim -- Aventis, Chugai | Lysosomal storage disease gene therapy -- Avigen |
| lepirudin -- Aventis | lysostaphin -- Nutrition 21 |
| leptin -- Amgen, IC Innovations | |
| Leptin gene therapy -- Chiron Corporation | |

FIG. 28Q

48/498

| | |
|--|---|
| M 23 -- Gruenenthal | MEDI 507 -- BioTransplant |
| M1 monoclonal antibodies -- Acorda | melanin concentrating hormone -- |
| Therapeutics | Neurocrine Biosciences |
| MA 16N7C2 -- Corvas Intl. | melanocortins -- OMRF |
| malaria vaccine -- GlaxoSmithKline, | Melanoma monoclonal antibodies -- Viragen |
| AdProTech, Antigenics, Apovia, Aventis | melanoma vaccine -- GlaxoSmithKline, |
| Pasteur, Axis Genetics, Behringwerke, | Akzo Nobel, Avant, Aventis Pasteur, |
| CDCP, Chiron Vaccines, Genzyme | Bavarian Nordic, Biovector, CancerVax, |
| Transgenics, Hawaii, MedImmune, NIH, | Genzyme Molecular Oncology, Humbolt, |
| NYU, Oxxon, Roche/Saramane, Biotech | ImClone Systems, Memorial, NYU, Oxxon |
| Australia, Rx Tech | Melanoma vaccine Magevac -- Therion |
| Malaria vaccine CDC/NIIMALVAC-1 | memory enhancers -- Scios |
| malaria vaccine, multicomponent | meningococcal B vaccine -- Chiron |
| mammaglobin -- Corixa | meningococcal vaccine -- CAMR |
| mammastatin -- Biotherapeutics | Meningococcal vaccine group B conjugate - |
| mannan-binding lectin -- NatlImmu | - North American Vaccine |
| mannan-MUC1 -- Psiron | Meningococcal vaccine group B |
| MAP 30 | recombinant -- BioChem Vaccines, |
| Marinovir -- Phytera | Microscience |
| MARstem -- Maret | Meningococcal vaccine group Y conjugate - |
| MB-015 -- Mochida | - North American Vaccine |
| MBP -- ImmuLogic | Meningococcal vaccine groups A B and C |
| MCI-028 -- Mitsubishi-Tokyo | conjugate -- North American Vaccine |
| MCIF -- Human Genome Sciences | Mepolizumab -- GlaxoSmithKline |
| MDC -- Advanced BioScience -- Akzo | Metastatin -- EntreMed, Takeda |
| Nobel, ICOS | Met-CkB7 -- Human Genome Sciences |
| MDX 11 -- Medarex | met-enkephalin -- TNI |
| MDX 210 -- Medarex | METH-1 -- Human Genome Sciences |
| MDX 22 -- Medarex | methioninase -- AntiCancer |
| MDX 22 | Methionine lyase gene therapy -- |
| MDX 240 -- Medarex | AntiCancer |
| MDX 33 | Met-RANTES -- Genexa Biomedical, |
| MDX 44 -- Medarex | Serono |
| MDX 447 -- Medarex | Metreleptin |
| MDX H210 -- Medarex | Microtubule inhibitor MAb |
| MDX RA -- Houston BioTech., Medarex | Immunogen/Abgenix |
| ME-104 -- Pharmexa | MGDF -- Kirin |
| Measles vaccine | MGV -- Progenics |
| Mecasermin -- Cephalon/Chiron, Chiron | micrin -- Endocrine |
| MEDI 488 -- MedImmune | microplasmin -- ThromboGenics |
| MEDI 500 | MIF -- Genetics Institute |

FIG. 28R

49/498

| | |
|---|---|
| migration inhibitory factor -- NIH | MAB 45-2D9- -- haematoporphyrin conjugate |
| Mim CD4.1 -- Xyte Therapies | MAB 4B4 |
| mirostipen -- Human Genome Sciences | MAB 4E3-CPA conjugate -- BCM Oncologia |
| Mitumomab (BEC-2) -- ImClone Systems, Merck KGaA | MAB 4E3-daunorubicin conjugate |
| MK 852 -- Merck | MAB 50-6 |
| MLN 1202 (Anti-CCR2 monoclonal antibody) -- Millenium Pharmaceuticals | MAB 50-61A -- Institut Pasteur |
| Mobenakin -- NIS | MAB 5A8 -- Biogen |
| molgramostim -- Genetics Institute, Novartis | MAB 791T/36-methotrexate conjugate |
| monoclonal antibodies -- Abgenix/Celltech, Immusol/ Medarex, Viragen/ Roslin Institute, Cambridge Antibody Tech./Elan | MAB 7c11.e8 |
| MAB 108 -- | MAB 7E11 C5-selenocystamine conjugate |
| MAB 10D5 -- | MAB 93KA9 -- Novartis |
| MAB 14.18-interleukin-2 immunocytokine -- Lexigen | MAB A5B7-cisplatin conjugate -- Biodynamics Research, Pharmacia |
| MAB 14G2a -- | MAB A5B7-I-131 |
| MAB 15A10 -- | MAB A7 |
| MAB 170 -- Biomira | MAB A717 -- Exocell |
| MAB 177Lu CC49 -- | MAB A7-zinostatin conjugate |
| MAB 17F9 | MAB ABX-RB2 -- Abgenix |
| MAB 1D7 | MAB ACA 11 |
| MAB 1F7 -- Immune Network | MAB AFP-I-131 -- Immunomedics |
| MAB 1H10-doxorubicin conjugate | MAB AP1 |
| MAB 26-2F | MAB AZ1 |
| MAB 2A11 | MAB B3-LysPE40 conjugate |
| MAB 2E1 -- RW Johnson | MAB B4 -- United Biomedical |
| MAB 2F5 | MAB B43 Genistein-conjugate |
| MAB 31.1 -- International BioImmune Systems | MAB B43.13-Tc-99m -- Biomira |
| MAB 32 -- Cambridge Antibody Tech., Peptech | MAB B43-PAP conjugate |
| MAB 323A3 -- Centocor | MAB B4G7-gelonin conjugate |
| MAB 3C5 | MAB BCM 43-daunorubicin conjugate -- BCM Oncologia |
| MAB 3F12 | MAB BIS-1 |
| MAB 3F8 | MAB BMS 181170 -- Bristol-Myers Squibb |
| MAB 42/6 | MAB BR55-2 |
| MAB 425 -- Merck KGaA | MAB BW494 |
| MAB 447-52D -- Merck Sharp & Dohme | MAB C 242-DM1 conjugate -- ImmunoGen |
| | MAB C242-PE conjugate |
| | MAB c30-6 |
| | MAB CA208-cytorhodin-S conjugate -- Hoechst Japan |
| | MAB CC49 -- Enzon |

FIG. 28S

50/498

| | |
|---|--|
| MAB ch14.18 – | MAB LL2-I-131 – Immunomedics |
| MAB CH14.18-GM-CSF fusion protein -- Lexigen | MAB LL2-Y-90 |
| MAB chCE7 | MAB LS2D617 -- Hybritech |
| MAB CI-137 -- AMRAD | MAB LYM-1-gelonin conjugate |
| MAB cisplatin conjugate | MAB LYM-1-I-131 |
| MAB CLB-CD19 | MAB LYM-1-Y-90 |
| MAB CLB-CD19v | MAB LYM-2 -- Peregrine |
| MAB CLL-1 -- Peregrine | MAB M195 |
| MAB CLL-1-GM-CSF conjugate | MAB M195-bismuth 213 conjugate -- Protein Design Labs |
| MAB CLL-1-IL-2 conjugate -- Peregrine | MAB M195-gelonin conjugate |
| MAB CLN IgG -- doxorubicin conjugates | MAB M195-I-131 |
| MAB conjugates – Tanox | MAB M195-Y-90 |
| MAB D612 | MAB MA 33H1 -- Sanofi |
| MAB Dal B02 | MAB MAD11 |
| MAB DC101 -- ImClone | MAB MGb2 |
| MAB EA 1 – | MAB MINT5 |
| MAB EC708 -- Biovation | MAB MK2-23 |
| MAB EP-5C7 -- Protein Design Labs | MAB MOC31 ETA(252-613) conjugate |
| MAB ERIC-1 -- ICRT | MAB MOC-31-In-111 |
| MAB F105 gene therapy | MAB MOC-31-PE conjugate |
| MAB FC 2.15 | MAB MR6 – |
| MAB G250 -- Centocor | MAB MRK-16 -- Aventis Pasteur |
| MAB GA6 | MAB MS11G6 |
| MAB GA733 | MAB MX-DTPA BrE-3 |
| MAB Gliomab-H -- Viventia Biotech | MAB MY9 |
| MAB HB2-saporin conjugate | MAB Nd2 -- Tosoh |
| MAB HD 37 – | MAB NG-1 -- Hygeia |
| MAB HD37-ricin chain-A conjugate | MAB NM01 – Nissin Food |
| MAB HNK20 -- Acambis | MAB OC 125 |
| MAB huN901-DM1 conjugate -- ImmunoGen | MAB OC 125-CMA conjugate |
| MAB I-131 CC49 -- Corixa | MAB OKI-1 -- Ortho-McNeil |
| MAB ICO25 | MAB OX52 -- Bioproducts for Science |
| MAB ICR12-CPG2 conjugate | MAB PMA5 |
| MAB ICR-62 | MAB PR1 |
| MAB IRac-ricin A conjugate | MAB prost 30 |
| MAB K1 | MAB R-24 |
| MAB KS1-4-methotrexate conjugate | MAB R-24 α Human GD3 -- Celltech |
| MAB L6 -- Bristol-Myers Squibb, Oncogen | MAB RFB4-ricin chain A conjugate |
| MAB LiCO 16-88 | MAB RFT5-ricin chain A conjugate |
| | MAB SC 1 |

FIG. 28T

51/498

| | |
|--|--|
| MAb SM-3 -- ICRT | Muc-1 vaccine -- Corixa |
| MAb SMART 1D10 -- Protein Design Labs | mucosal tolerance -- Aberdeen |
| MAb SMART ABL 364 -- Novartis | mullerian inhibiting subst |
| MAb SN6f | muplestim -- Genetics Institute, Novartis, |
| MAb SN6f-deglycosylated ricin A chain | DSM Anti-Infectives |
| conjugate -- | murine MAb -- KS Biomedix |
| MAb SN6j | Mutant somatropin -- JCR Pharmaceutical |
| MAb SN7-ricin chain A conjugate | MV 833 -- Toagosei |
| MAb T101-Y-90 conjugate -- Hybritech | Mycoplasma pulmonis vaccine |
| MAb T-88 -- Chiron | Mycoprex -- XOMA |
| MAb TB94 -- Cancer ImmunoBiology | myeloperoxidase -- Henogen |
| MAb TEC 11 | myostatin -- Genetics Institute |
| MAb TES-23 -- Chugai | Nacolomab tafenatox -- Pharmacia |
| MAb TM31 -- Avant | Nagrecor -- Scios |
| MAb TNT-1 -- Cambridge Antibody Tech., | nagrestipen -- British Biotech |
| Peregrine | NAP-5 -- Corvas Intl. |
| MAb TNT-3 | NAPc2 -- Corvas Intl. |
| MAb TNT-3 -- IL2 fusion protein -- | nartograstim -- Kyowa |
| MAb TP3-A α -211 | Natalizumab -- Protein Design Labs |
| MAb TP3-PAP conjugate -- | Nateplase -- NIH, Nihon Schering |
| MAb UJ13A -- ICRT | nateplase -- Schering AG |
| MAb UN3 | NBI-3001 -- Neurocrine Biosci. |
| MAb ZME-018-gelonin conjugate | NBI-5788 -- Neurocrine Biosci. |
| MAb-BC2 -- GlaxoSmithKline | NBI-6024 -- Neurocrine Biosci. |
| MAb-DM1 conjugate -- ImmunoGen | Nef inhibitors -- BRI |
| MAb-ricin-chain-A conjugate -- XOMA | Neisseria gonorrhoea vaccine -- Antex |
| MAb-temoporfin conjugates | Biologics |
| Monopharm C -- Viventia Biotech | Neomycin B-arginine conjugate |
| monteplase -- Eisai | Nerelimomab -- Chiron |
| montirelin hydrate -- Gruenenthal | Nerve growth factor -- Amgen -- Chiron, |
| moroctocog alfa -- Genetics Institute | Genentech |
| Moroctocog-alfa -- Pharmacia | Nerve growth factor gene therapy |
| MP 4 | nesiritide citrate -- Scios |
| MP-121 -- Biopharm | neuregulin-2 -- CeNeS |
| MP-52 -- Biopharm | neurocan -- NYU |
| MRA -- Chugai | neuronal delivery system -- CAMR |
| MS 28168 -- Mitsui Chemicals, Nihon | Neurophil inhibitory Factor -- Corvas |
| Schering | Neuroprotective vaccine -- University of |
| MSH fusion toxin -- Ligand | Auckland |
| MSI-99 -- Genaera | neurotrophic chimaeras -- Regeneron |
| MT 201 -- Micromet | neurotrophic factor -- NsGene, CereMedix |

FIG. 28U

52/498

| | |
|------------------------------------|--|
| NeuroVax -- Immune Response | Oncophage -- Antigenics |
| neurturin -- Genentech | Oncostatin M -- Bristol-Myers Squibb |
| neutral endopeptidase -- Genentech | OncoVax-CL -- Jenner Biotherapies |
| NGF enhancers -- NeuroSearch | OncoVax-P -- Jenner Biotherapies |
| NHL vaccine -- Large Scale Biology | onercept -- Yeda |
| NIP45 -- Boston Life Sciences | onychomycosis vaccine -- Boehringer |
| NKI-B20 | Ingelheim |
| NM 01 -- Nissin Food | opebecan -- XOMA |
| NMI-139 -- NitroMed | opioids -- Arizona |
| NMMP -- Genetics Institute | Oprelvekin -- Genetics Institute |
| NN-2211 -- Novo Nordisk | Oregovomab -- AltaRex |
| Noggin -- Regeneron | Org-33408 b-- Akzo Nobel |
| Nonacog alfa | Orolip DP -- EpiCept |
| Norelin -- Biostar | oryzacystatin |
| Norwalk virus vaccine | OSA peptides -- GenSci Regeneration |
| NRLU 10 -- NeoRx | osteoblast-cadherin GF -- Pharis |
| NRLU 10 PE -- NeoRx | Osteocalcin-thymidine kinase gene therapy |
| NT-3 -- Regeneron | osteogenic protein -- Curis |
| NT-4/5 -- Genentech | osteopontin -- OraPharma |
| NU 3056 | osteoporosis peptides -- Integra, Telios |
| NU 3076 | osteoprotegerin -- Amgen, SnowBrand |
| NX 1838 -- Gilead Sciences | otitis media vaccines -- Antex Biologics |
| NY ESO-1/CAG-3 antigen -- NIH | ovarian cancer -- University of Alabama |
| NYVAC-7 -- Aventis Pasteur | OX40-IgG fusion protein -- Cantab, Xenova |
| NZ-1002 -- Novazyme | P 246 -- Diatide |
| obesity therapy -- Nobex | P 30 -- Alfacell |
| OC 10426 -- Ontogen | p1025 -- Active Biotech |
| OC 144093 -- Ontogen | P-113 [^] -- Demegen |
| OCIF -- Sankyo | P-16 peptide -- Transition Therapeutics |
| Oct-43 -- Otsuka | p43 -- Ramot |
| Odulimomab -- Immunotech | P-50 peptide -- Transition Therapeutics |
| OK PSA - liposomal | p53 + RAS vaccine -- NIH, NCI |
| OKT3-gamma-1-ala-ala | PACAP(1-27) analogue |
| OM 991 | paediatric vaccines -- Chiron |
| OM 992 | Pafase -- ICOS |
| Omalizumab -- Genentech | PAGE-4 plasmid DNA -- IDEC |
| oncoimmunin-L -- NIH | PAI-2 -- Biotech Australia, Human |
| Oncolysin B -- ImmunoGen | Therapeutics |
| Oncolysin CD6 -- ImmunoGen | Palifermin (keratinocyte growth factor) -- |
| Oncolysin M -- ImmunoGen | Amgen |
| Oncolysin S -- ImmunoGen | Palivizumab -- MedImmune |

FIG. 28V

53/498

| | |
|---|---|
| PAM 4 -- Merck | PEG-uricase -- Mountain View |
| pamiteplase -- Yamanouchi | Pegvisomant -- Genentech |
| pancreatin, Minitabs -- Eurand | PEGylated proteins, PolyMASC -- Valentis |
| Pangen -- Fournier | PEGylated recombinant native human leptin |
| Pantarin -- Selective Genetics | -- Roche |
| Parainfluenza virus vaccine -- Pharmacia, | Pemtumomab |
| Pierre Fabre | Penetratin -- Cyclacel |
| paraoxanase -- Esperion | Pepscan -- Antisoma |
| parathyroid hormone -- Abiogen, Korea | peptide G -- Peptech, ICRT |
| Green Cross | peptide vaccine -- NIH, NCI |
| Parathyroid hormone (1-34) -- | Pexelizumab |
| Chugai/Suntory | pexiganan acetate -- Genaera |
| Parkinson's disease gene therapy -- Cell | Pharmaprojects No. 3179 -- NYU |
| Genesys/ Ceregene | Pharmaprojects No. 3390 -- Ernest Orlando |
| Parvovirus vaccine -- MedImmune | Pharmaprojects No. 3417 -- Sumitomo |
| PCP-Scan -- Immunomedics | Pharmaprojects No. 3777 -- Acambis |
| PDGF -- Chiron | Pharmaprojects No. 4209 -- XOMA |
| PDGF cocktail -- Theratechnologies | Pharmaprojects No. 4349 -- Baxter Intl. |
| peanut allergy therapy -- Dynavax | Pharmaprojects No. 4651 |
| PEG anti-ICAM MAb -- Boehringer | Pharmaprojects No. 4915 -- Avanir |
| Ingelheim | Pharmaprojects No. 5156 -- Rhizogenics |
| PEG asparaginase -- Enzon | Pharmaprojects No. 5200 -- Pfizer |
| PEG glucocerebrosidase | Pharmaprojects No. 5215 -- Origene |
| PEG hirudin -- Knoll | Pharmaprojects No. 5216 -- Origene |
| PEG interferon-alpha-2a -- Roche | Pharmaprojects No. 5218 -- Origene |
| PEG interferon-alpha-2b + ribavirin -- | Pharmaprojects No. 5267 -- ML |
| Biogen, Enzon, ICN Pharmaceuticals, | Laboratories |
| Schering-Plough | Pharmaprojects No. 5373 -- MorphoSys |
| PEG MAb A5B7 -- | Pharmaprojects No. 5493 -- Metabolex |
| Pegacaristim -- Amgen -- Kirin Brewery -- | Pharmaprojects No. 5707 -- Genentech |
| ZymoGenetics | Pharmaprojects No. 5728 -- Autogen |
| Pegaldesleukin -- Research Corp | Pharmaprojects No. 5733 -- BioMarin |
| pegaspargase -- Enzon | Pharmaprojects No. 5757 -- NIH |
| pegfilgrastim -- Amgen | Pharmaprojects No. 5765 -- Gryphon |
| PEG-interferon Alpha -- Viragen | Pharmaprojects No. 5830 -- AntiCancer |
| PEG-interferon Alpha 2A -- Hoffman La- | Pharmaprojects No. 5839 -- Dyax |
| Roche | Pharmaprojects No. 5849 -- Johnson & |
| PEG-interferon Alpha 2B -- Schering- | Johnson |
| Plough | Pharmaprojects No. 5860 -- Mitsubishi- |
| PEG-r-hirudin -- Abbott | Tokyo |
| PEG-rHuMGDF -- Amgen | |

FIG. 28W

54/498

| | |
|---|---|
| Pharmaprojects No. 5869 -- Oxford GlycoSciences | Plasminogen activators -- Abbott Laboratories, American Home Products, Boehringer Mannheim, Chiron |
| Pharmaprojects No. 5883 -- Asahi Brewery | Corporation, DuPont Pharmaceuticals, Eli Lilly, Shionogi, Genentech, Genetics Institute, GlaxoSmithKline, Hemispherx Biopharma, Merck & Co, Novartis, Pharmacia Corporation, Wakamoto, Yeda |
| Pharmaprojects No. 5947 -- StressGen | plasminogen-related peptides -- Bio-Tech. General/MGH |
| Pharmaprojects No. 5961 -- Theratechnologies | platelet factor 4 -- RepliGen |
| Pharmaprojects No. 5962 -- NIH | Platelet-derived growth factor -- Amgen -- ZymoGenetics |
| Pharmaprojects No. 5966 -- NIH | plusonemin-- Hayashibara |
| Pharmaprojects No. 5994 -- Pharming | PMD-2850 -- Protherics |
| Pharmaprojects No. 5995 -- Pharming | Pneumococcal vaccine -- Antex Biologics, Aventis Pasteur |
| Pharmaprojects No. 6023 -- IMMUCON | Pneumococcal vaccine intranasal -- BioChem Vaccines/Biovector |
| Pharmaprojects No. 6063 -- Cytoclonal | PR1A3 |
| Pharmaprojects No. 6073 -- SIDDCO | PR-39 |
| Pharmaprojects No. 6115 -- Genzyme | pralmorelin -- Kaken |
| Pharmaprojects No. 6227 -- NIH | Pretarget-Lymphoma -- NeoRx |
| Pharmaprojects No. 6230 -- NIH | Priliximab -- Centocor |
| Pharmaprojects No. 6236 -- NIH | PRO 140 -- Progenics |
| Pharmaprojects No. 6243 -- NIH | PRO 2000 -- Procept |
| Pharmaprojects No. 6244 -- NIH | PRO 367 -- Progenics |
| Pharmaprojects No. 6281 -- Senetek | PRO 542 -- Progenics |
| Pharmaprojects No. 6365 -- NIH | pro-Apo A-I -- Esperion |
| Pharmaprojects No. 6368 -- NIH | prolactin -- Genzyme |
| Pharmaprojects No. 6373 -- NIH | Prosaptide TX14(A) -- Bio-Tech. General |
| Pharmaprojects No. 6408 -- Pan Pacific | prostate cancer antibodies -- Immunex, UroCor |
| Pharmaprojects No. 6410 -- Athersys | prostate cancer antibody therapy -- Genentech/UroGenesys, Genotherapeutics |
| Pharmaprojects No. 6421 -- Oxford GlycoSciences | prostate cancer immunotherapeutics -- The PSMA Development Company |
| Pharmaprojects No. 6522 -- Maxygen | prostate cancer vaccine -- Aventis Pasteur, Zonagen, Corixa, Dendreon, Jenner |
| Pharmaprojects No. 6523 -- Pharis | Biotherapies, Therion Biologics |
| Pharmaprojects No. 6538 -- Maxygen | |
| Pharmaprojects No. 6554 -- APALEXO | |
| Pharmaprojects No. 6560 -- Ardana | |
| Pharmaprojects No. 6562 -- Bayer | |
| Pharmaprojects No. 6569 -- Eos | |
| Phenoxazine | |
| Phenylase -- Ibex | |
| Pigment epithelium derived factor -- plasminogen activator inhibitor-1, recombinant -- DuPont Pharmaceuticals | |

FIG. 28X

55/498

| | |
|--|--|
| prostate-specific antigen -- EntreMed | RD 62198 |
| protein A -- RepliGen | rDnase -- Genentech |
| protein adhesives -- Enzon | RDP-58 -- SangStat |
| protein C -- Baxter Intl., PPL Therapeutics, | RecepTox-Fce -- Keryx |
| ZymoGenetics | RecepTox-GnRH -- Keryx, MTR |
| protein C activator -- Gilead Sciences | Technologies |
| protein kinase R antags -- NIH | RecepTox-MBP -- Keryx, MTR |
| protirelin -- Takeda | Technologies |
| protocadherin 2 -- Caprion | recFSH -- Akzo Nobel, Organon |
| Pro-urokinase -- Abbott, Bristol-Myers | REGA 3G12 |
| Squibb, Dainippon, Tosoh -- Welfide | Regavirumab -- Teijin |
| P-selectin glycoprotein ligand-1 -- Genetics | relaxin -- Connetics Corp |
| Institute | Renal cancer vaccine -- Macropharm |
| pseudomonal infections -- InterMune | repifermin -- Human Genome Sciences |
| Pseudomonas vaccine -- Cytovax | Respiratory syncytial virus PFP-2 vaccine -- |
| PSGL-Ig -- American Home Products | Wyeth-Lederle |
| PSP-94 -- Procyon | Respiratory syncytial virus vaccine -- |
| PTH 1-34 -- Nobex | GlaxoSmithKline, Pharmacia, Pierre Fabre |
| Quilimmune-M -- Antigenics | Respiratory syncytial virus vaccine |
| R 744 -- Roche | inactivated |
| R 101933 | Respiratory syncytial virus-parainfluenza |
| R 125224 -- Sankyo | virus vaccine -- Aventis Pasteur, |
| RA therapy -- Cardion | Pharmacia |
| Rabies vaccine recombinant -- Aventis | Retepase -- Boehringer Mannheim, |
| Pasteur, BioChem Vaccines, Kaketsuken | Hoffman La-Roche |
| Pharmaceuticals | Retropep -- Retroscreen |
| RadioTheraCIM -- YM BioSciences | RFB4 (dsFv) PE38 |
| Ramot project No. 1315 -- Ramot | RFI 641 -- American Home Products |
| Ramot project No. K-734A -- Ramot | RFTS -- UAB Research Foundation |
| Ramot project No. K-734B -- Ramot | RG 12986 -- Aventis Pasteur |
| Ranibizumab (Anti-VEGF fragment) -- | RG 83852 -- Aventis Pasteur |
| Genentech | RG-1059 -- RepliGen |
| RANK -- Immunex | rGCR -- NIH |
| ranpirnase -- Alfacell | rGLP-1 -- Restoragen |
| ranpirnase-anti-CD22 MAb -- Alfacell | rGRF -- Restoragen |
| RANTES inhibitor -- Milan | rh Insulin -- Eli Lilly |
| RAPID drug delivery systems -- ARIAD | RHAMM targeting peptides -- Cangene |
| rasburicase -- Sanofi | rHb1.1 -- Baxter Intl. |
| rBPI-21, topical -- XOMA | rhCC10 -- Claragen |
| RC 529 -- Corixa | rhCG -- Serono |
| rCFTR -- Genzyme Transgenics | Rheumatoid arthritis gene therapy |

FIG. 28Y

56/498

| | |
|---|--|
| Rheumatoid arthritis vaccine -- Veterans Affairs Medical Center | SB RA 31012 -- |
| rhLH -- Serono | SC 56929 -- Pharmacia |
| Ribozyme gene therapy -- Genset | SCA binding proteins -- Curis, Enzon |
| Rickettsial vaccine recombinant | scFv(14E1)-ETA Berlex Laboratories, Schering AG |
| RIGScan CR -- Neoprobe | ScFv(FRP5)-ETA -- |
| RIP-3 -- Rigel | ScFv6C6-PE40 -- |
| Rituximab -- Genentech | SCH 55700 -- Celltech |
| RK-0202 -- RxKinetix | Schistosomiasis vaccine -- Glaxo Wellcome/Medeva, Brazil |
| RLT peptide -- Esperion | SCPF -- Advanced Tissue Sciences |
| rM/NEI -- IVAX | scuPA-suPAR complex -- Hadasit |
| rmCRP -- Immtech | SD-9427 -- Pharmacia |
| RN-1001 -- Renovo | SDF-1 -- Ono |
| RN-3 -- Renovo | SDZ 215918 -- Novartis |
| RNAse conjugate -- Immunomedics | SDZ 280125 -- Novartis |
| RO 631908 -- Roche | SDZ 89104 -- Novartis |
| Rotavirus vaccine -- Merck | SDZ ABL 364 -- Novartis |
| RP 431 -- DuPont Pharmaceuticals | SDZ MMA 383 -- Novartis |
| RP-128 -- Resolution | Secretin -- Ferring, Repligen |
| RPE65 gene therapy -- | serine protease inhbs -- Pharis |
| RPR 110173 -- Aventis Pasteur | sermorelin acetate -- Serono |
| RPR 115135 -- Aventis Pasteur | SERP-1 -- Viron |
| RPR 116258A -- Aventis Pasteur | sertenef -- Dainippon |
| rPSGL-Ig -- American Home Products | serum albumin, Recombinant human -- Aventis Behring |
| r-SPC surfactant -- Byk Gulden | serum-derived factor -- Hadasit |
| RSV antibody -- Medimmune | Sevirumab -- Novartis |
| Ruplizumab -- Biogen | SGN 14 -- Seattle Genetics |
| rV-HER-2/neu -- Therion Biologics | SGN 15 -- Seattle Genetics |
| SA 1042 -- Sankyo | SGN 17/19 -- Seattle Genetics |
| sacrosidase -- Orphan Medical | SGN 30 -- Seattle Genetics |
| Sant 7 | SGN-10 -- Seattle Genetics |
| Sargramostim -- Immunex | SGN-11 -- Seattle Genetics |
| saruplase -- Gruenenthal | SH 306 -- DuPont Pharmaceuticals |
| Satumomab -- Cytogen | Shanvac-B -- Shantha |
| SB 1 -- COR Therapeutics | Shigella flexneri vaccine -- Avant, Acambis, Novavax |
| SB 207448 -- GlaxoSmithKline | Shigella sonnei vaccine -- |
| SB 208651 -- GlaxoSmithKline | sICAM-1 -- Boehringer Ingelheim |
| SB 240683 -- GlaxoSmithKline | Silteplase -- Genzyme |
| SB 249415 -- GlaxoSmithKline | |
| SB 249417 -- GlaxoSmithKline | |
| SB 6 -- COR Therapeutics | |

FIG. 28Z

57/498

| | |
|--|--|
| SIV vaccine -- Endocon, Institut Pasteur | Staphylococcus aureus vaccine conjugate -- |
| SK 896 -- Sanwa Kagaku Kenkyusho | Nabi |
| SK-827 -- Sanwa Kagaku Kenkyusho | Staphylococcus therapy -- Tripep |
| Skeletex -- CellFactors | Staphylokinase -- Biovation, Prothera, |
| SKF 106160 -- GlaxoSmithKline | Thrombogenetics |
| S-nitroso-AR545C -- | Streptococcal A vaccine -- M6 |
| SNTP -- Active Biotech | Pharmaceuticals, North American Vaccine |
| somatomedin-1 -- GroPep, Mitsubishi- | Streptococcal B vaccine -- Microscience |
| Tokyo, NIH | Streptococcal B vaccine recombinant -- |
| somatomedin-1 carrier protein -- Insmed | Biochem Vaccines |
| somatostatin -- Ferring | Streptococcus pyogenes vaccine |
| Somatotropin/ | STRL-33 -- NIH |
| Human Growth Hormone -- Bio-Tech. | Subalin -- SRC VB VECTOR |
| General, Eli Lilly | SUIS -- United Biomedical |
| somatropin -- Bio-Tech. General, Alkermes, | SUIS-LHRH -- United Biomedical |
| ProLease, Aventis Behring, Biovector, | SUN-E3001 -- Suntory |
| Cangene, Dong-A, Eli Lilly, Emisphere, | super high affinity monoclonal antibodies -- |
| Enact, Genentech, Genzyme Transgenics, | YM BioSciences |
| Grandis/InfiMed, CSL, InfiMed, MacroMed, | Superoxide dismutase -- Chiron, Enzon, |
| Novartis, Novo Nordisk, Pharmacia | Ube Industries, Bio-Tech, Yeda |
| Serono, TranXenoGen | superoxide dismutase-2 -- OXIS |
| somatropin derivative -- Schering AG | suppressin -- UAB Research Foundation |
| somatropin, AIR -- Eli Lilly | SY-161-P5 -- ThromboGenics |
| Somatropin, inhaled -- Eli Lilly/Alkermes | SY-162 -- ThromboGenics |
| somatropin, Kabi -- Pharmacia | Systemic lupus erythematosus vaccine -- |
| somatropin, Orasome -- Novo Nordisk | MedClone/VivoRx |
| Sonermin -- Dainippon Pharmaceutical | T cell receptor peptides -- Xoma |
| SP(V5.2)C -- Supertek | T cell receptor peptide vaccine |
| SPf66 | T4N5 liposomes -- AGI Dermatics |
| sphingomyelinase -- Genzyme | TACI, soluble -- ZymoGenetics |
| SR 29001 -- Sanofi | targeted apoptosis -- Antisoma |
| SR 41476 -- Sanofi | tasonermin -- Boehringer Ingelheim |
| SR-29001 -- Sanofi | TASP |
| SS1(dsFV)-PE38 -- NeoPharm | TASP-V |
| β 2 microglobulin -- Avidex | Tat peptide analogues -- NIH |
| β 2-microglobulin fusion proteins -- NIH | TBP I -- Yeda |
| β -amyloid peptides -- CeNeS | TBP II |
| β -defensin -- Pharis | TBV25H -- NIH |
| Staphylococcus aureus infections -- | Tc 99m ior cea1 -- Center of Molecular |
| Inhibitex/ZLB | Immunology |
| | Tc 99m P 748 -- Diatide |

FIG. 28AA

58/498

| | |
|--|---|
| Tc 99m votumumab -- Intracell | Tissue factor -- Genentech |
| Tc-99m rh-Annexin V -- Theseus Imaging | Tissue factor pathway inhibitor |
| teceleukin -- Biogen | TJN-135 -- Tsumura |
| tenecteplase -- Genentech | TM 27 -- Avant |
| Teriparatide -- Armour Pharmaceuticals, Asahi Kasei, Eli Lilly | TM 29 -- Avant |
| terlipressin -- Ferring | TMC-151 -- Tanabe Seiyaku |
| testisin -- AMRAD | TNF tumour necrosis factor -- Asahi Kasei |
| Tetrafibricin -- Roche | TNF Alpha -- CytImmune |
| TFPI -- EntreMed | TNF antibody -- Johnson & Johnson |
| tgD-IL-2 -- Takeda | TNF binding protein -- Amgen |
| TGF-Alpha -- ZymoGenetics | TNF degradation product -- Oncotech |
| TGF- β -- Kolon | TNF receptor -- Immunex |
| TGF- β 2 -- Insmad | TNF receptor 1, soluble -- Amgen |
| TGF- β 3 -- OSI | TNF Tumour necrosis factor-alpha -- Asahi Kasei, Genetech, Mochida |
| Thalassaemia gene therapy -- Crucell | TNF-Alpha inhibitor -- Tripep |
| TheraCIM-h-R3 -- Center of Molecular Immunology, YM BioSciences | TNFR:Fc gene therapy -- Targeted Genetics |
| Theradigm-HBV -- Epimmune | TNF-SAM2 |
| Theradigm-HPV -- Epimmune | Tolerimab -- Innogenetics |
| Theradigm-malaria -- Epimmune | Toxoplasma gondii vaccine -- GlaxoSmithKline |
| Theradigm-melanoma -- Epimmune | TP 9201 -- Telios |
| TheraFab -- Antisoma | TP10 -- Avant |
| ThGRF 1-29 -- Theratechnologies | TP20 -- Avant |
| ThGRF 1-44 -- Theratechnologies | tPA -- Centocor |
| Thrombin receptor activating peptide -- Abbott | trafermin -- Scios |
| thrombomodulin -- Iowa, Novocastra | TRAIL/Apo2L -- Immunex |
| Thrombopoietin -- Dragon Pharmaceuticals, Genentech | TRAIL-R1 MAb -- Cambridge Antibody Technologies |
| thrombopoietin, Pliva -- Recepton | transferrin-binding proteins -- CAMR |
| Thrombospondin 2 -- | Transforming growth factor-beta-1 -- Genentech |
| thrombostatin -- Thromgen | transport protein -- Genesis |
| thymalfasin -- SciClone | Trastuzumab -- Genetech |
| thymocartin -- Gedeon Richter | TRH -- Ferring |
| thymosin Alpha1 -- NIH | Triabin -- Schering AG |
| thyroid stimulating hormone -- Genzyme | Triconal |
| tICAM-1 -- Bayer | Triflavin |
| Tick anticoagulant peptide -- Merck | troponin I -- Boston Life Sciences |
| TIF -- Xoma | TRP-2 ^A -- NIH |
| Tifacogin -- Chiron, NIS, Pharmacia | trypsin inhibitor -- Mochida |

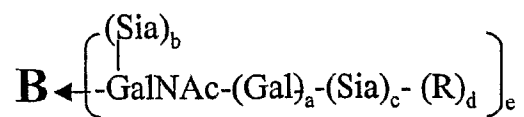
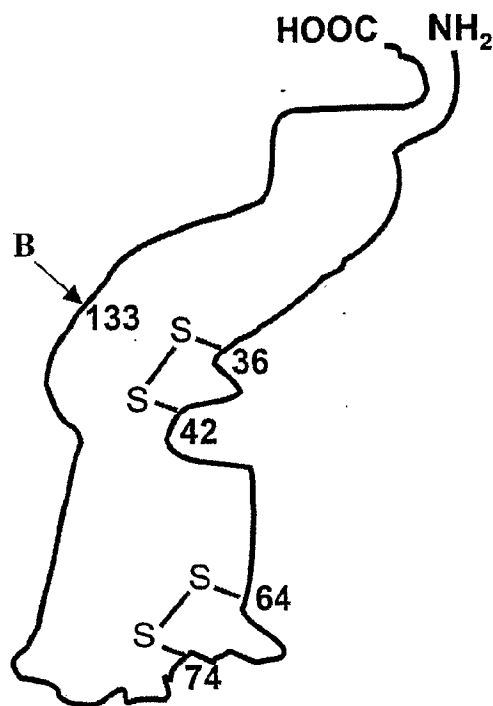
FIG. 28BB

59/498

| | |
|---|--|
| TSP-1 gene therapy -- | Vascular endothelial growth factors -- R&D |
| TT-232 | Systems |
| TTS-CD2 -- Active Biotech | vascular targeting agents -- Peregrine |
| Tuberculosis vaccine -- Aventis Pasteur, | vasopermeation enhancement agents -- |
| Genesis | Peregrine |
| Tumor Targeted Superantigens -- Active | vasostatin -- NIH |
| Biotech -- Pharmacia | VCL -- Bio-Tech. General |
| tumour vaccines -- PhotoCure | VEGF -- Genentech, Scios |
| tumour-activated prodrug antibody | VEGF inhibitor -- Chugai |
| conjugates -- Millennium/ImmunoGen | VEGF-2 -- Human Genome Sciences |
| tumstatin -- ILEX | VEGF-Trap -- Regeneron |
| Tuvirumab -- Novartis | viscumin, recombinant -- Madaus |
| TV-4710 -- Teva | Vitaxin |
| TWEAK receptor -- Immunex | Vitrage -- ISTA Pharmaceuticals |
| TXU-PAP | West Nile virus vaccine -- Bavarian Nordic |
| TY-10721 -- TOA Eiyo | WP 652 |
| Type I diabetes vaccine -- Research Corp | WT1 vaccine -- Corixa |
| Typhoid vaccine CVD 908 | WX-293 -- Willex BioTech. |
| U 143677 -- Pharmacia | WX-360 -- Willex BioTech. |
| U 81749 -- Pharmacia | WX-UK1 -- Willex BioTech. |
| UA 1248 -- Arizona | XMP-500 -- XOMA |
| UGIF -- Sheffield | XomaZyme-791 -- XOMA |
| UIC 2 | XTL 001 -- XTL Biopharmaceuticals |
| UK 101 | XTL 002 -- XTL Biopharmaceuticals |
| UK-279276 -- Corvas Intl. | yeast delivery system -- GlobelImmune |
| urodilatin -- Pharis | Yersinia pestis vaccine |
| urofollitrophin -- Serono | YIGSR-Stealth -- Johnson & Johnson |
| Urokinase -- Abbott | Yisum Project No. D-0460 -- Yisum |
| uteroferin-- Pepgen | YM 207 -- Yamanouchi |
| V 20 -- GLYCODESIGN | YM 337 -- Protein Design Labs |
| V2 vasopressin receptor gene therapy | Yttrium-90 labelled biotin |
| vaccines -- Active Biotech | Yttrium-90-labeled anti-CEA MAb T84.66 -- |
| Varicella zoster glycoprotein vaccine -- | ZD 0490 -- AstraZeneca |
| Research Corporation Technologies | ziconotide -- Elan |
| Varicella zoster virus vaccine live -- Cantab | ZK 157138 -- Berlex Laboratories |
| Pharmaceuticals | Zolimomab aritox |
| Vascular endothelial growth factor -- | Zorcell -- Immune Response |
| Genentech, University of California | ZRXL peptides -- Novartis |

FIG. 28CC

60/498



a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, sialyl or
oligosialyl

FIG. 29A

61/498

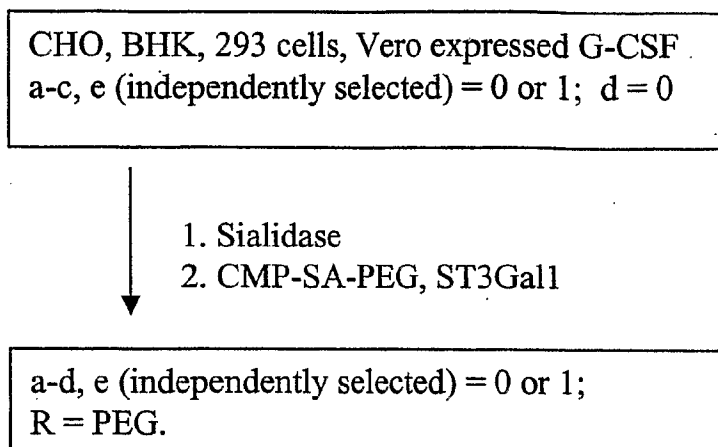


FIG. 29B

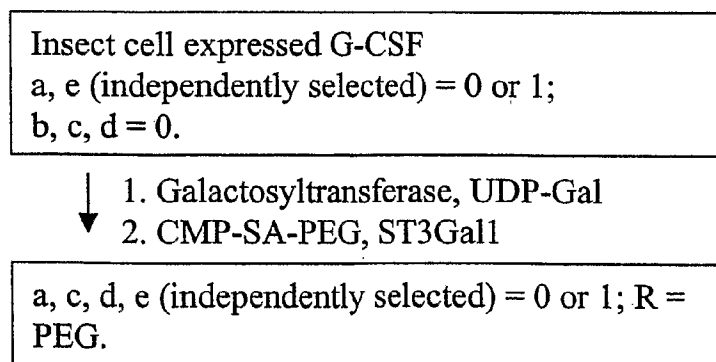


FIG. 29C

62/498

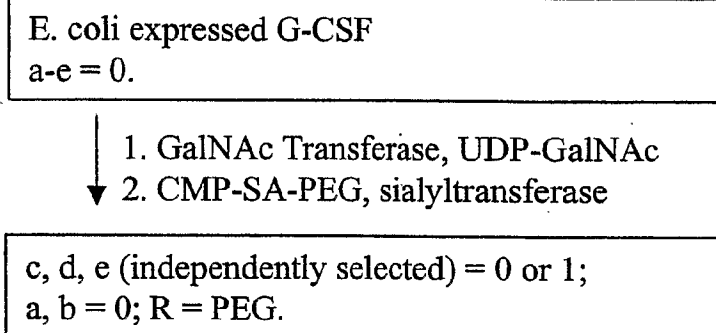


FIG. 29D

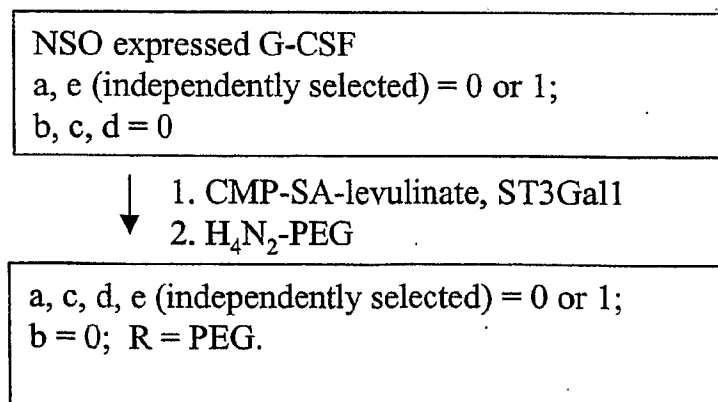


FIG. 29E

63/498

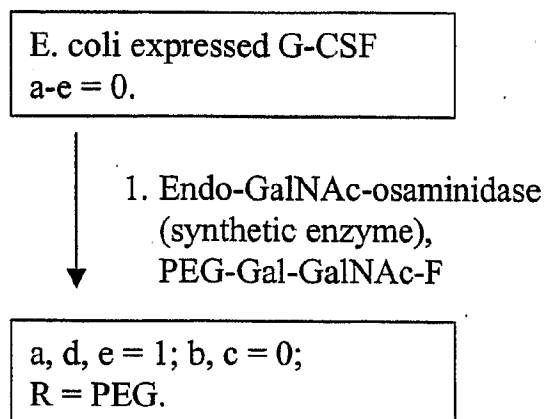


FIG. 29F

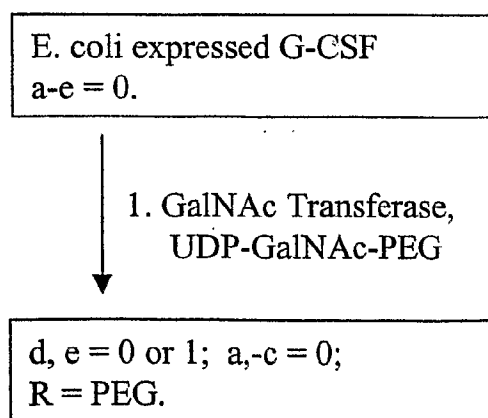
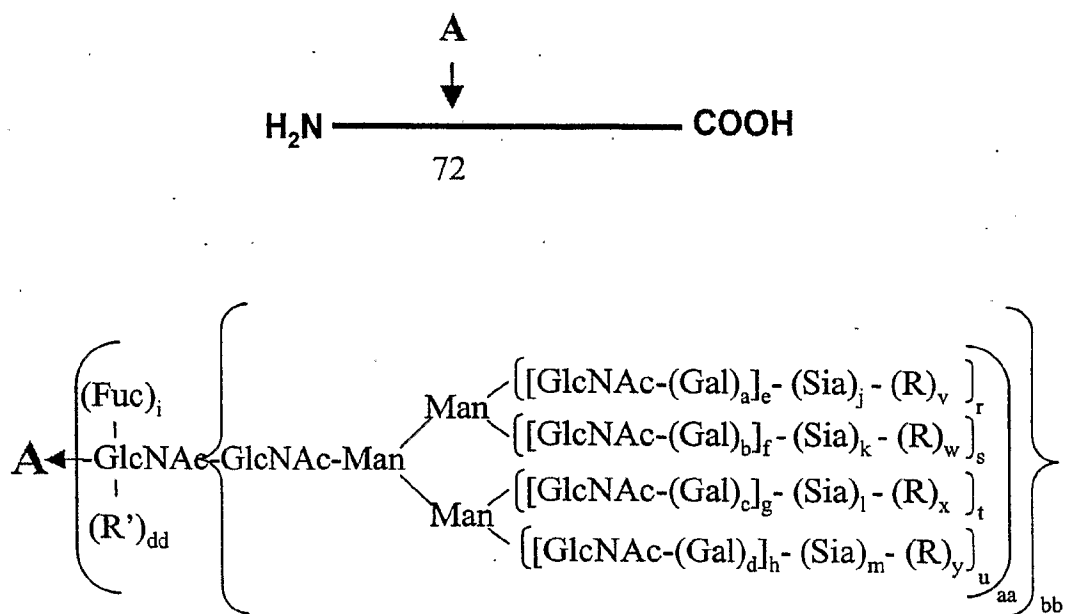


FIG. 29G

64/498



a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 30A

65/498

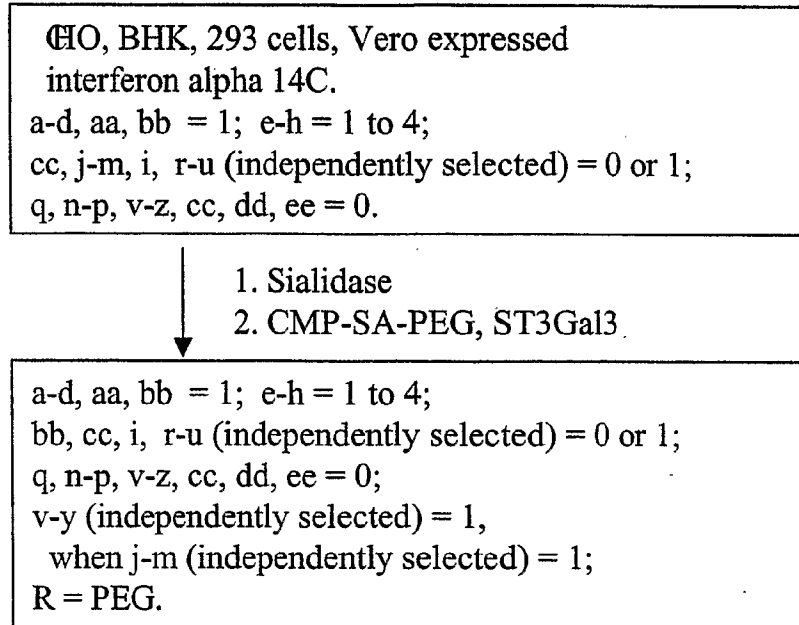


FIG. 30B

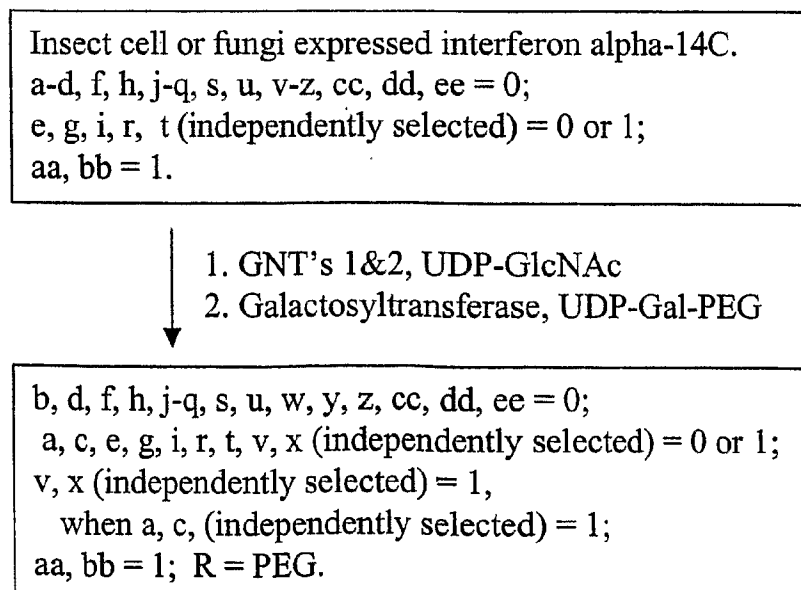


FIG. 30C

66/498

Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

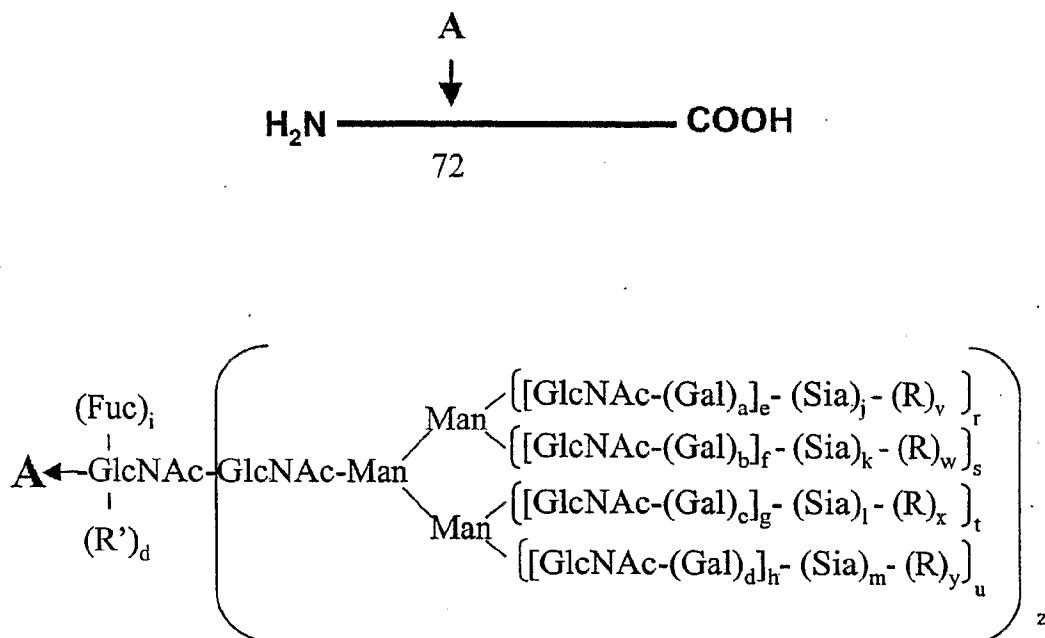
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 30D

67/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 30E

68/498

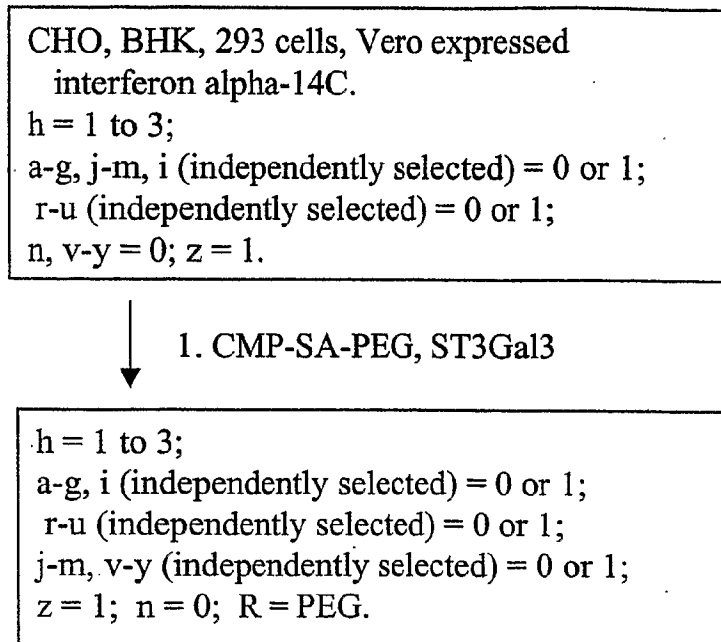


FIG. 30F

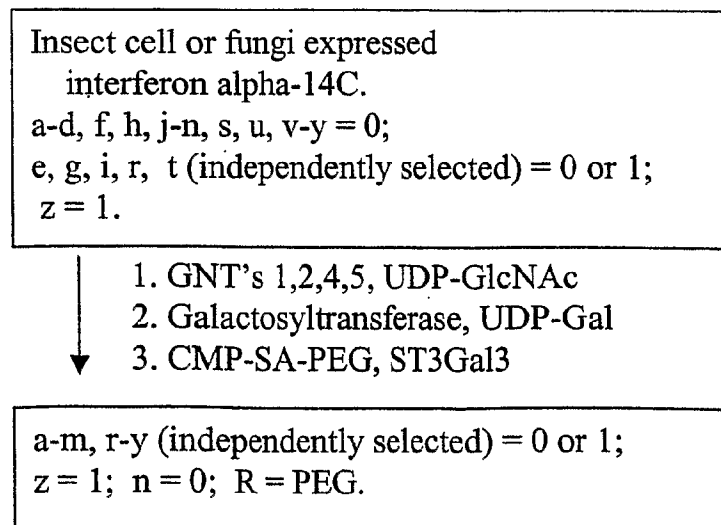


FIG. 30G

69/498

Yeast expressed interferon alpha-14C.
 a-n = 0; r-y (independently selected) = 0 to 1;
 z = 1; R (branched or linear) = Man,
 oligomannose.

1. mannosidases
2. GNT's 1,2,4,5, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal
- ▼ 4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 30H

NSO expressed interferon alpha 14C.
 a-i, r-u (independently selected) = 0 or 1;
 j-m, n, v-y = 0; z = 1.

1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
- ▼ 2. H₄N₂-PEG

a-i, j-m, r-y (independently selected) = 0 or 1;
 n = 0; z = 1; R = PEG.

FIG. 30I

70/498

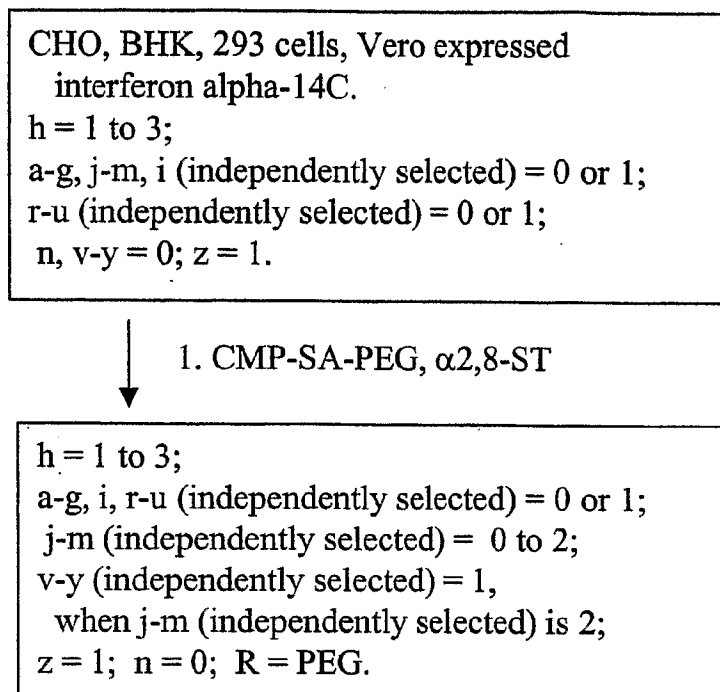


FIG. 30J

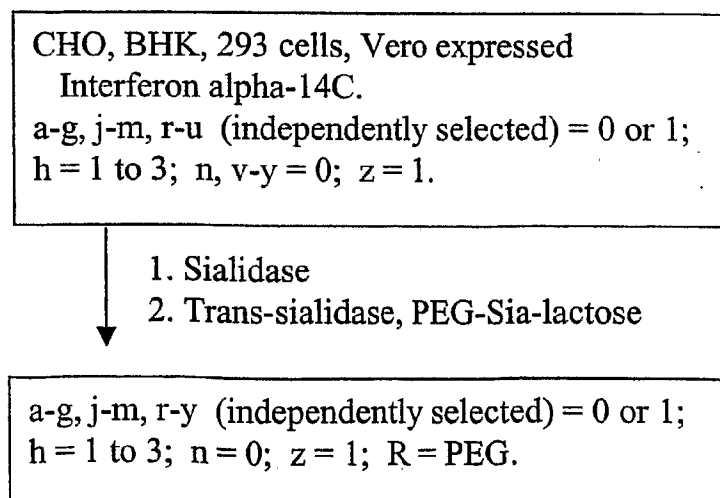


FIG. 30K

71/498

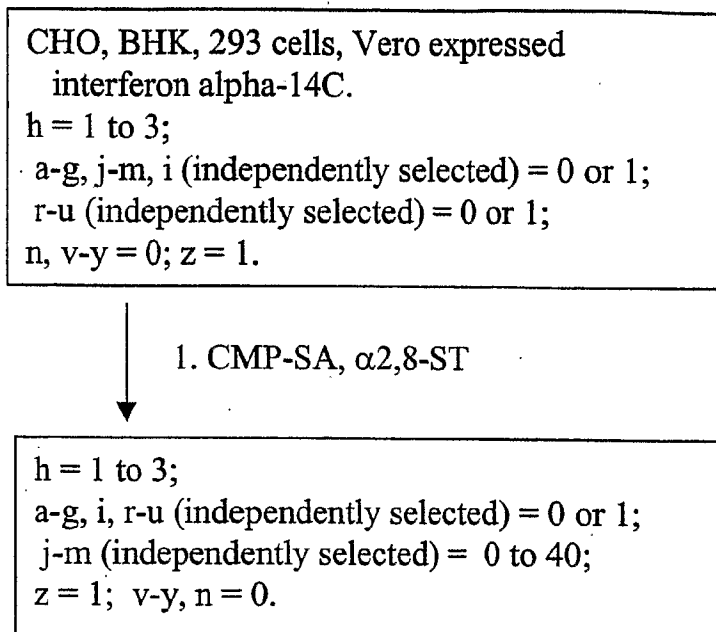


FIG. 30L

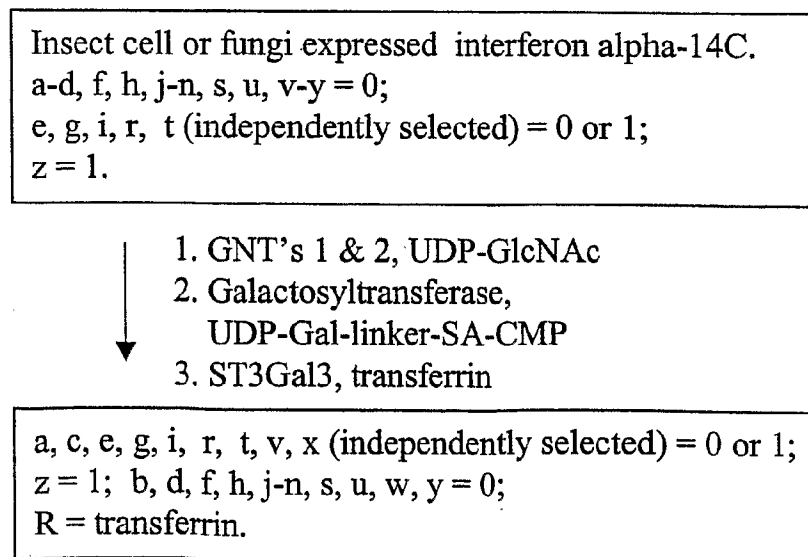


FIG. 30M

72/498

Insect cell or fungi expressed interferon alpha-14C.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
 2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
 3. ST3Gal3, transferrin

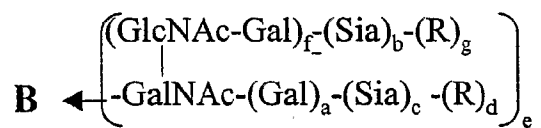
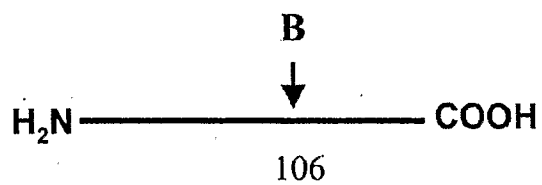
i (independently selected) = 0 or 1;

a-h, j-m, r-z = 0;

n = 1; R' = -Gal-linker-transferrin.

FIG. 30N

73/498



a-c, e, f (independently selected) = 0 or 1;
 d, g = 0; R = polymer, glycoconjugate.

FIG. 300

74/498

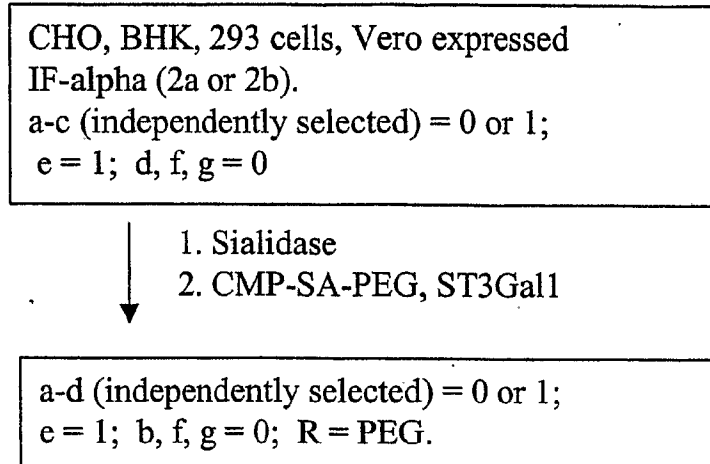


FIG. 30P

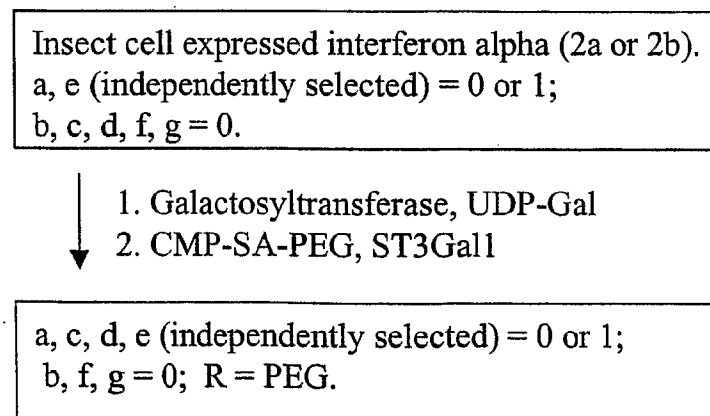


FIG. 30Q

75/498

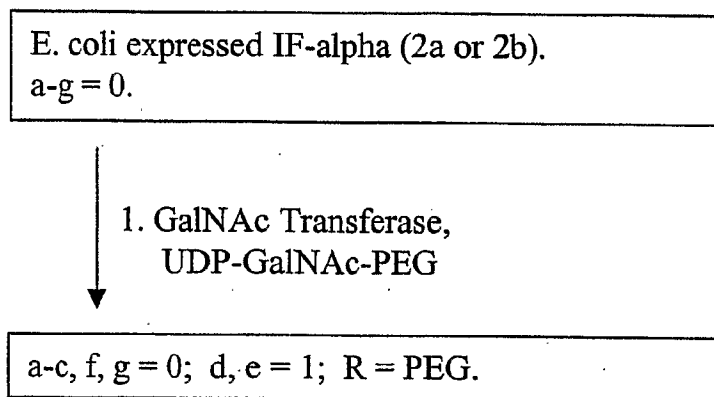


FIG. 30R

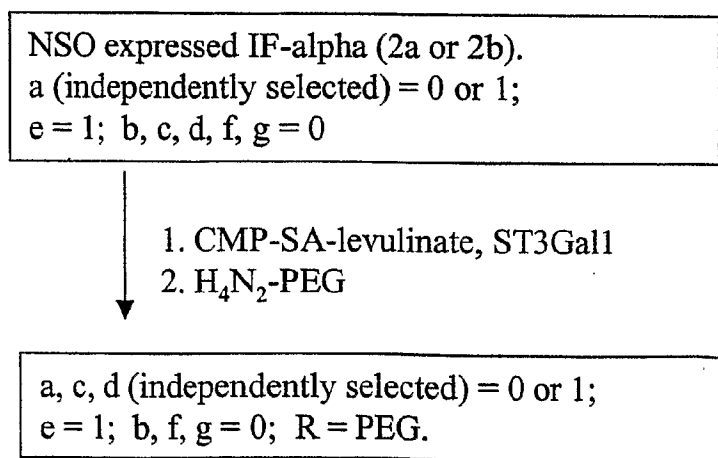


FIG. 30S

76/498

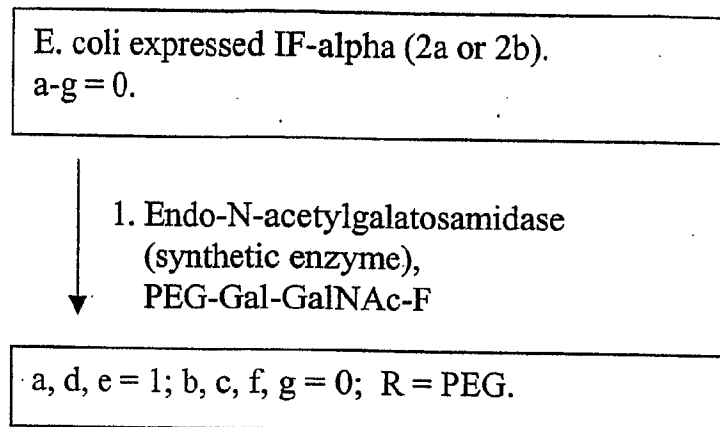


FIG. 30T

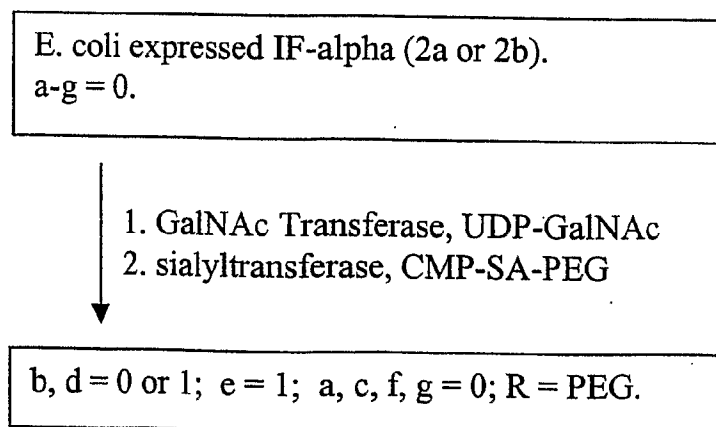


FIG. 30U

77/498

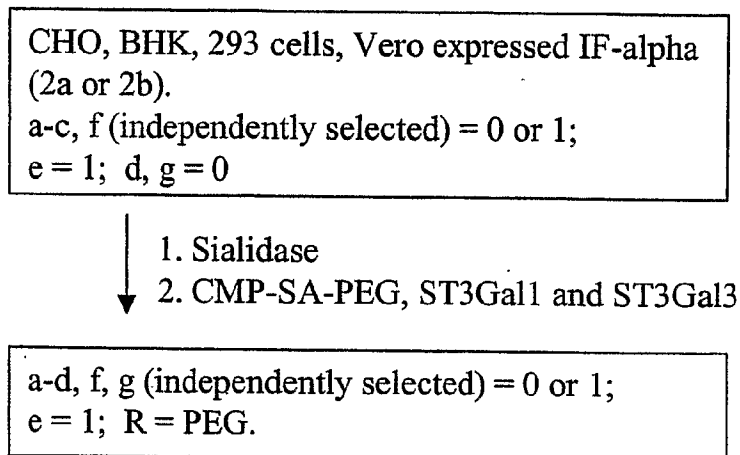


FIG. 30V

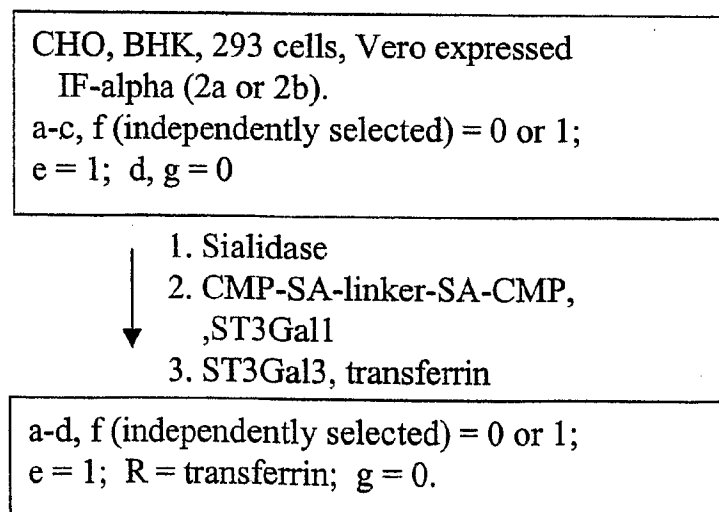


FIG. 30W

79/498

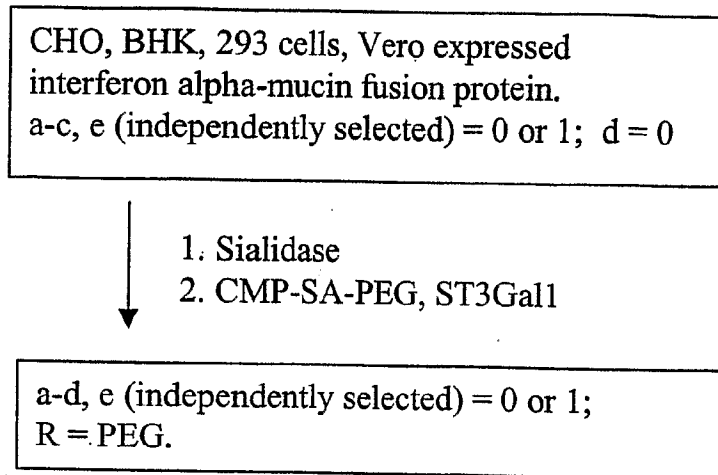


FIG. 30Y

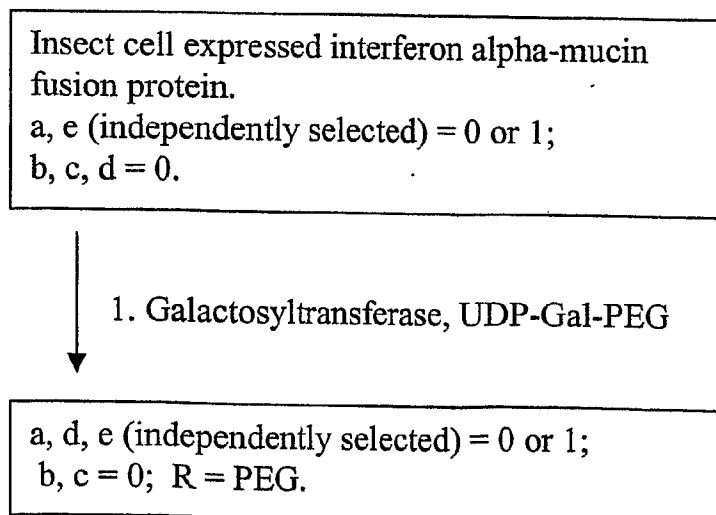


FIG. 30Z

80/498

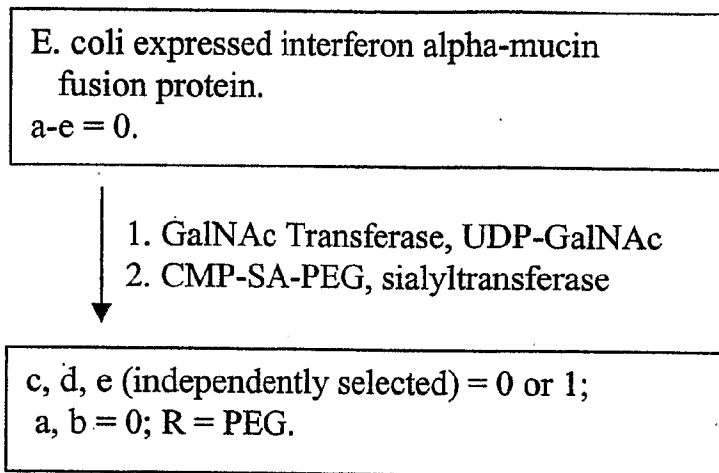
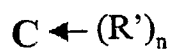
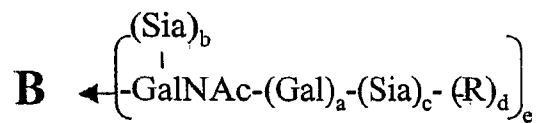
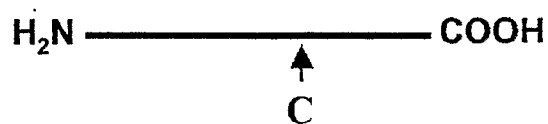
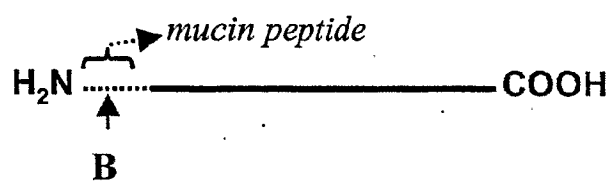
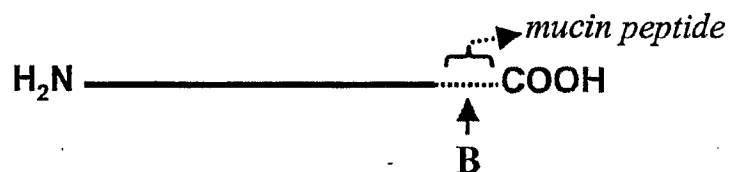


FIG. 30AA

81/498



a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 30BB

82/498

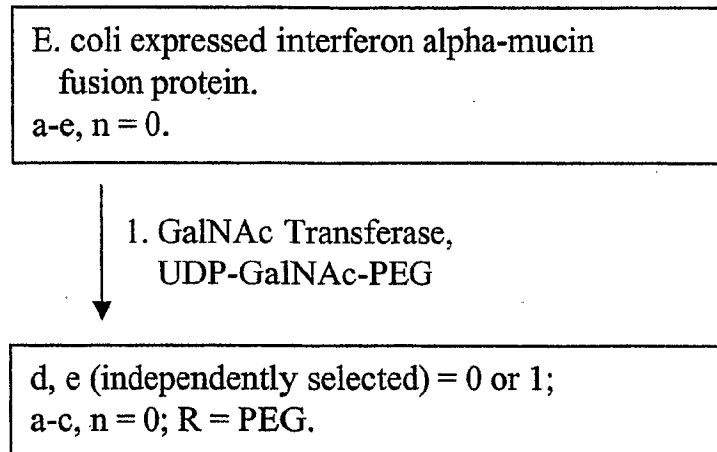


FIG. 30CC

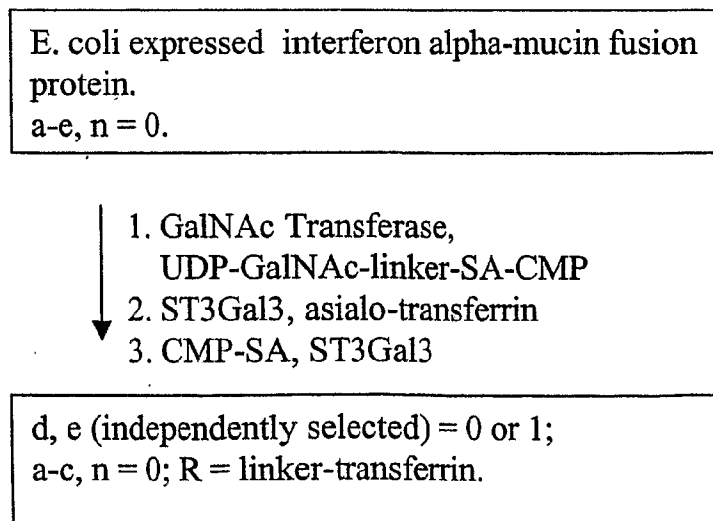


FIG. 30DD

83/498

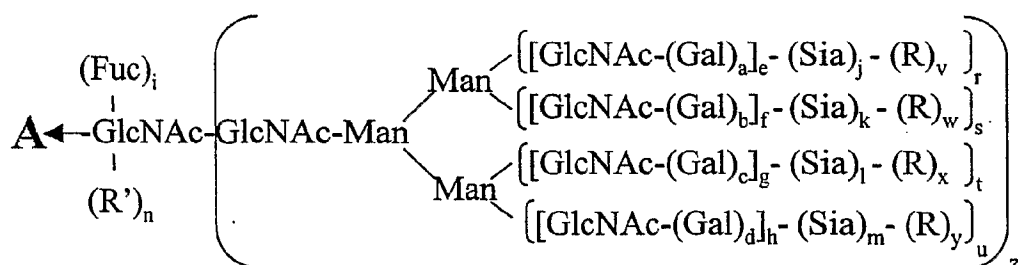
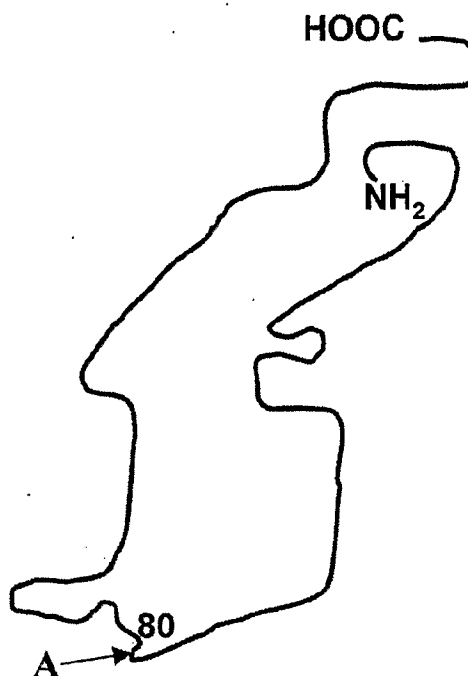
E. coli expressed Interferon alpha (no fusion).
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
2. ST3Gal3, transferrin

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 30EE

84/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 31A

85/498

CHO, BHK, 293 cells, Vero expressed IF-beta
 h = 1 to 3;
 a-g, j-m, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;
 a-g, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 31B

Insect cell expressed IF-beta
 a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, r, t (independently selected) = 0 or 1;
 z = 1.



1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
2. CMP-SA-PEG, ST3Gal3,
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 j, l, v, x (independently selected) = 0 or 1;
 z = 1; R = PEG.

FIG. 31C

86/498

Yeast expressed IF-beta

a-n = 0; z = 1;

r-y (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed IF-beta

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

- ↓
1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 31E

87/498

Insect cell expressed IF-beta
 a-d, f, h, j-n, s, u, v-y = 0; e, g, i, r, t
 (independently selected) = 0 or 1; z = 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 31F

Yeast expressed IF-beta
 a-n = 0; z = 1;
 r-y (independently selected) = 0 to 1;
 R (branched or linear) = Man, oligomannose.

- ↓
1. mannosidases
 2. GNT's 1,2,4,5, UDP-GlcNAc
 3. Galactosyltransferase, UDP-Gal
 4. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 31G

88/498

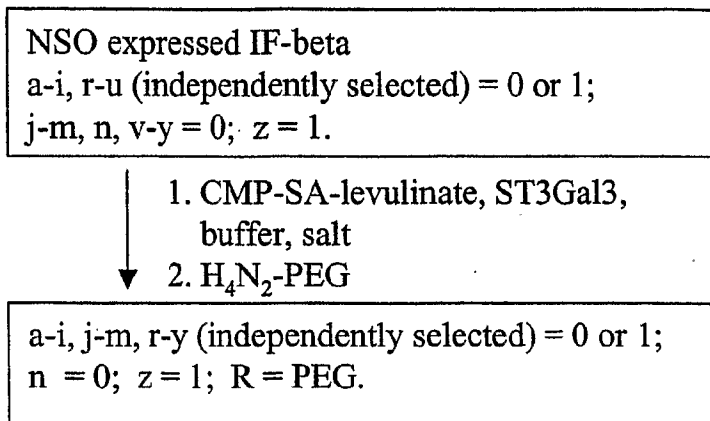


FIG. 31H

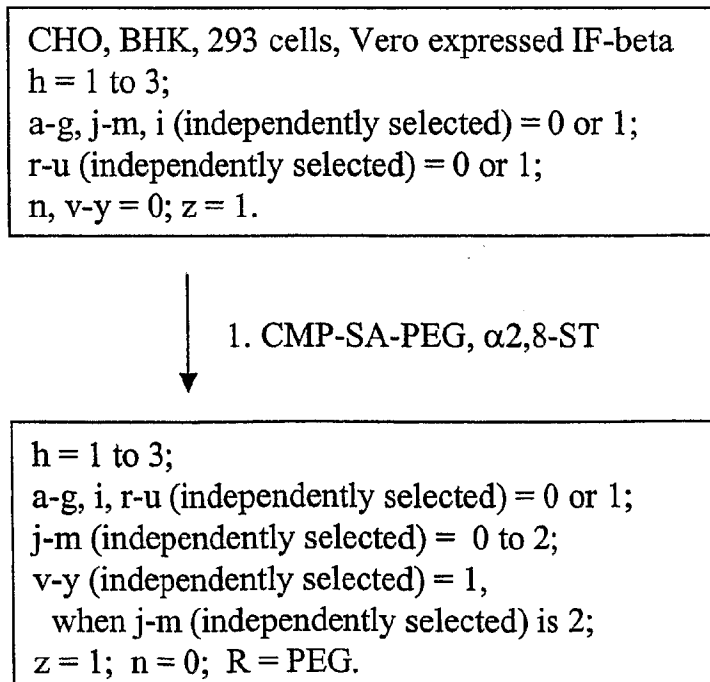


FIG. 31I

89/498

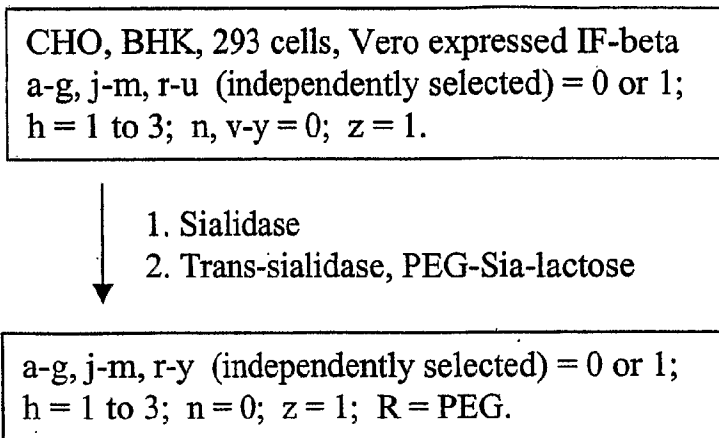


FIG. 31J

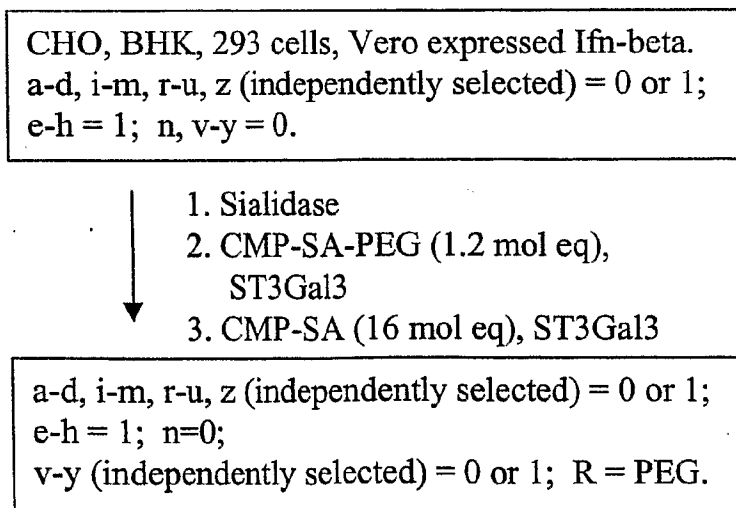


FIG. 31K

90/498

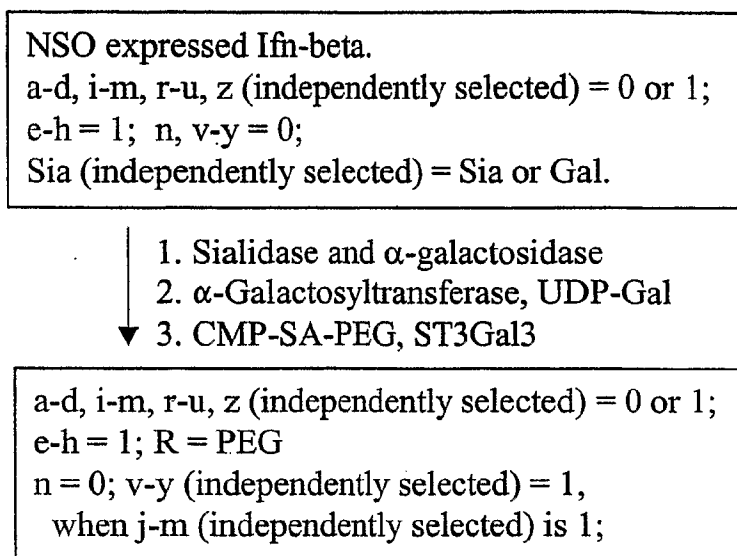


FIG. 31L

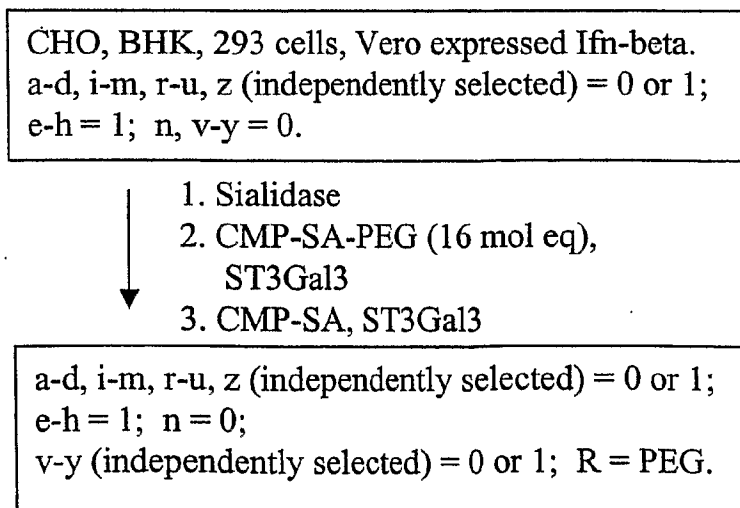


FIG. 31M

91/498

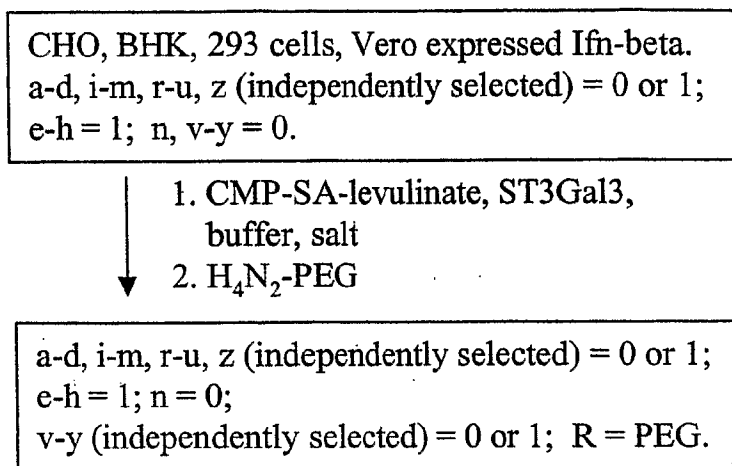


FIG. 31N

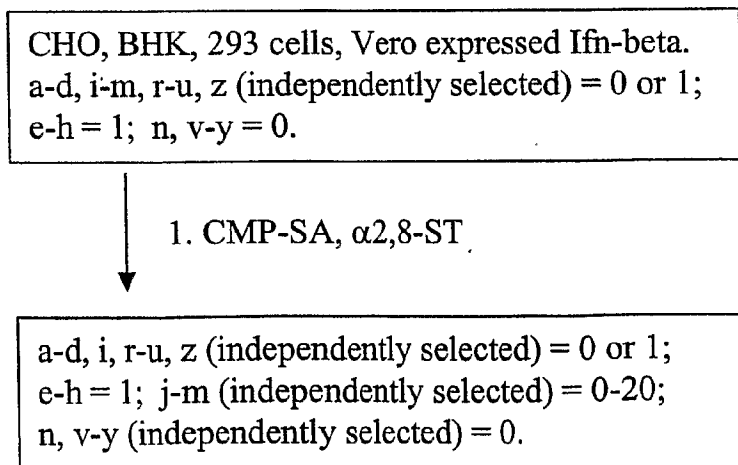
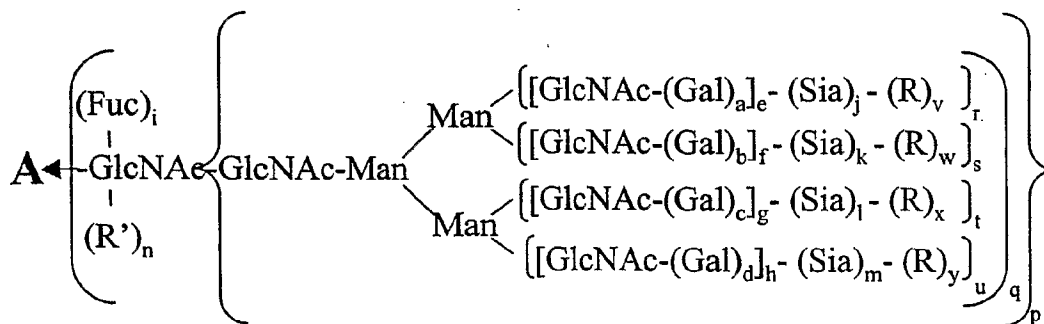
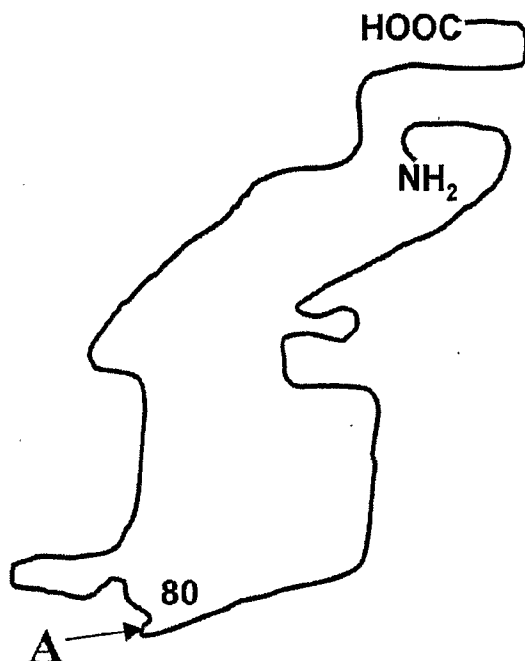


FIG. 31O

92/498



a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group;

R' = H, glycosyl group, modifying group,
glycoconjugate.

FIG. 31P

93/498

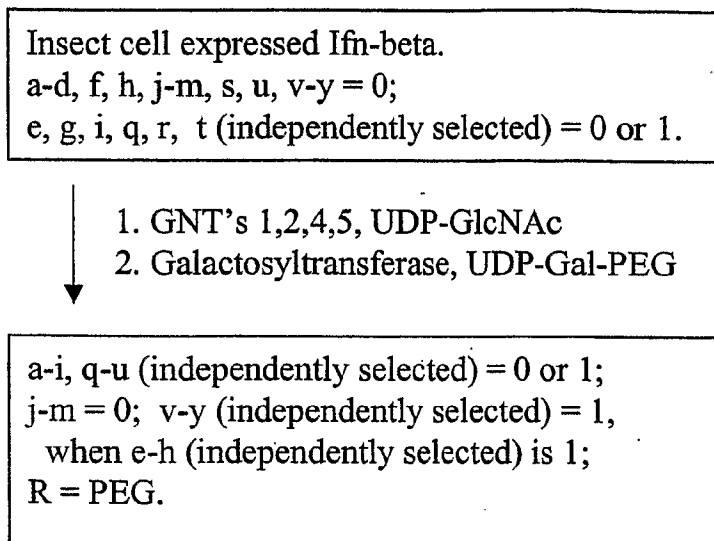


FIG. 31Q

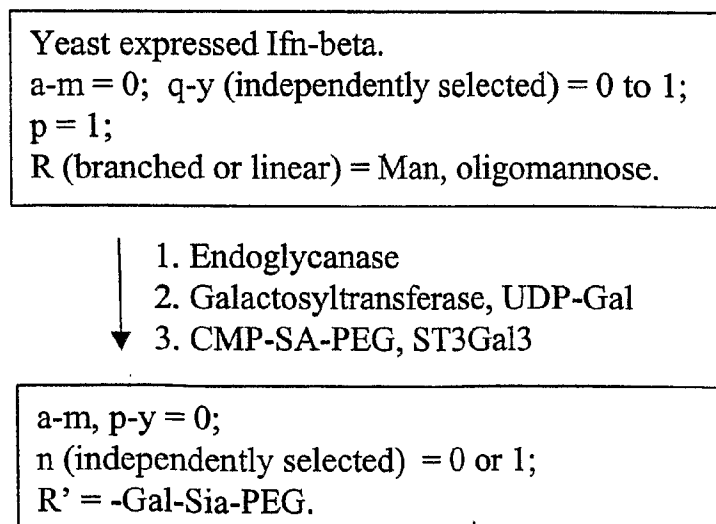


FIG. 31R

94/498

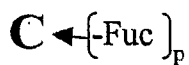
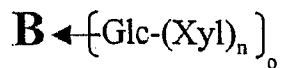
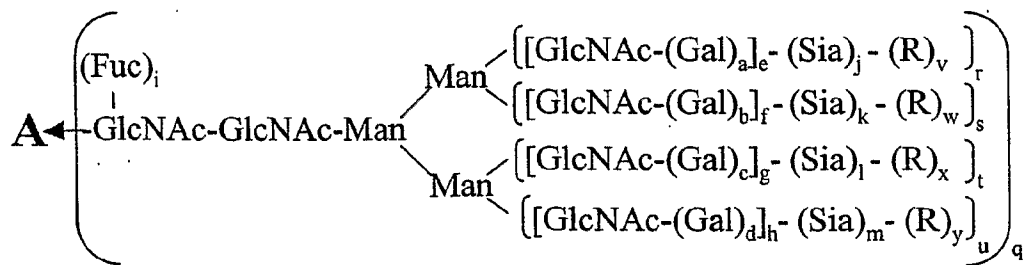
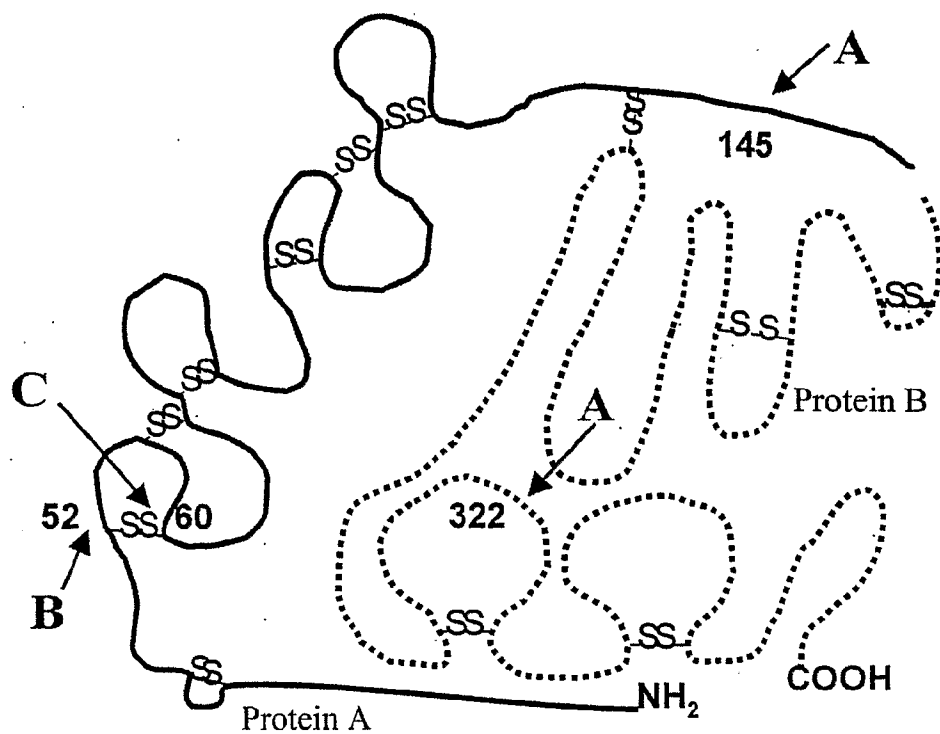
CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 31S

95/498



a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A..

FIG. 32A

96/498

BHK expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mole eq),
ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
v, x, (independently selected) = 1,
when j, l (respectively, independently selected) is 1;
R = PEG.

FIG. 32B

CHO, BHK, 293 cells, Vero expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mole eq),
ST3Gal3
 3. CMP-SA (8 mol eq), ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
v or x, (independently selected) = 1,
when j or l, (respectively, independently selected) is 1;
R = PEG.

FIG. 32C

97/498

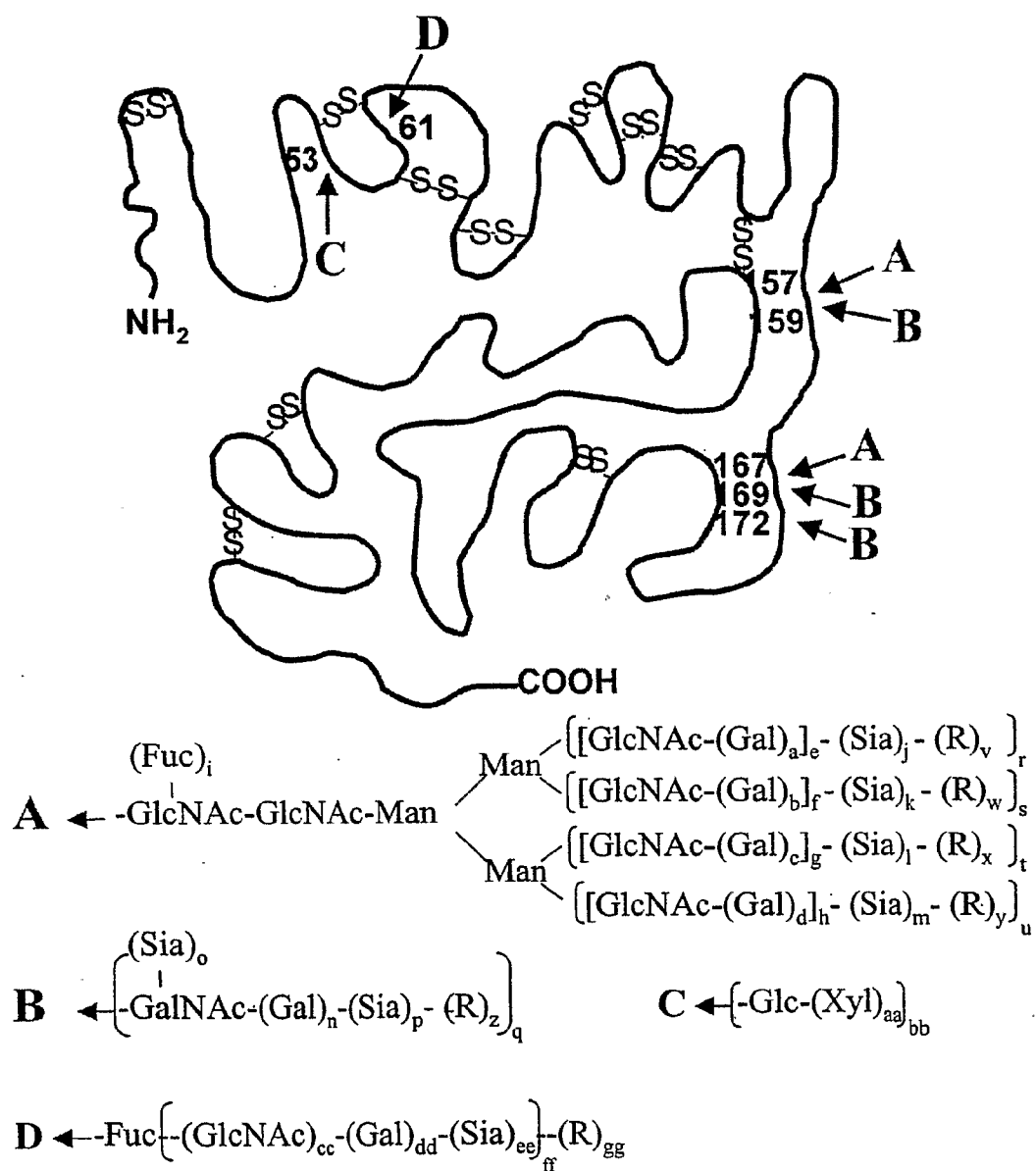
NSO expressed Factor VII or VIIa
a--u (independently selected) = 0 or 1;
v-y = 0; n = 0-4;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;
n = 0-4; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
Sia = Sia; R = PEG.

FIG. 32D

98/498



a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 33A

99/498

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 R = PEG.

FIG. 33B

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3
3. ST3Gal1, CMP-SA

a-d, n, p, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 o, z = 0; R = PEG.

FIG. 33C

100/498

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

- ↓
1. sialidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA, ST3Gal3
 - ↓
 4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1; R = PEG;
 o, v-y, gg = 0;
 j-m, p, ee (independently selected) = 0 or 1, but when
 p = 1, z = 1.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

↓ CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1; R = PEG;
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =
 0 or 1.

FIG. 33E

101/498

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 33F

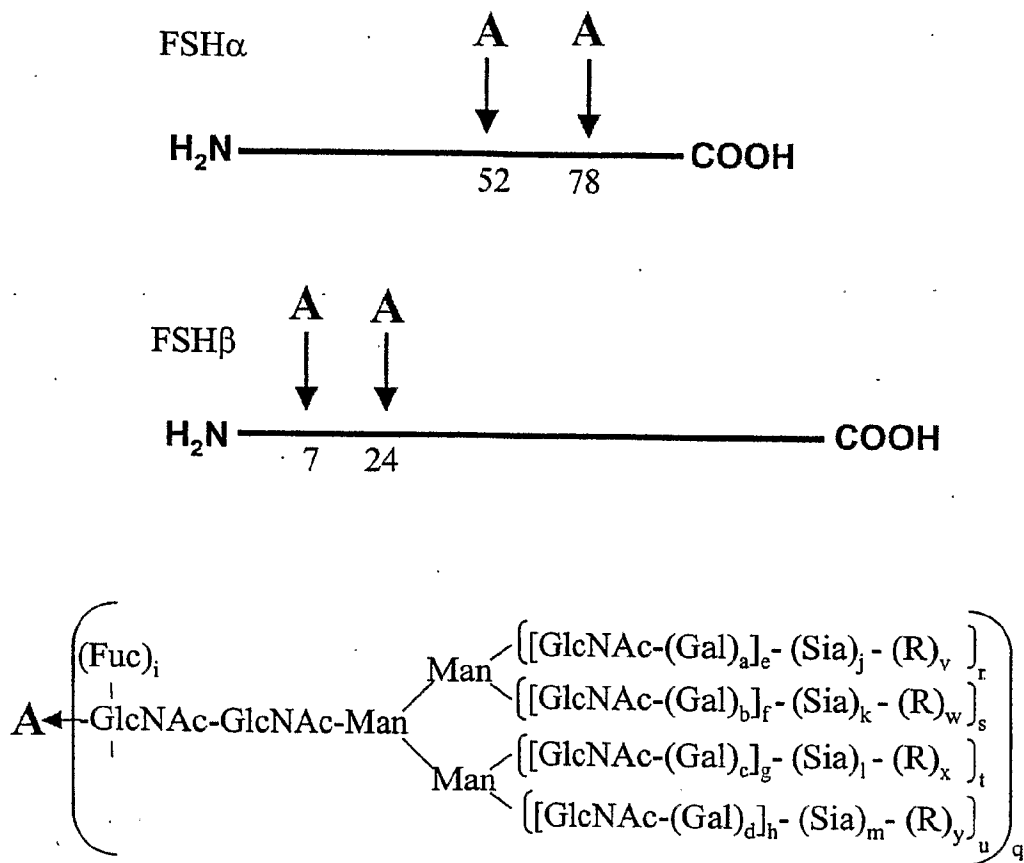
CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1;
 e-h, aa = 1 to 4;
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG, α 2,8-ST

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee (independently selected) = 0 to 2;
 v-y, gg (independently selected) = 1, when j-m
 (independently selected) is 2;

FIG. 33G

102/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 34A

103/498

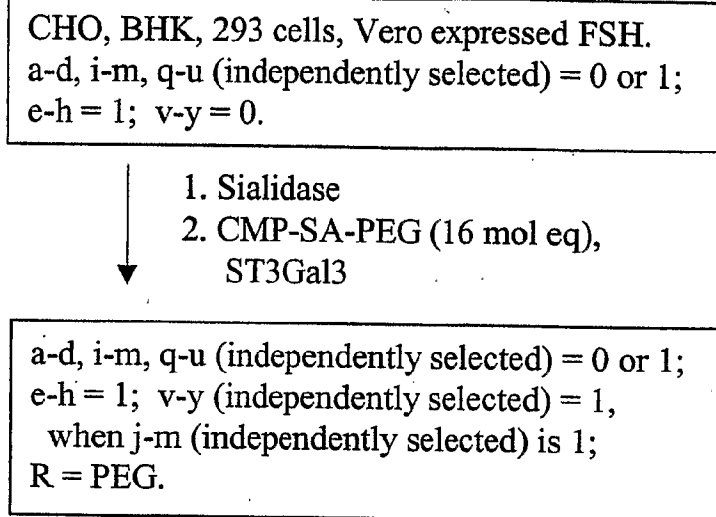


FIG. 34B

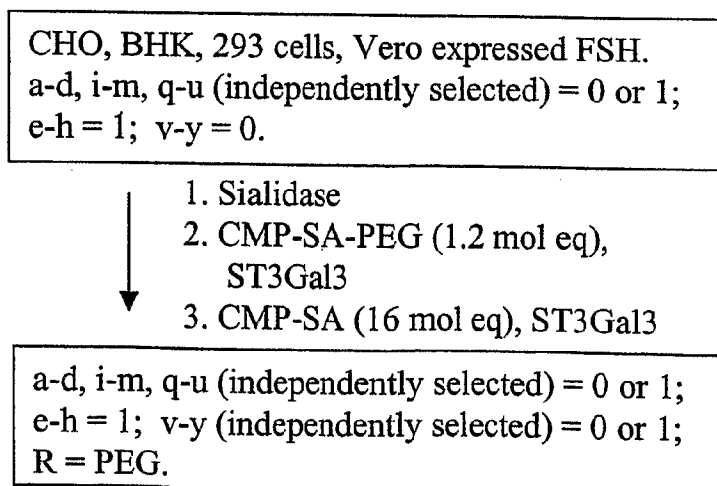


FIG. 34C

104/498

NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ↓ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 34D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ↓ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 34E

105/498

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 34F

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 34G

106/498

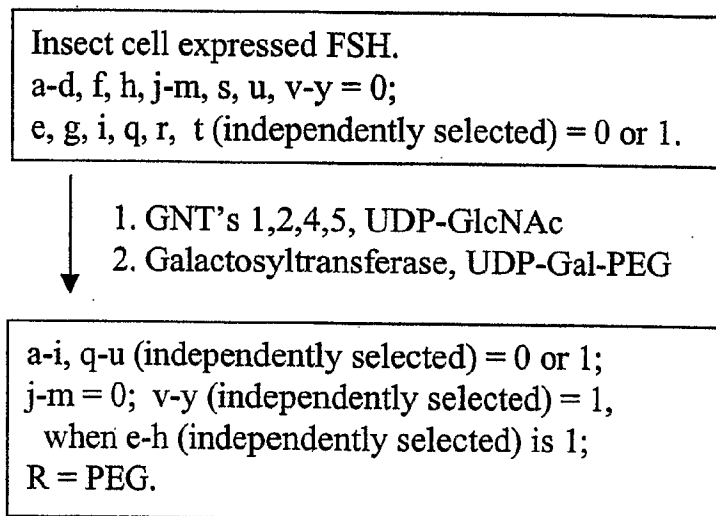


FIG. 34H

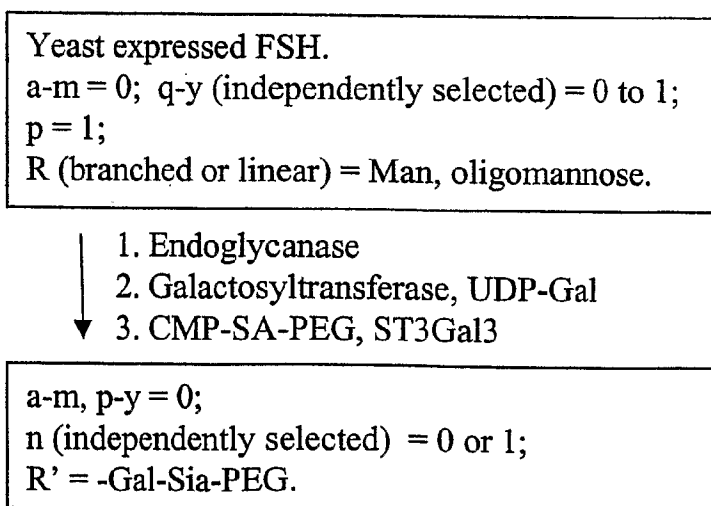


FIG. 34I

107/498

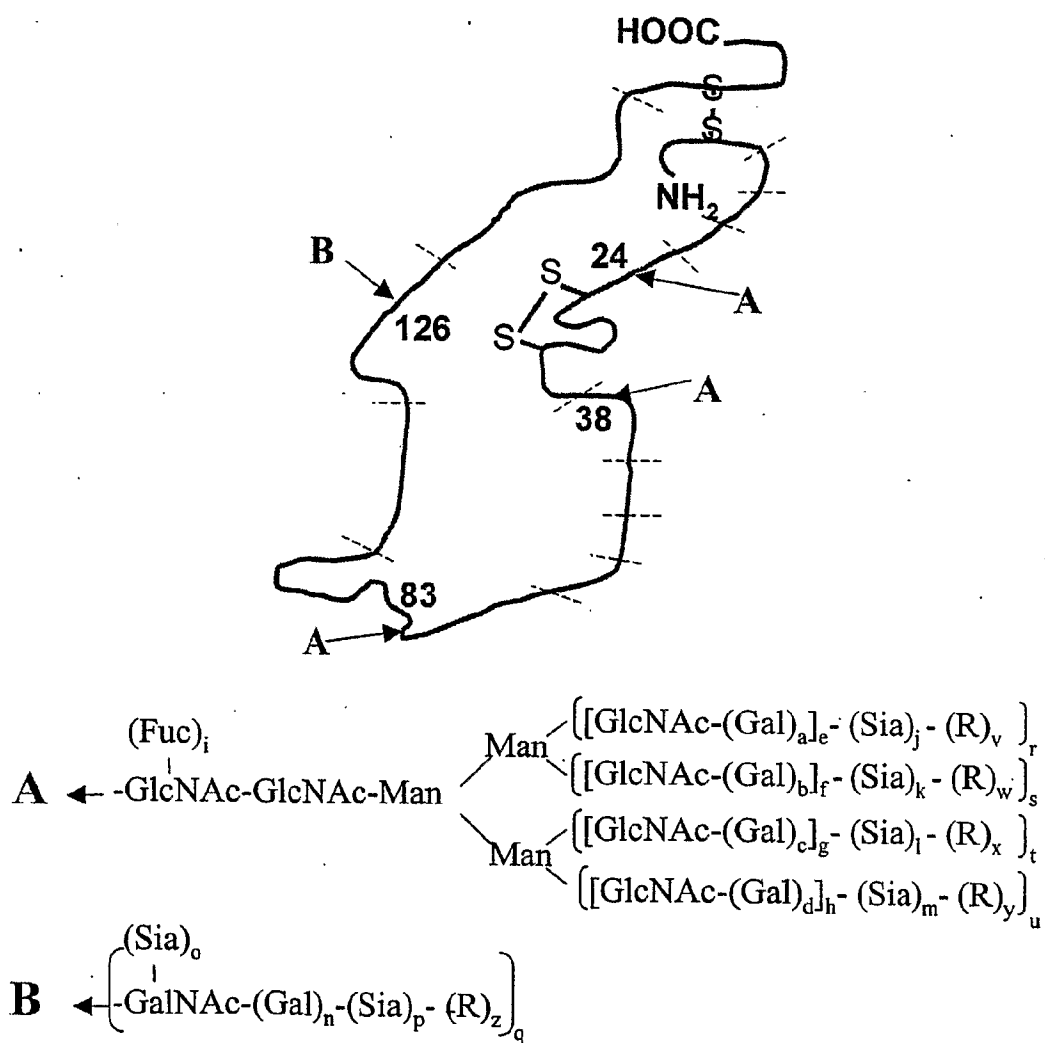
CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated chorionic gonadrophin (CG) produced in CHO.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-CG.

FIG. 34J

108/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35A

109/498

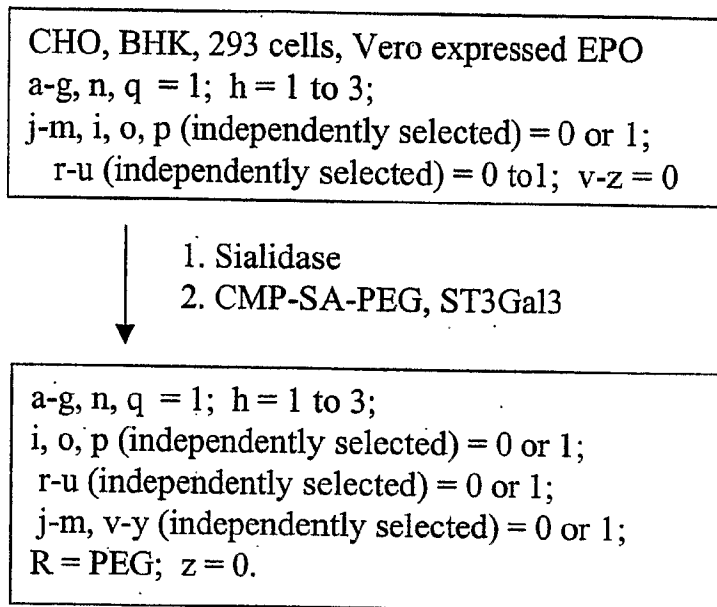


FIG. 35B

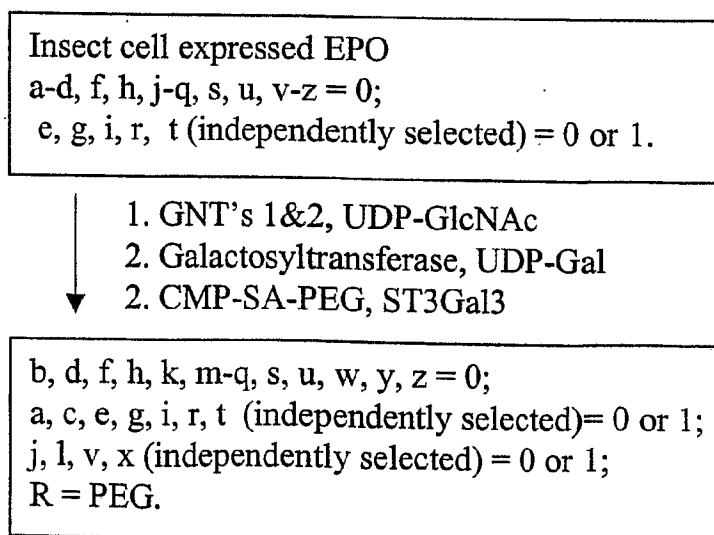


FIG. 35C

110/498

CHO, BHK, 293 cells, Vero expressed EPO
 a-q, r-u (independently selected) = 0 or 1;
 v-z = 0.

- ↓
1. sialidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA, ST3Gal3
 4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;
 i-m, o, r-u (independently selected) = 0 or 1;
 v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed EPO
 a-g, n, q = 1; h = 1 to 3;
 j-m, i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 v-z = 0

- ↓
1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;
 i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1;
 j-m, v-y (independently selected) = 0 or 1;
 R = PEG; z = 0.

FIG. 35E

111/498

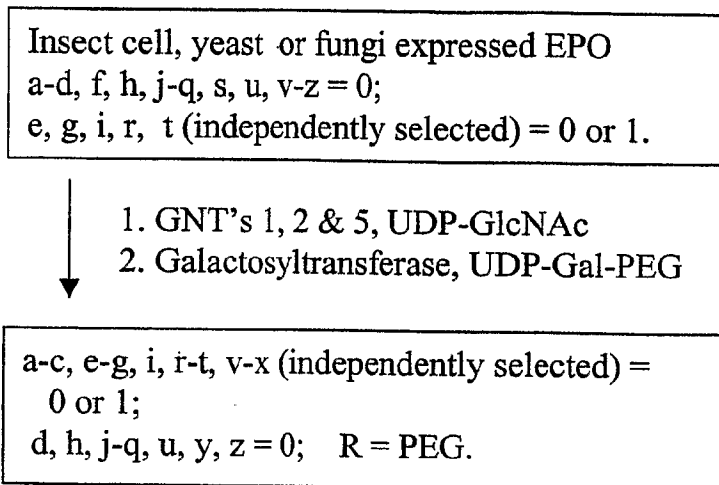


FIG. 35F

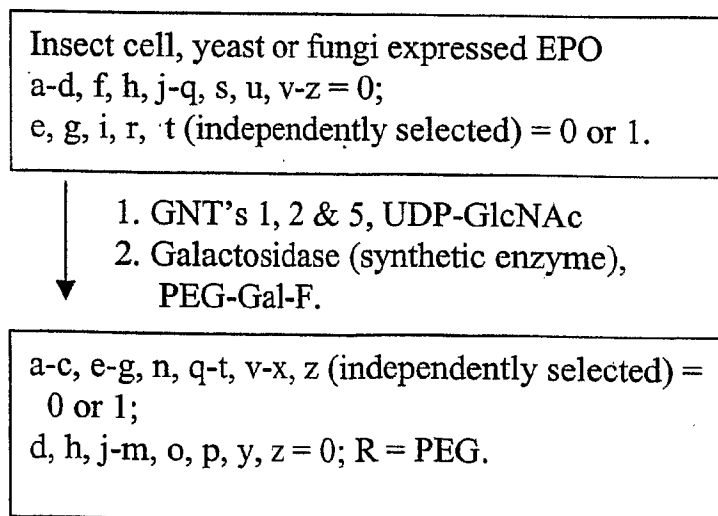


FIG. 35G

112/498

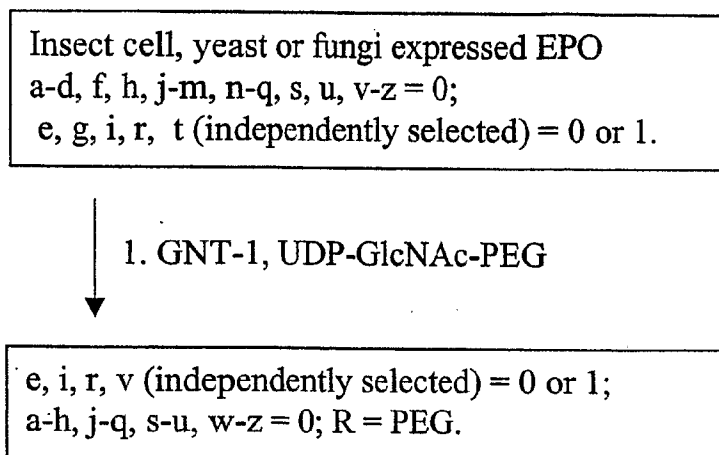


FIG. 35H

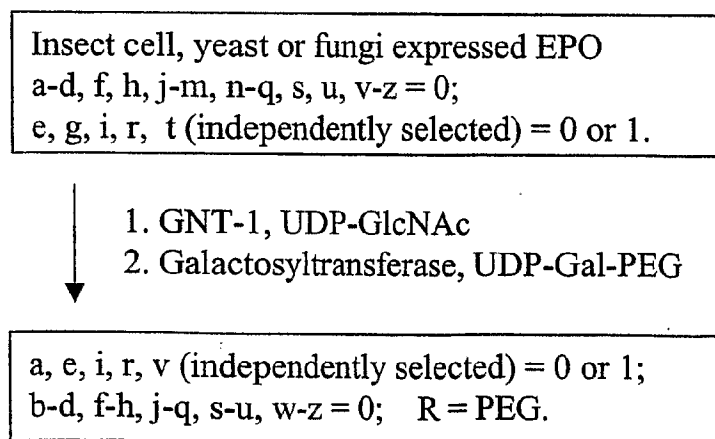


FIG. 35I

113/498

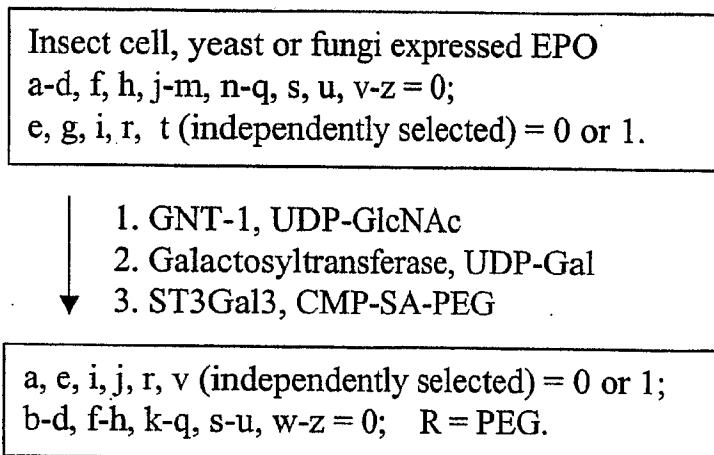


FIG. 35J

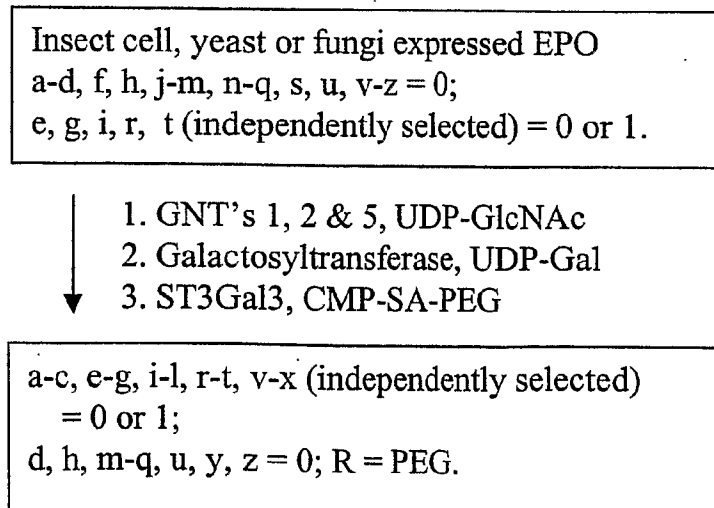


FIG. 35K

114/498

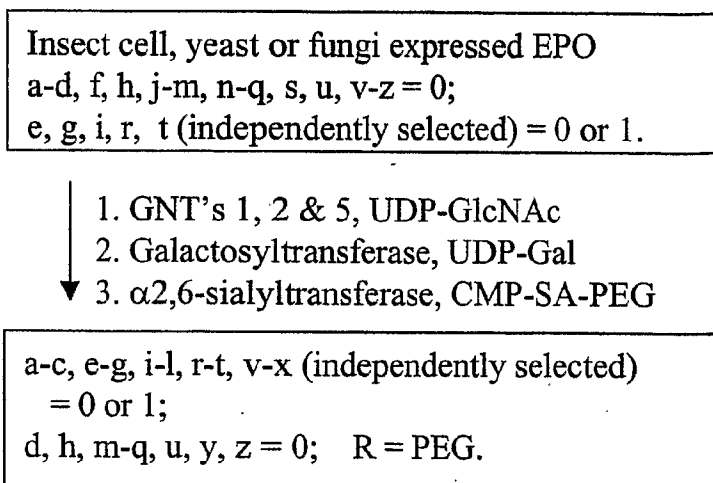


FIG. 35L

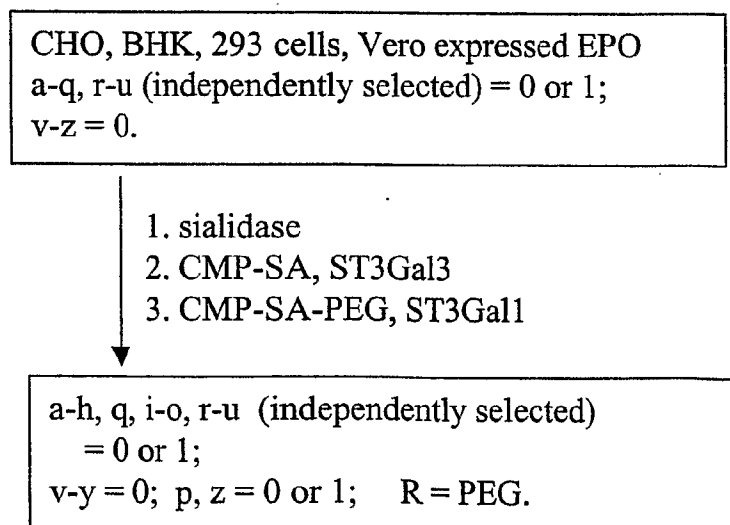


FIG. 35M

115/498

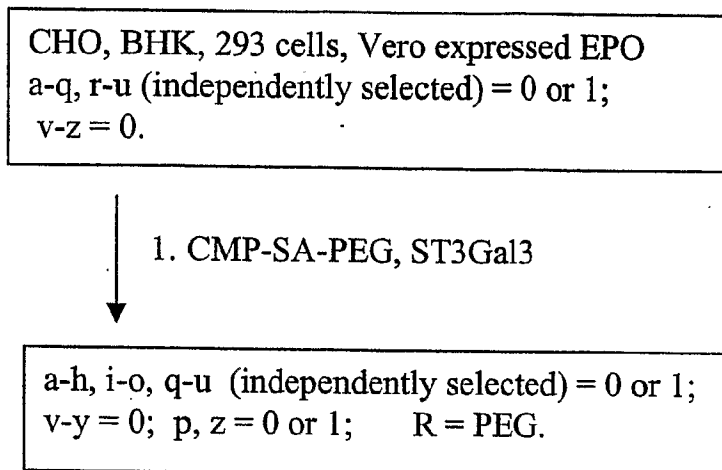


FIG. 35N

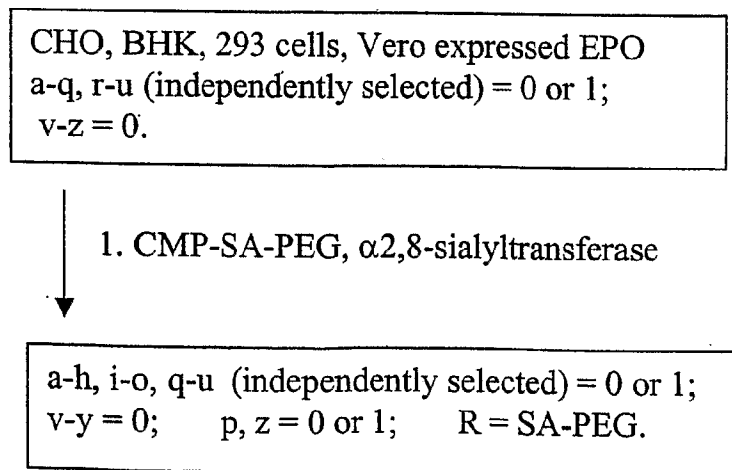


FIG. 35O

116/498

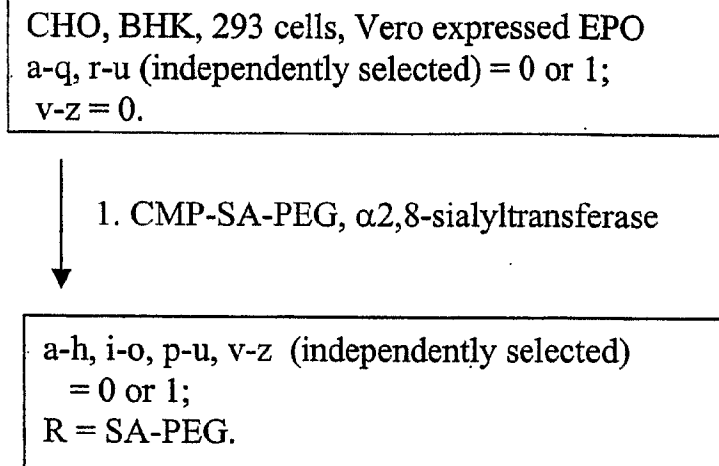


FIG. 35P

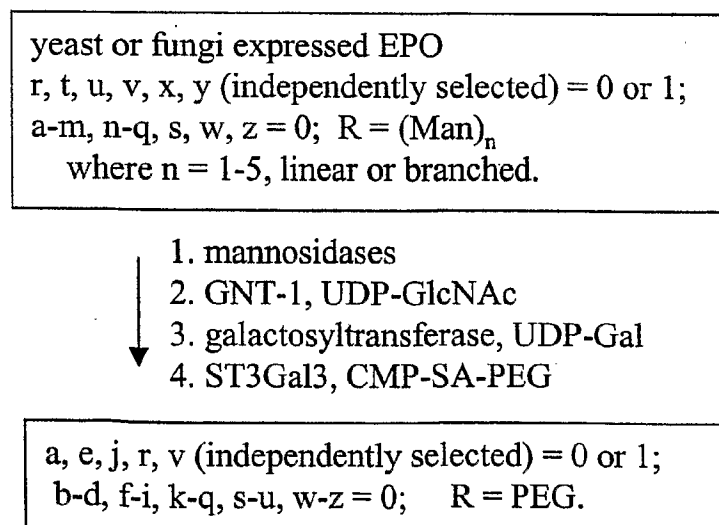


FIG. 35Q

117/498

yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 $a-m, n-q, s, w, z = 0$; $R = (\text{Man})_n$
 where $n = 1-5$, linear or branched.

- ↓
1. mannosidases
 2. GNT-1, UDP-GlcNAc-PEG

e, r, v (independently selected) = 0 or 1;
 $a-h, i-q, s-u, w-z = 0$; $R = \text{PEG}$.

FIG. 35R

yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 $a-m, n-q, s, w, z = 0$; $R = (\text{Man})_n$
 where $n = 1-5$, linear or branched.

- ↓
1. mannosidase-I
 2. GNT-1, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal
 4. ST3Gal3, CMP-SA-PEG

$a, e, j, r, t-u, v, x, y$ (independently selected)
 = 0 or 1;
 $b-d, f-i, k-q, s, w, z = 0$;
 $(R)_v = \text{PEG}$; $(R)_x$ and $(R)_y = \text{Man}$.

FIG. 35S

118/498

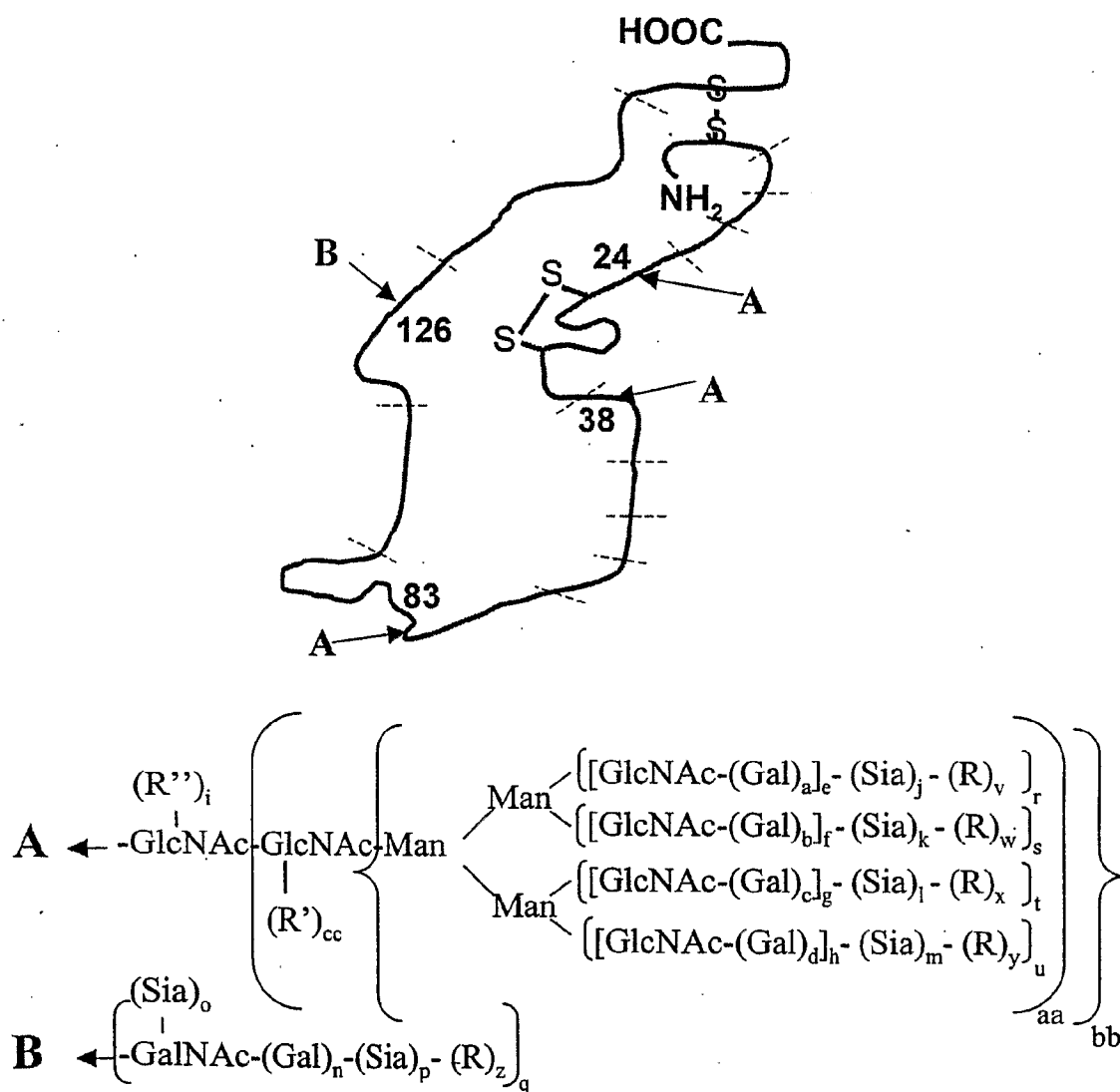


FIG. 35T

119/498

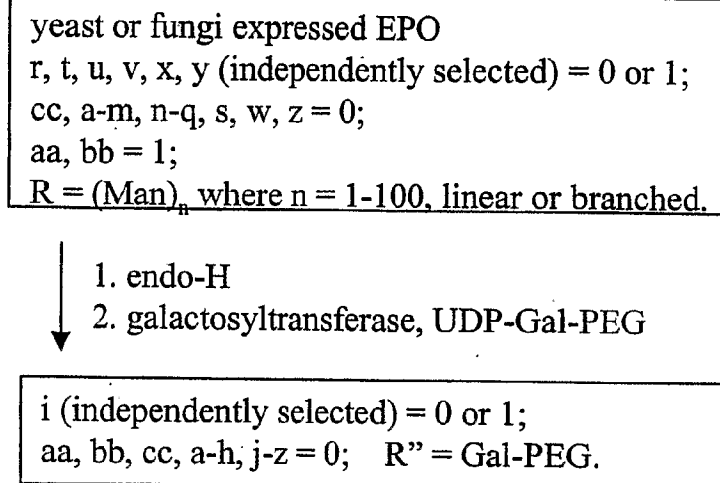


FIG. 35U

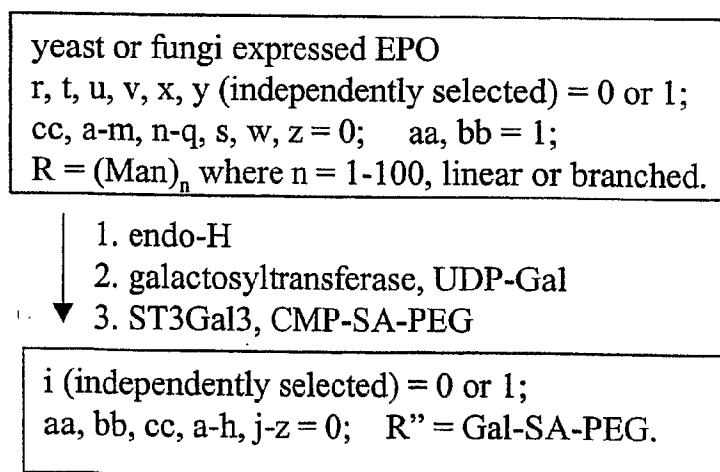


FIG. 35V

120/498

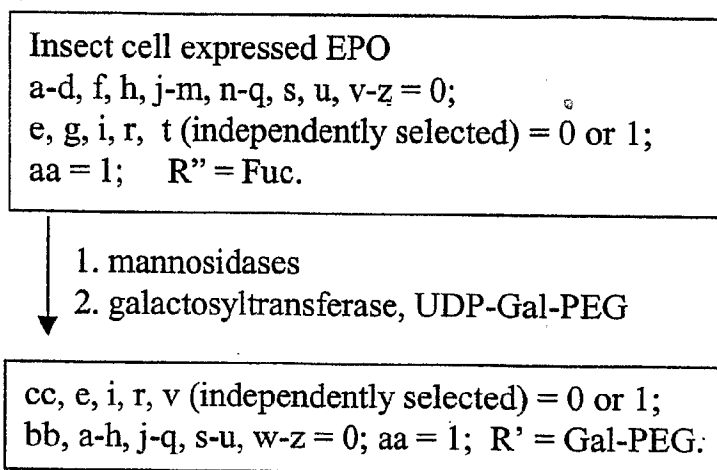


FIG. 35W

121/498

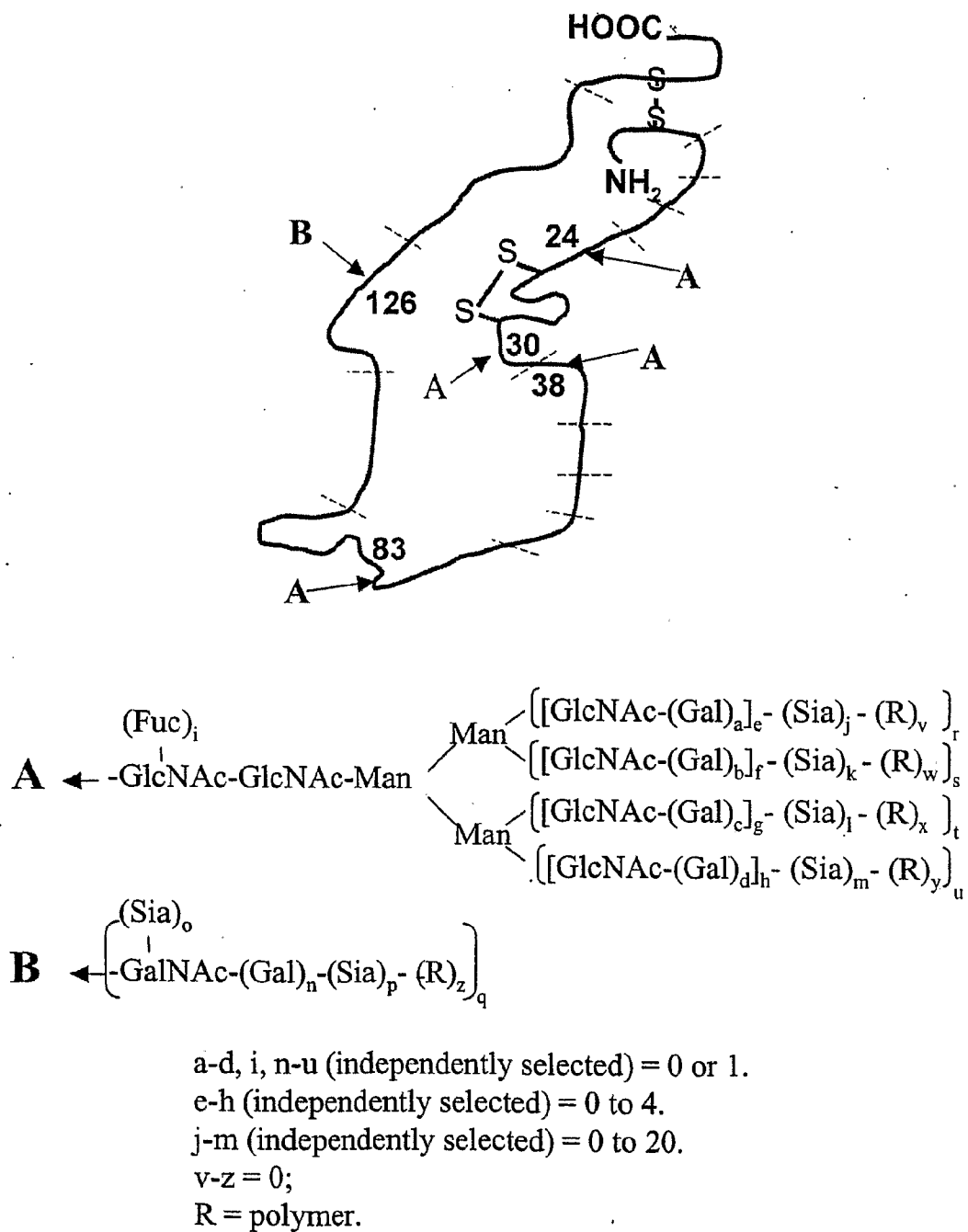


FIG. 35X

122/498

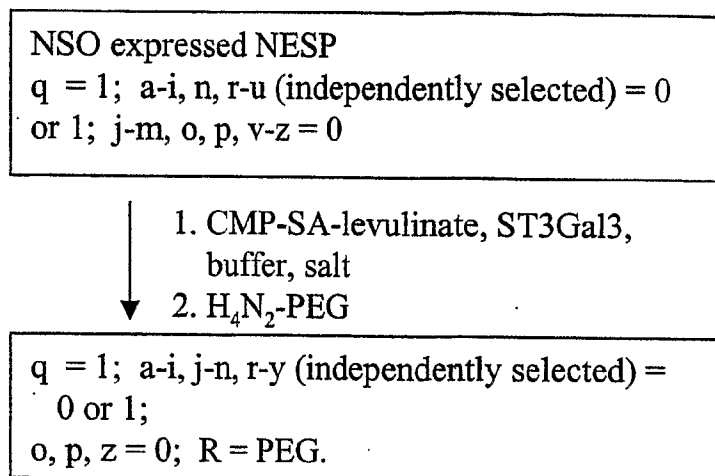


FIG. 35Y

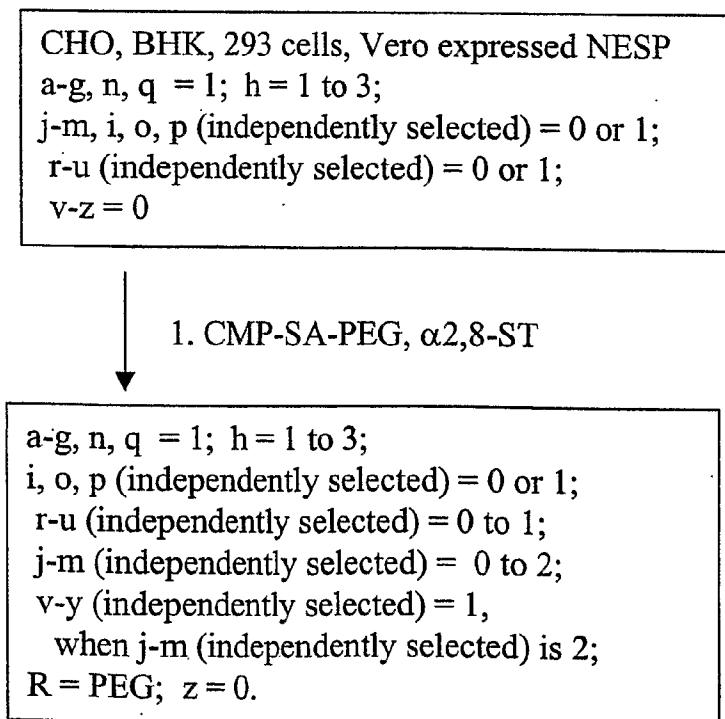


FIG. 35Z

123/498

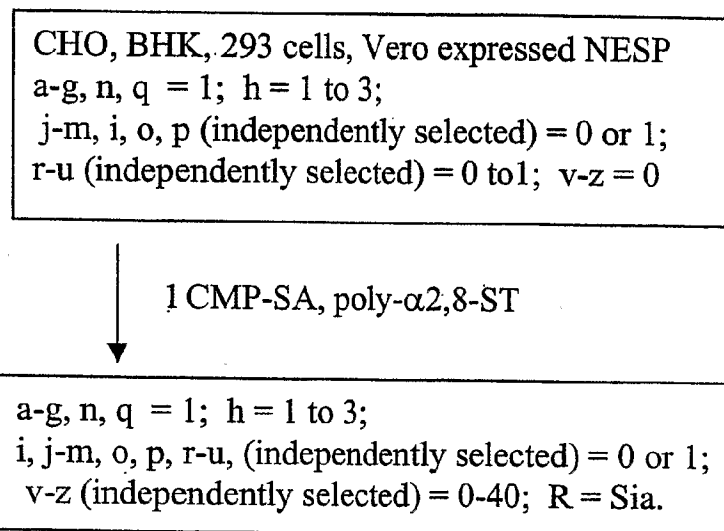
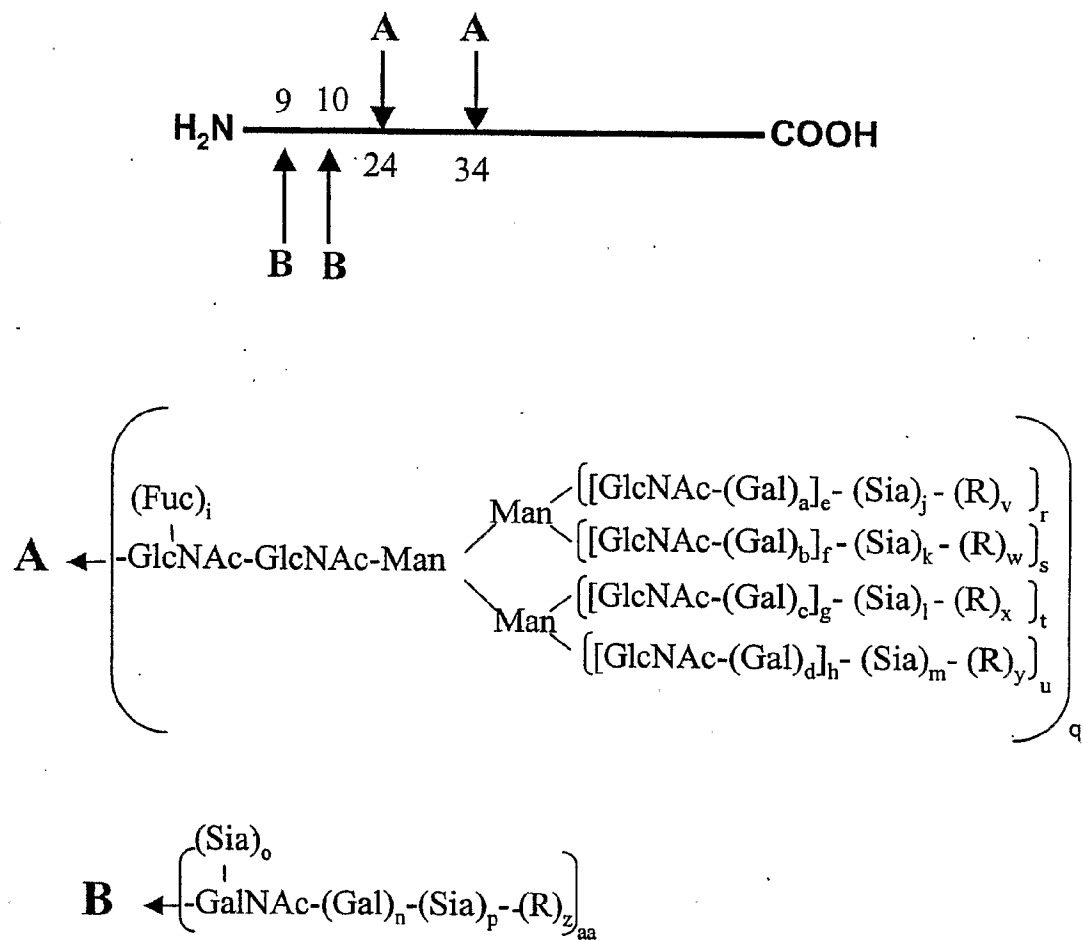


FIG. 35AA

124/498



a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 36A

125/498

CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
o, p, z = 0; n, e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 36B

CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3 &
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;
o, z = 0; n, e-h = 1;
v-y (independently selected) = 0 or 1; R = PEG.

FIG. 36C

126/498

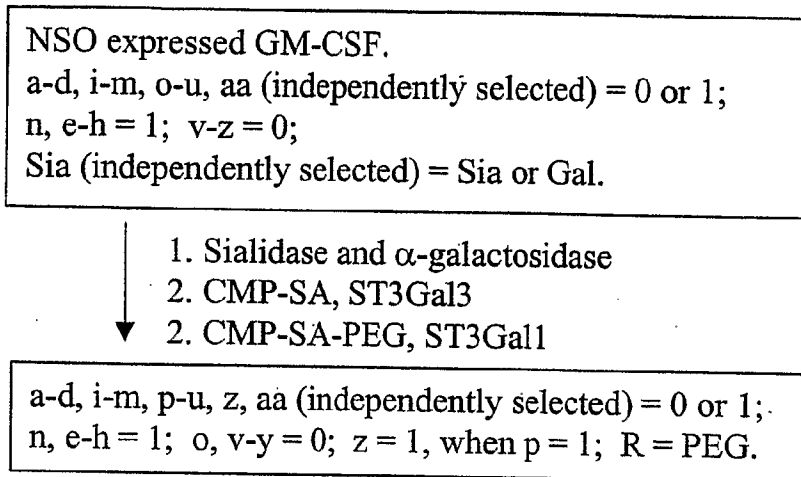


FIG. 36D

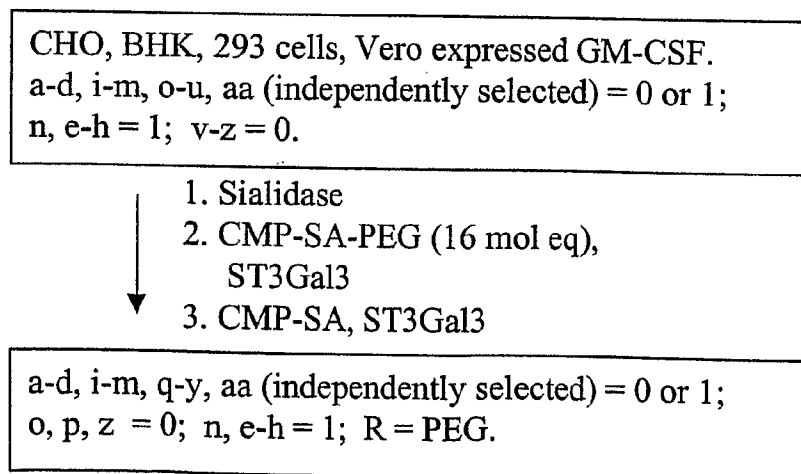


FIG. 36E

127/498

CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;
z = 0; n, e-h = 1; R = PEG.

FIG. 36F

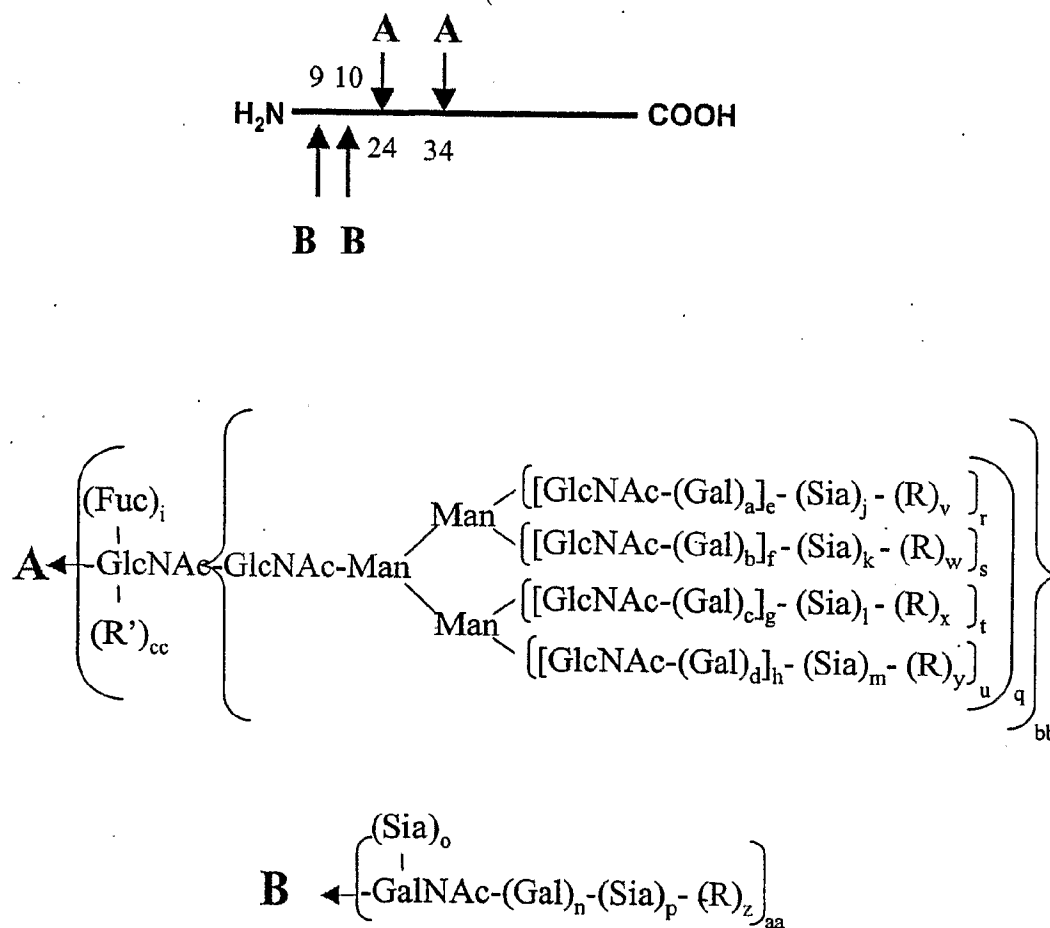
CHO, BHK, 293 cells, Vero expressed GMCSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

1. CMP-SA, α 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; j-m (independently selected) = 0-20;
v-z (independently selected) = 0.

FIG. 36G

128/498



a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group. glycoconjugate.

FIG. 36H

129/498

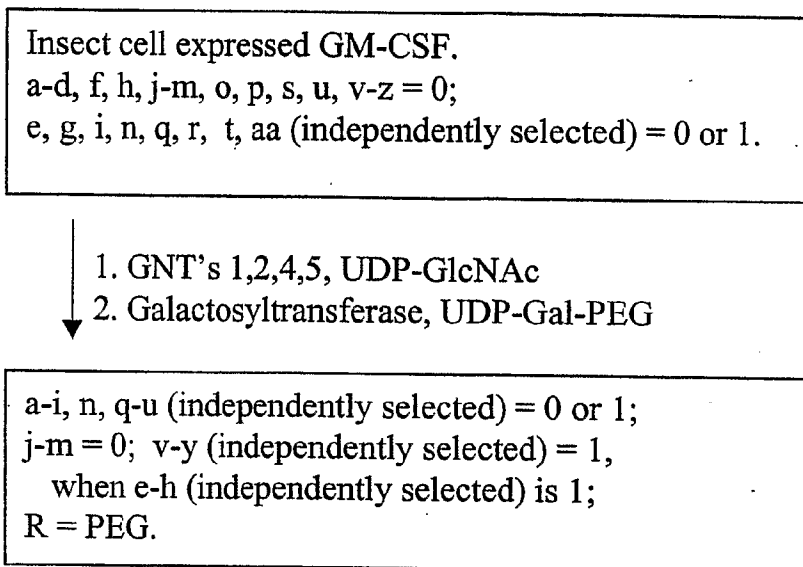


FIG. 36I

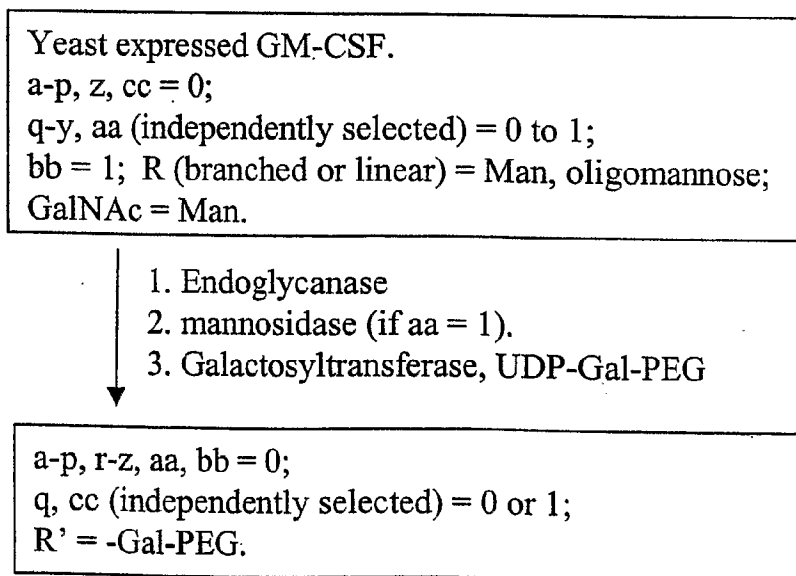


FIG. 36J

130/498

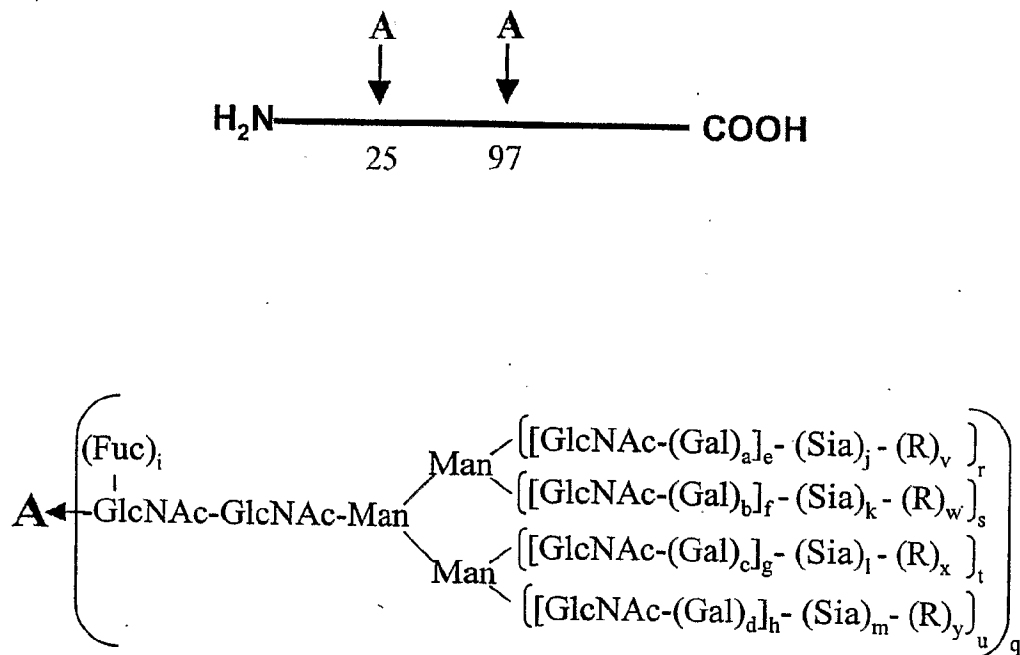
CHO, BHK, 293 cells, Vero expressed GM-CSF.
a--m, o-u, aa, bb (independently selected) = 0 or 1;
n, v-z, cc = 0.

- ↓
1. sialidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-linker-SA-CMP, ST3Gal1
 3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 36K

131/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

$$v-y=0; R = \text{polymer.}$$

FIG. 37A

132/498

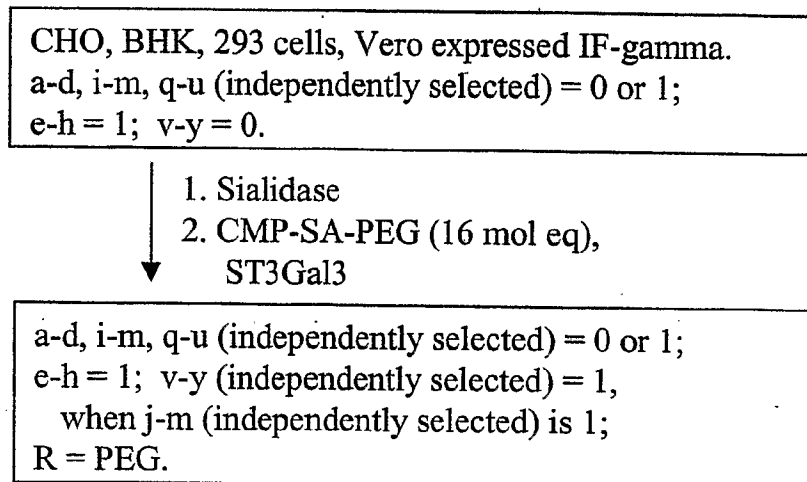


FIG. 37B

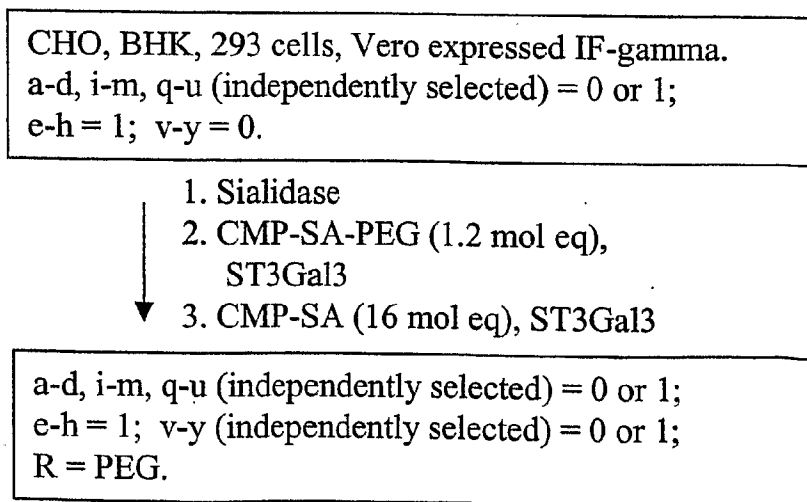


FIG. 37C

133/498

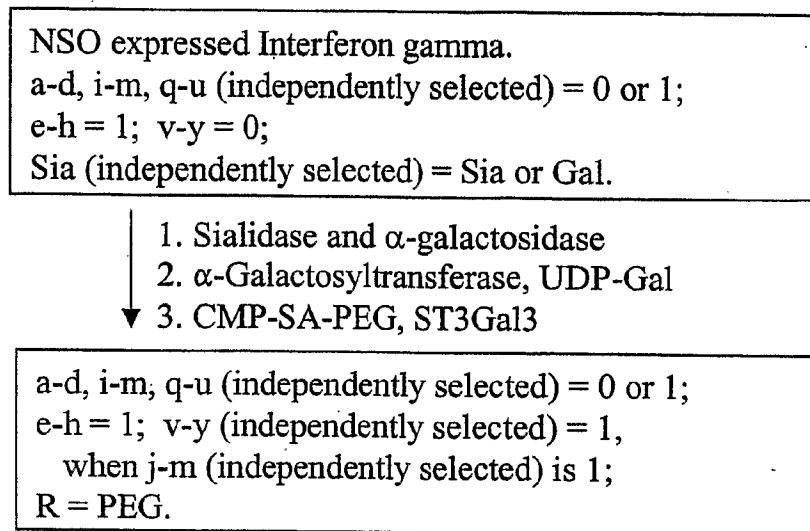


FIG. 37D

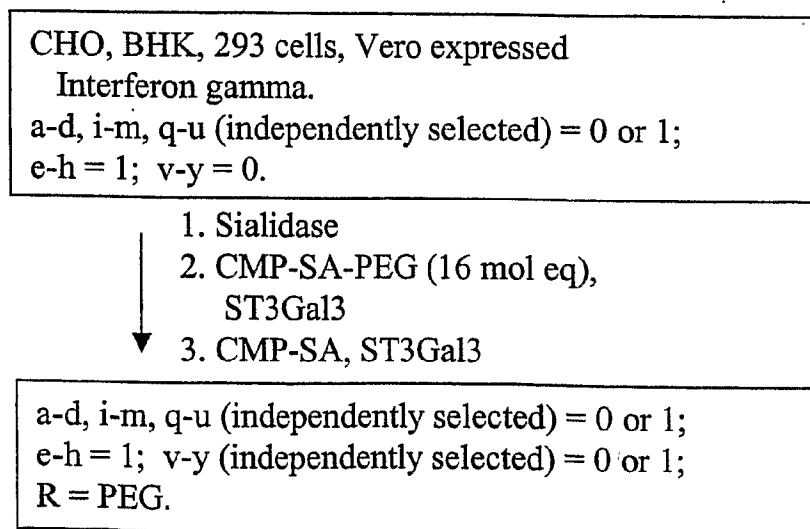


FIG. 37E

134/498

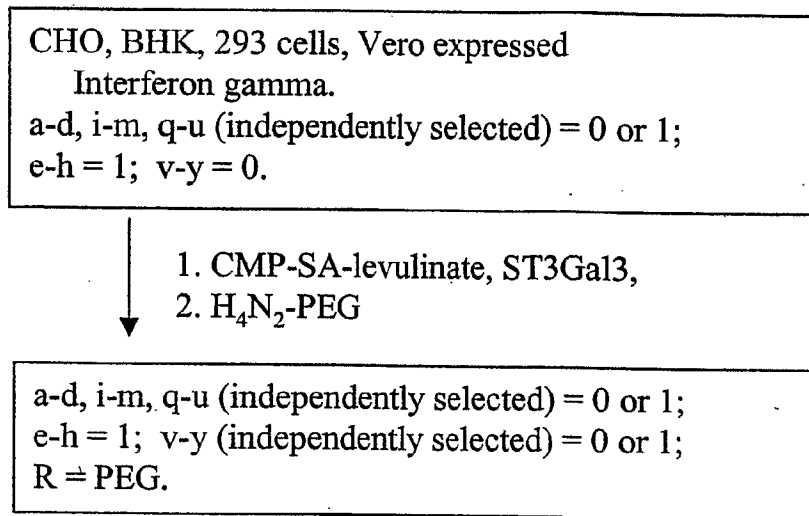


FIG. 37F

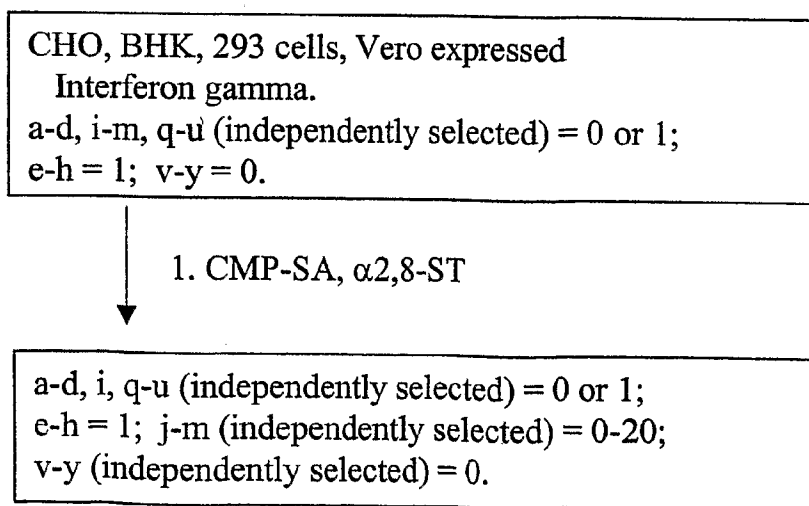


FIG. 37G

135/498

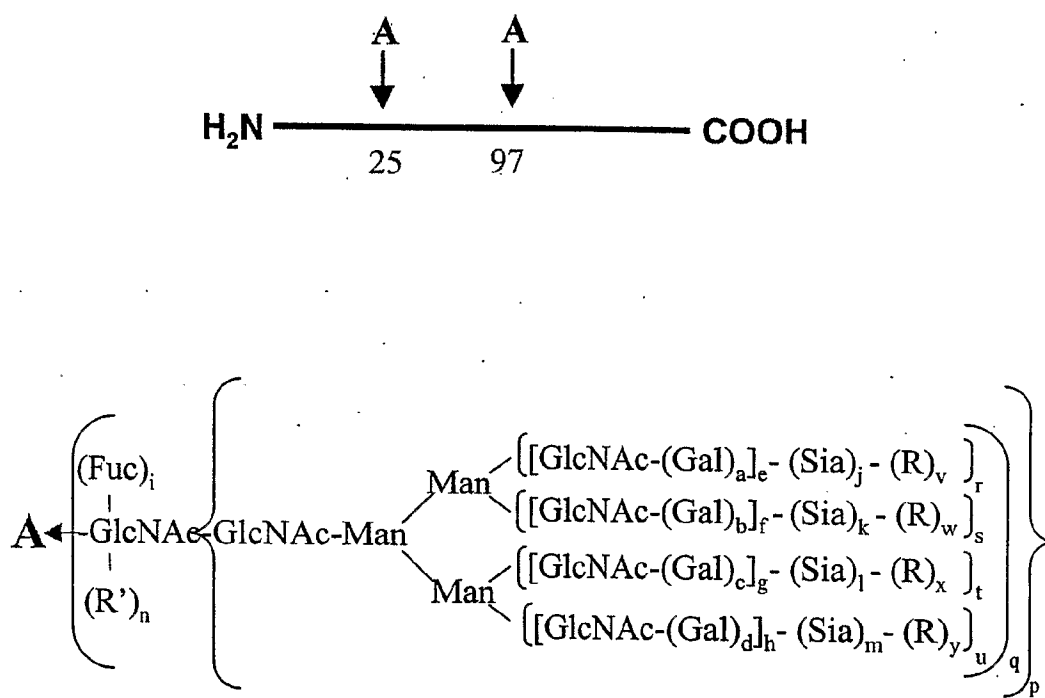


FIG. 37H

136/498

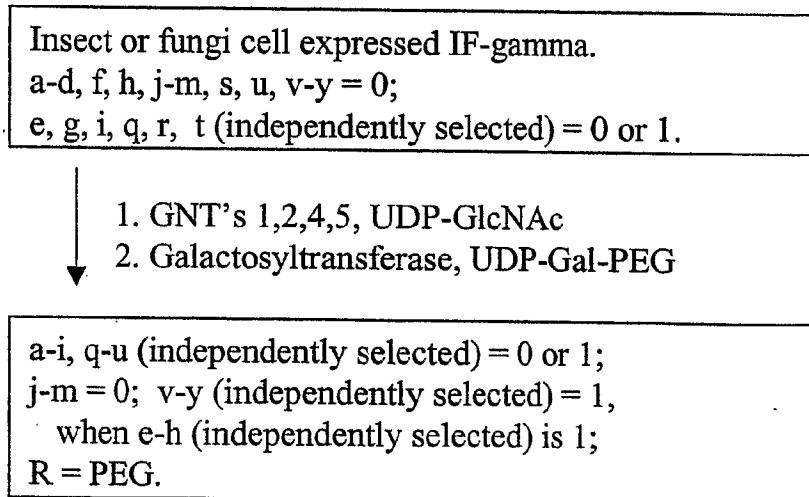


FIG. 37I

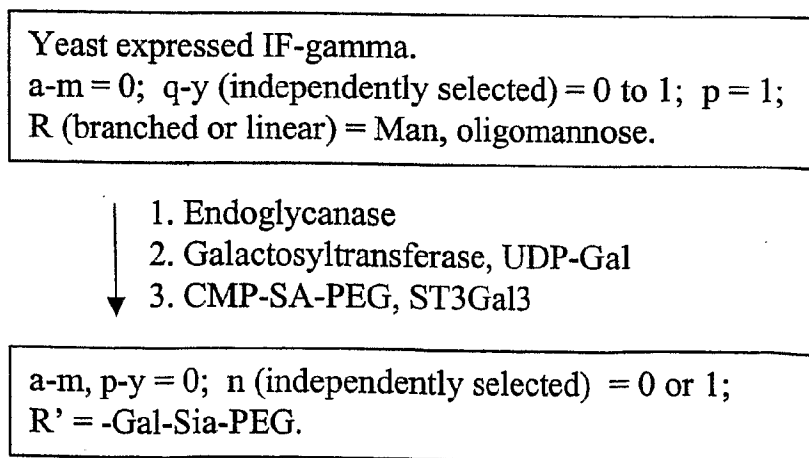


FIG. 37J

137/498

CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP, ST3Gal3
 2. Galactosyltransferase, transferrin treated with endoglycanase.

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 37K

CHO, BHK, 293 cells, Vero expressed
Interferon gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1; n, v-y = 0.

- ↓
1. CMP-SA-PEG,
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1;
n, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 37L

138/498

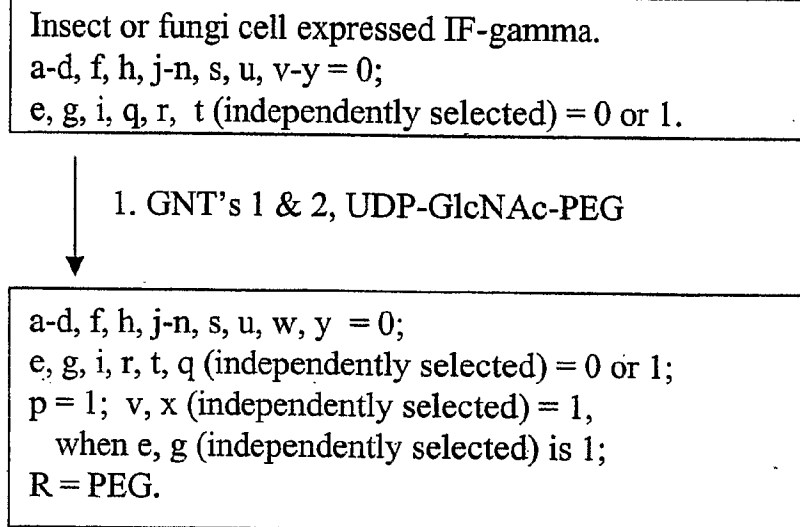


FIG. 37M

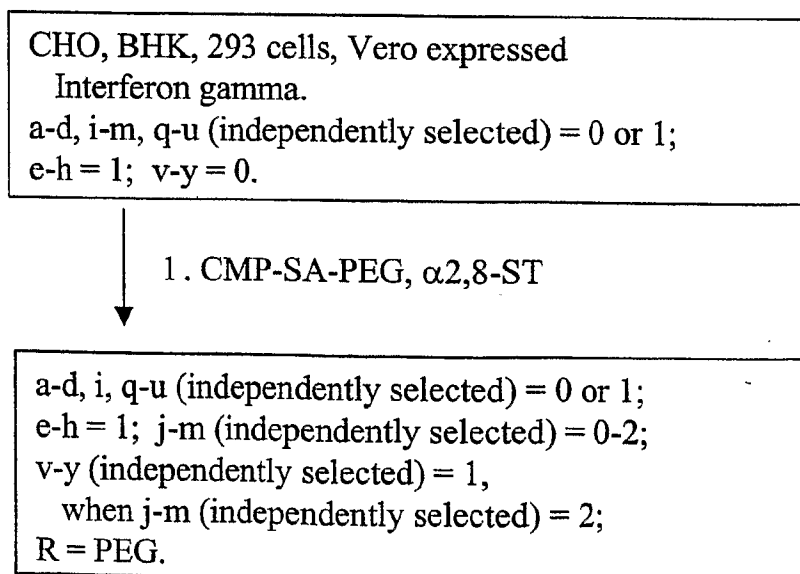
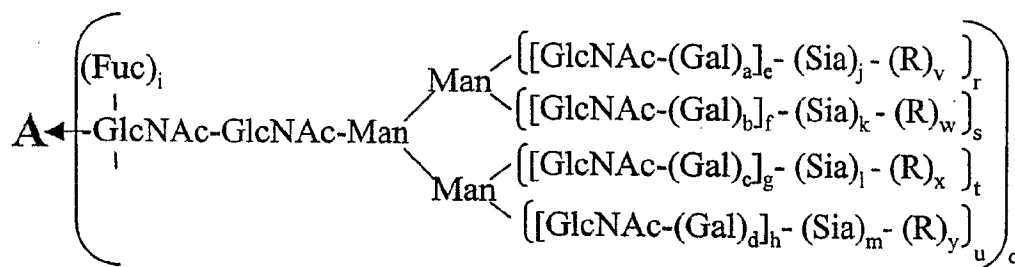
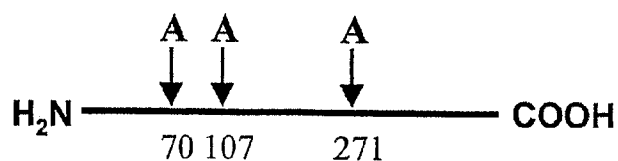


FIG. 37N

139/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 38A

140/498

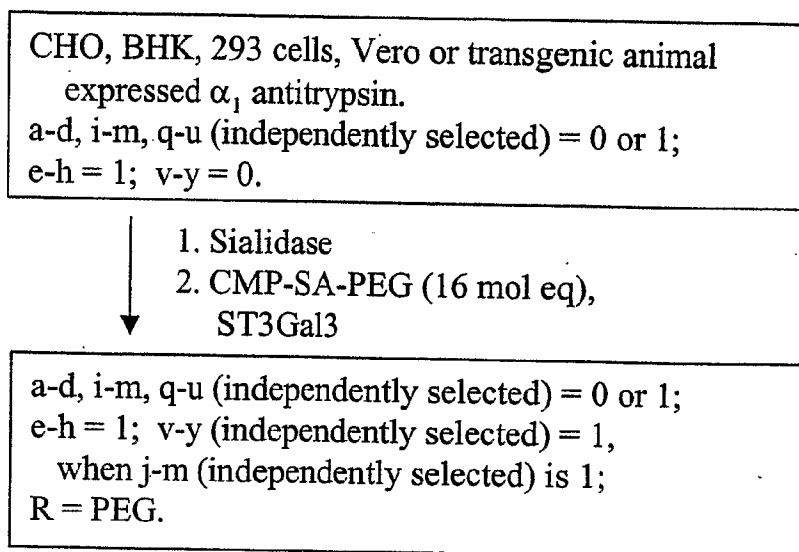


FIG. 38B

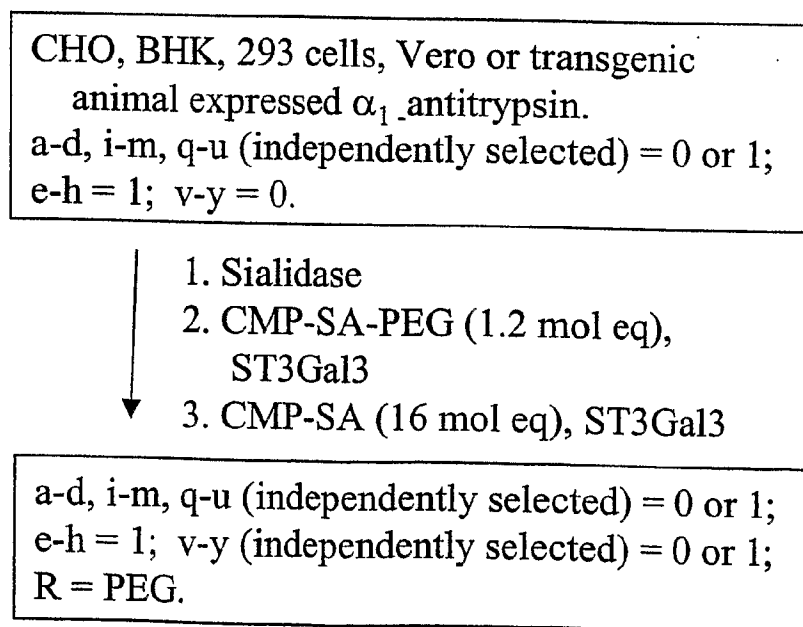


FIG. 38C

141/498

CHO, BHK, 293 cells, Vero or transgenic animal
expressed alpha-1 antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38D

CHO, BHK, 293 cells, Vero or transgenic animal
expressed α_1 -antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38E

142/498

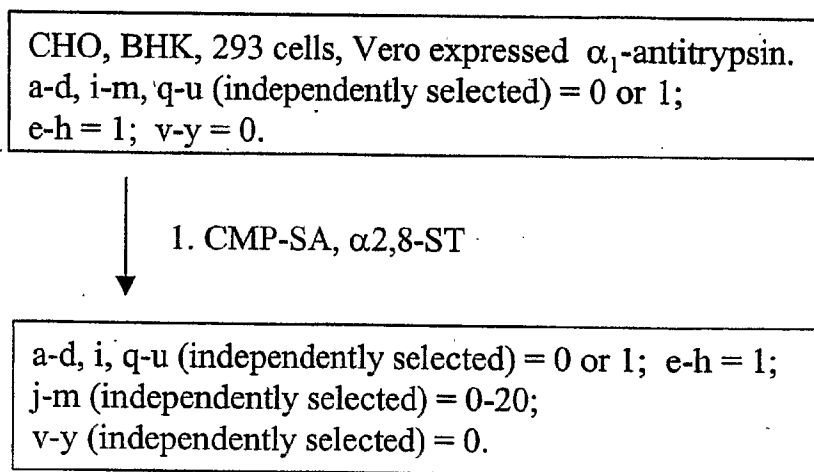
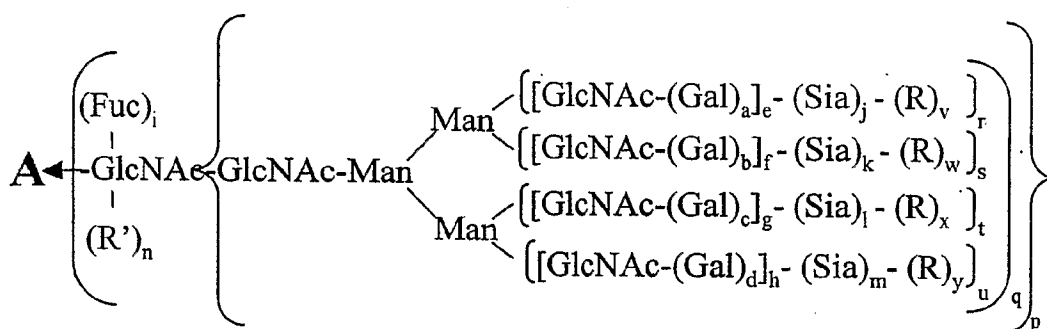
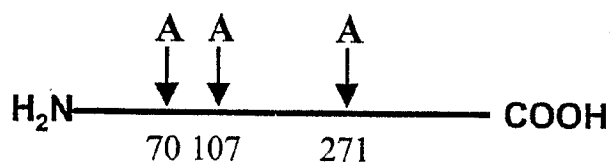


FIG. 38F

143/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

$$v-y=0;$$

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 38G

144/498

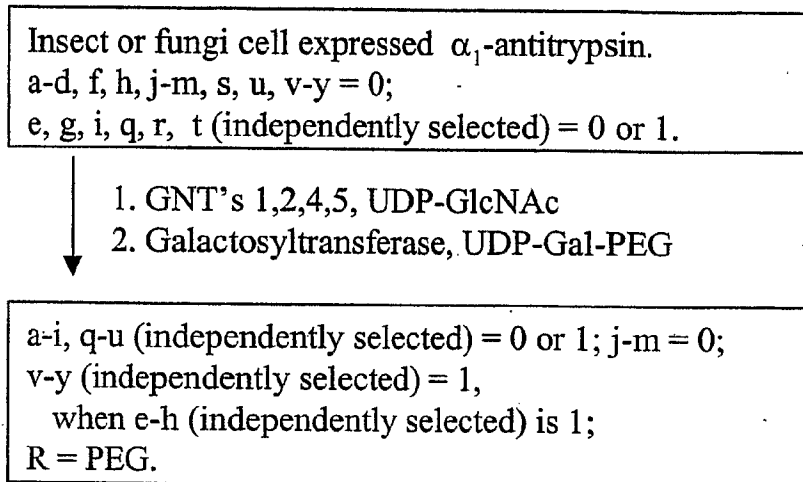


FIG. 38H

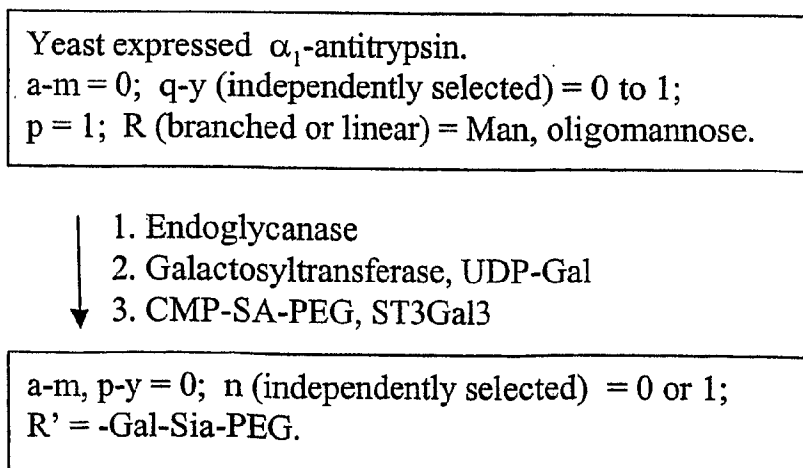


FIG. 38I

145/498

CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin treated
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 38J

147/498

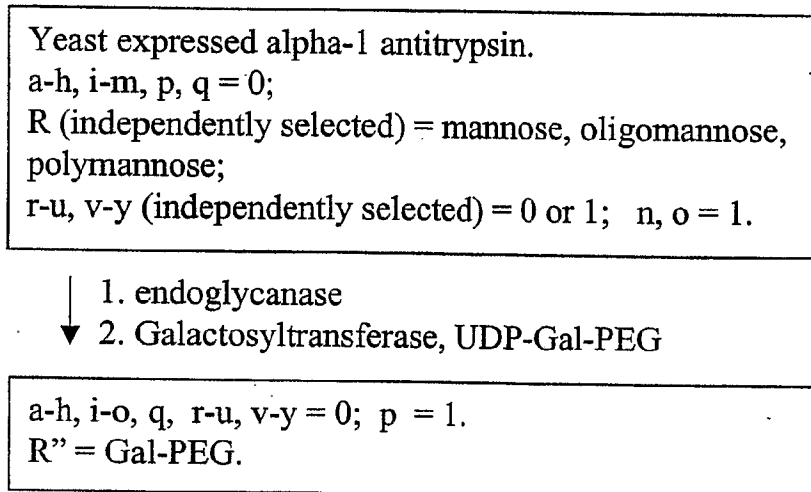


FIG. 38L

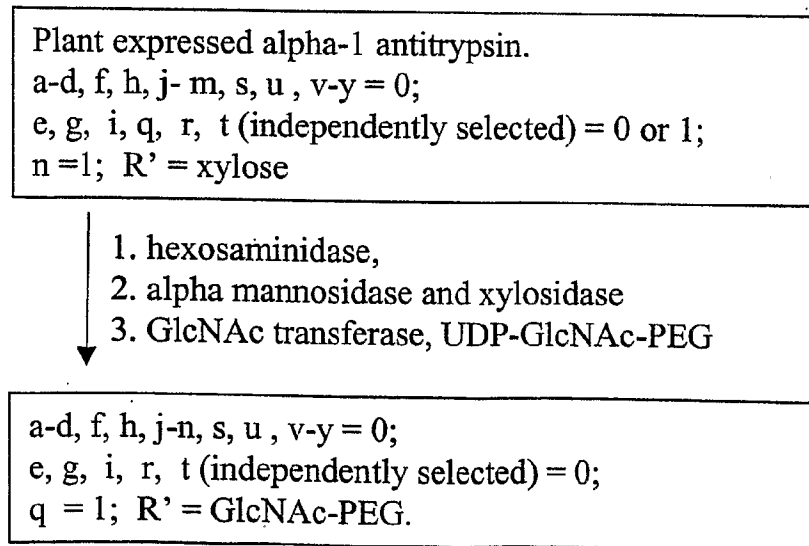


FIG. 38M

148/498

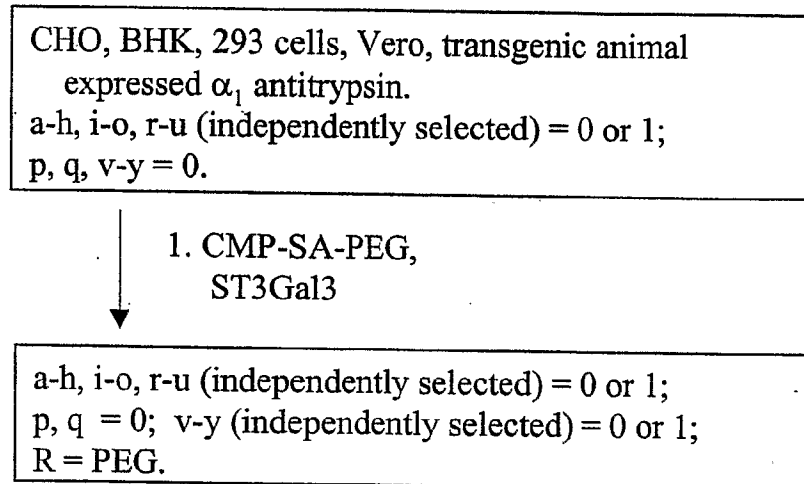
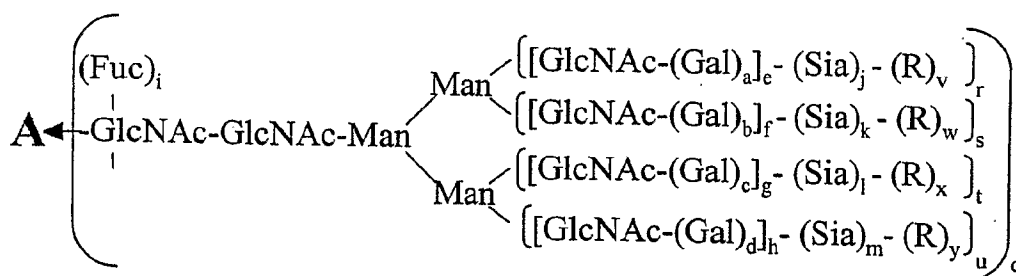
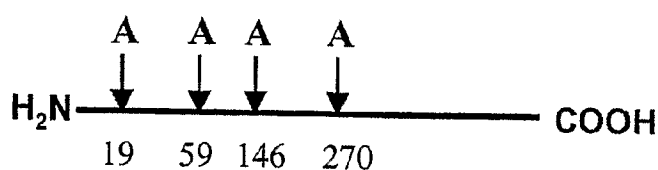


FIG. 38N

149/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 39A

150/498

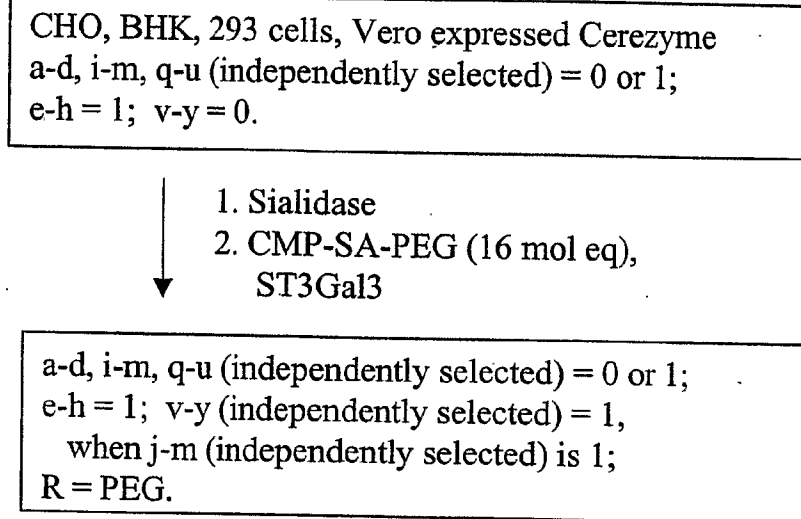


FIG. 39B

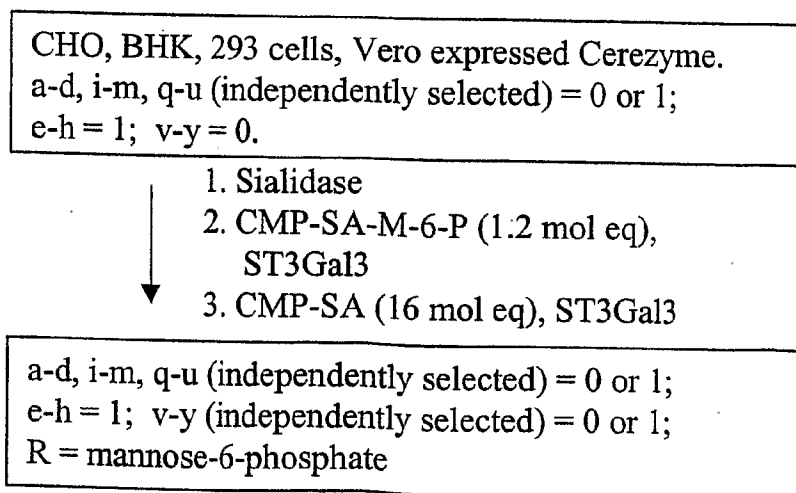


FIG. 39C

151/498

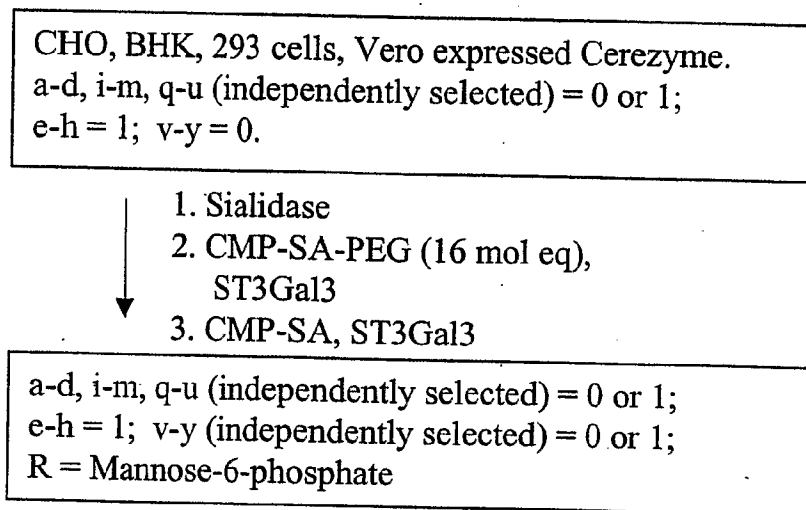


FIG. 39D

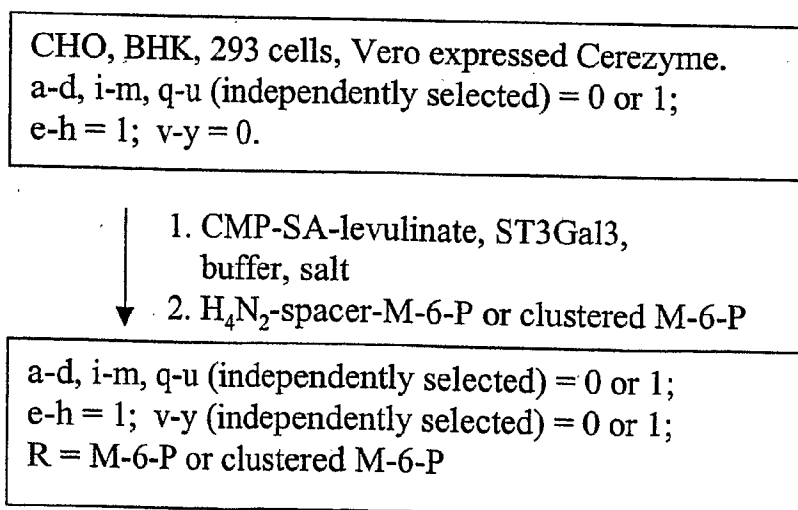


FIG. 39E

152/498

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

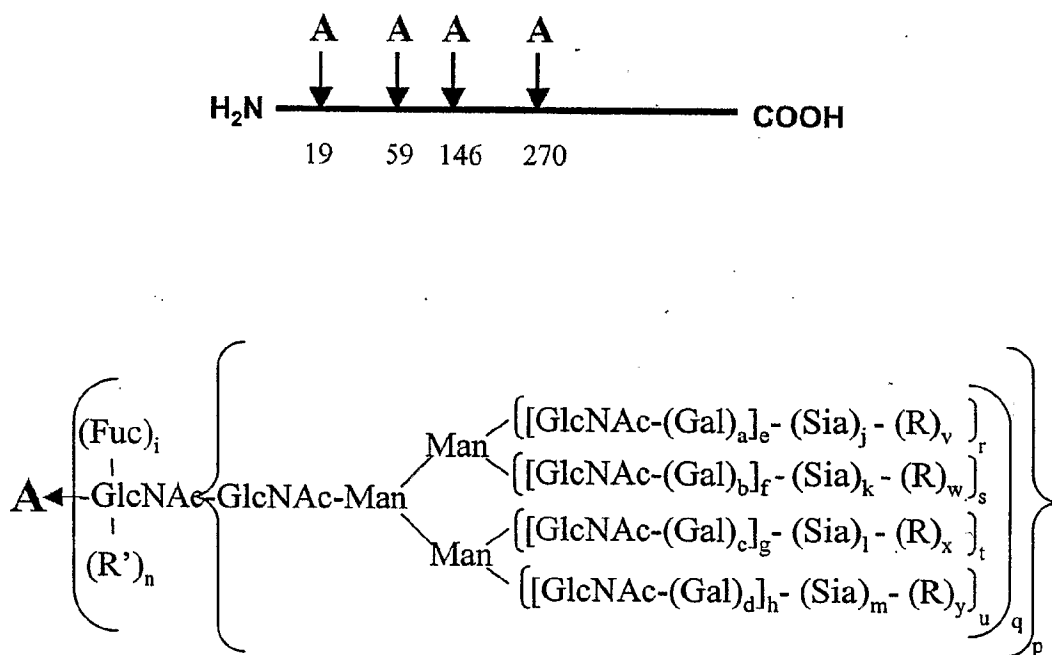


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 39F

153/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 39G

154/498

Insect cell expressed Cerezyme.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 39H

Yeast expressed Cerezyme.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3


a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 39I

155/498

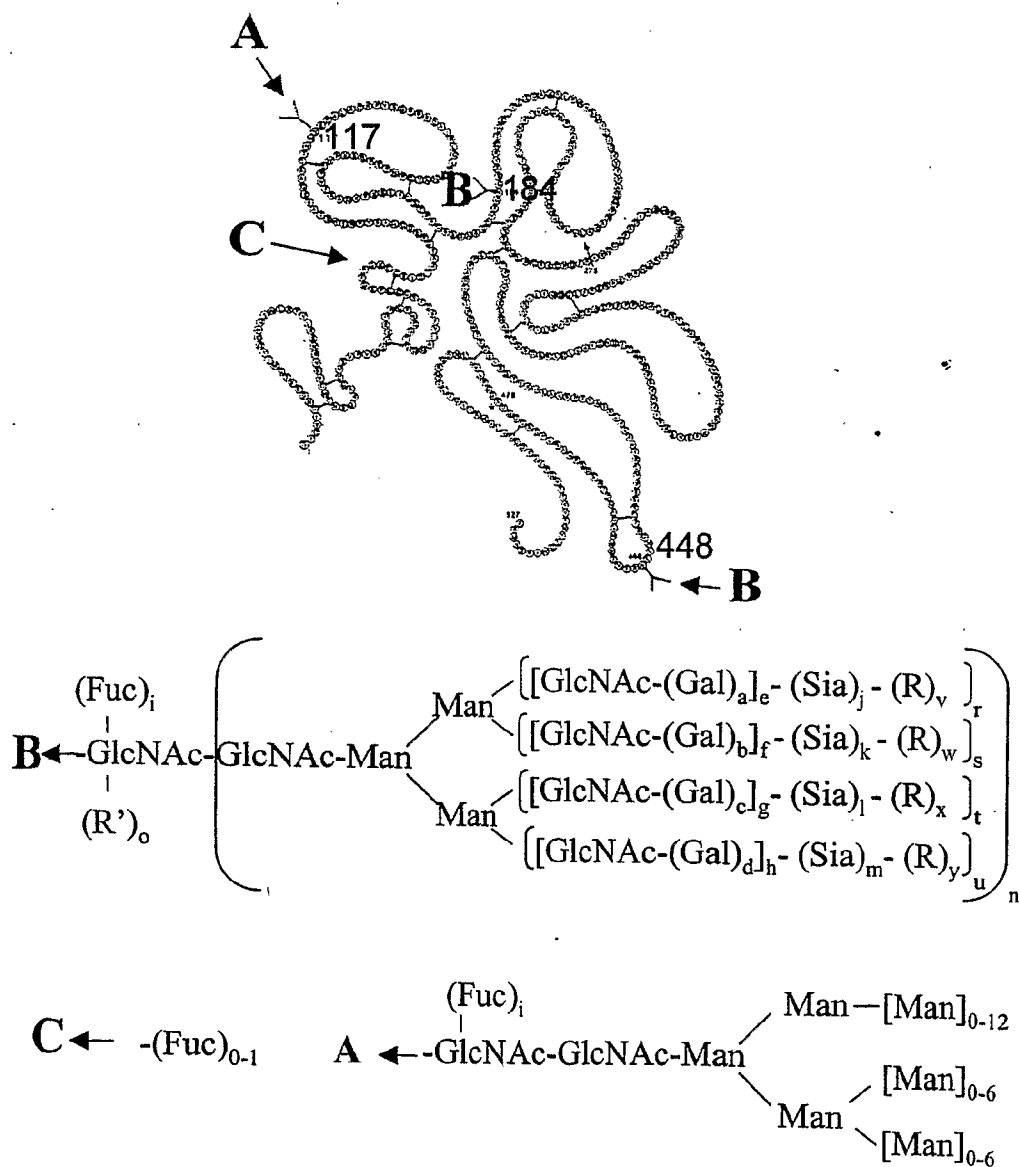
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- 
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0; v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 39J

156/498



a-d, i, n-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 4.
 j-m (independently selected) = 0 to 20.
 R = polymer; R' = sugar, glycoconjugate.

FIG. 40A

157/498

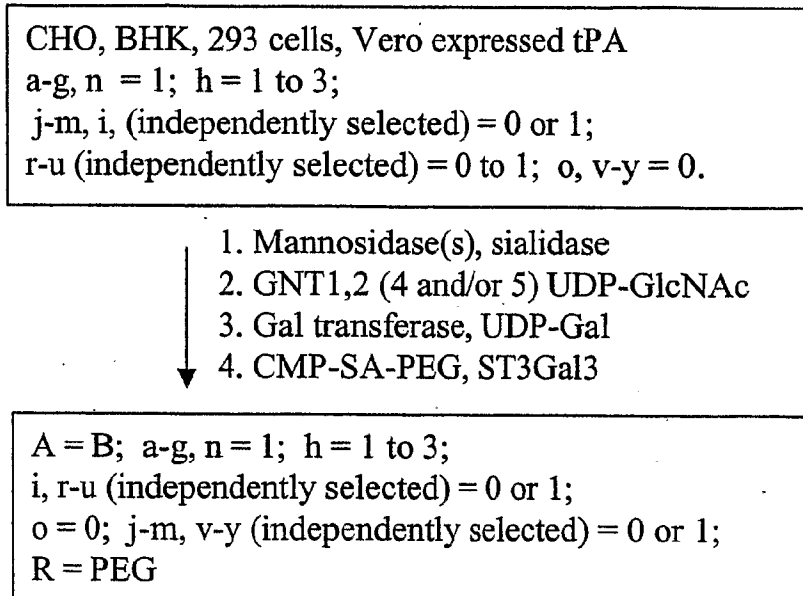


FIG. 40B

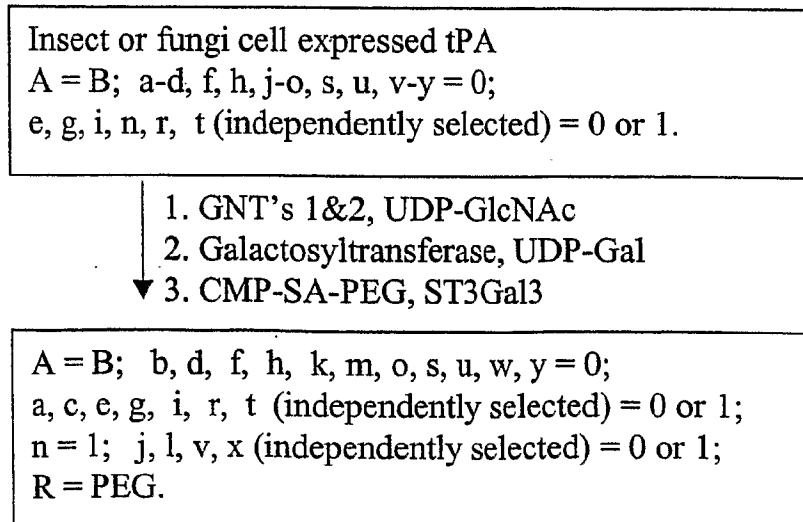


FIG. 40C

158/498

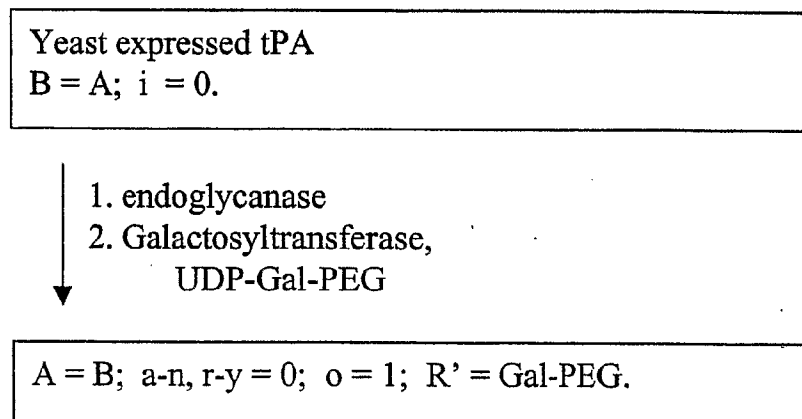


FIG. 40D

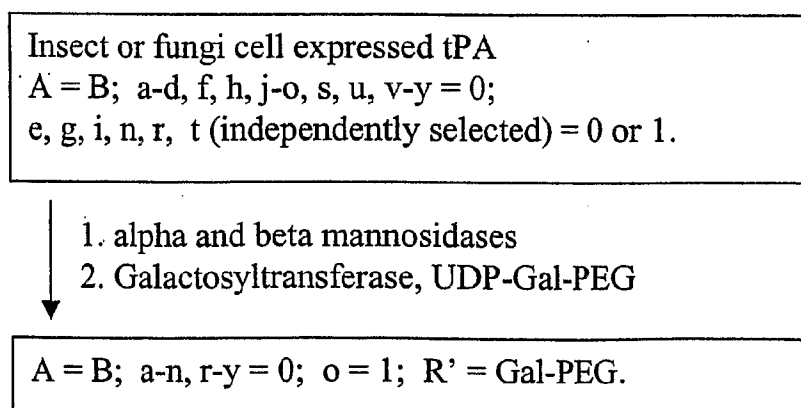


FIG. 40E

159/498

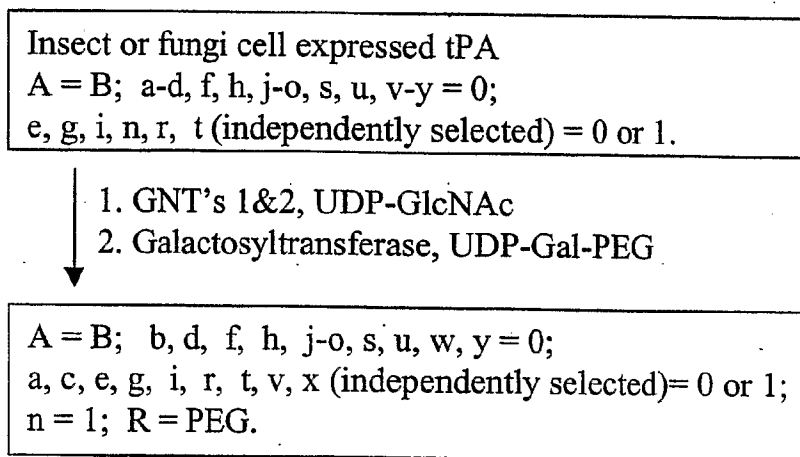


FIG. 40F

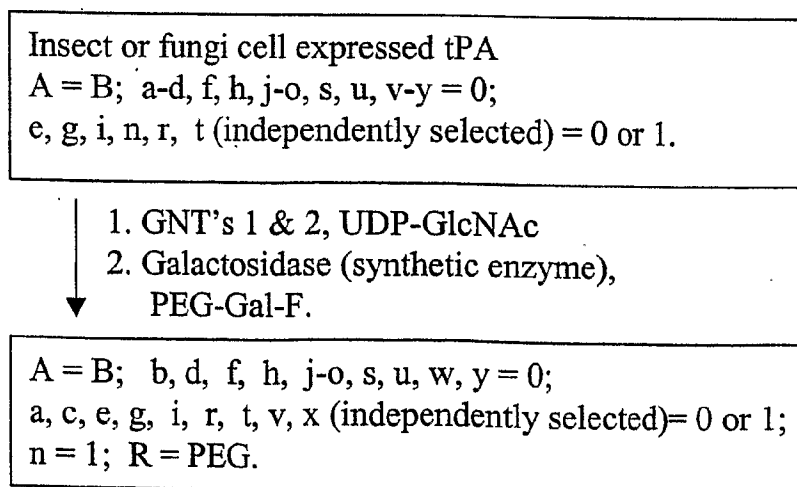
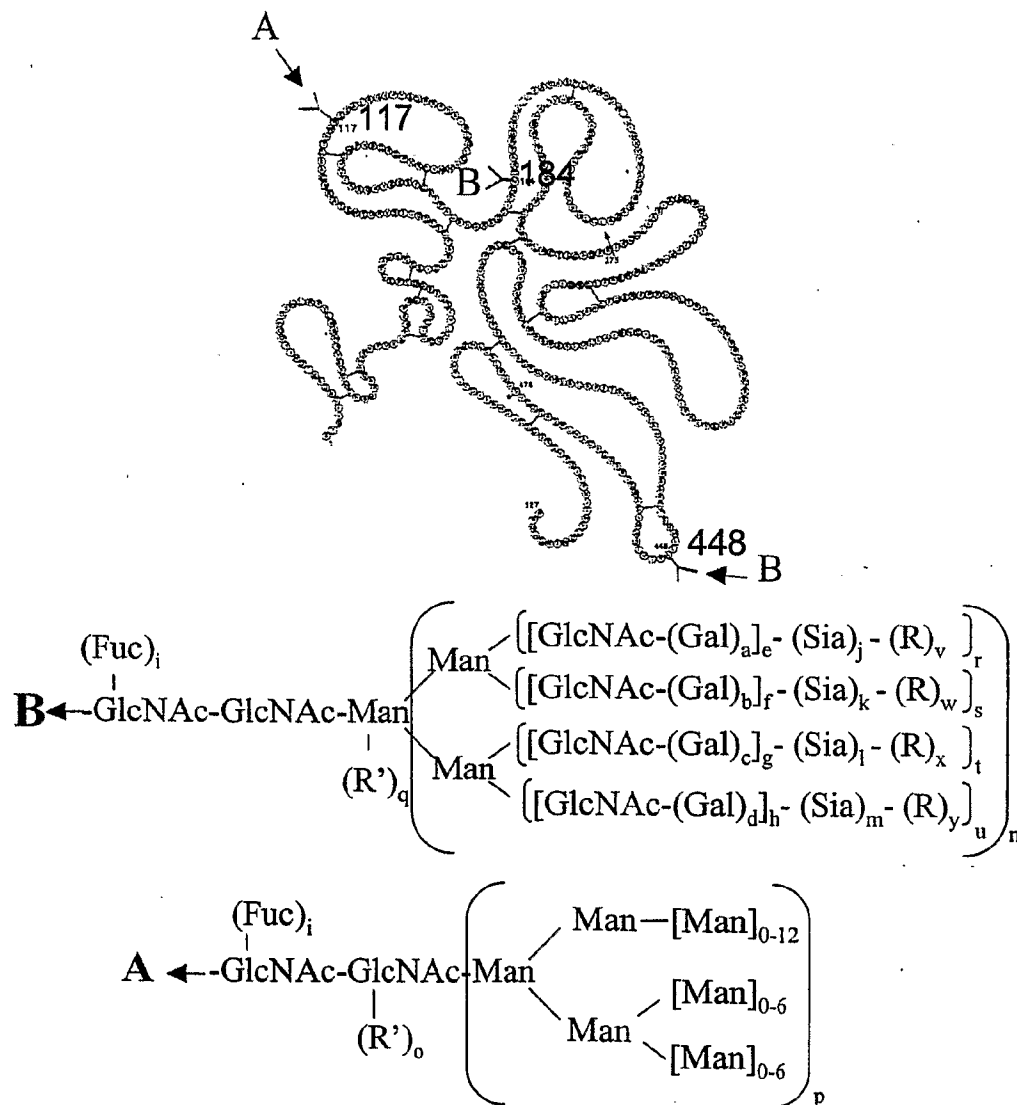


FIG. 40G

160/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40H

161/498

NSO expressed tPA

A = B; a-m, r-u (independently selected) = 0 or 1;
n = 1; o, p, q, v-y = 0

- ↓
1. sialidase, alpha-galactosidase
 2. CMP-SA-levulinate, ST3Gal3,
 3. H₄N₂-PEG

A = B; a-m, r-y (independently selected) = 0 or 1;
n = 1; o, p, q = 0;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 40I

CHO, BHK, 293 cells, Vero expressed tPA

a-g, n, p = 1; h = 1 to 3;
j-m, i, (independently selected) = 0 or 1;
r-u (independently selected) = 0 to 1; q, o, v-y = 0.

- ↓
1. alpha and beta Mannosidases
 2. CMP-SA, ST3Gal3
 3. Galactosyltransferase, UDP-Gal-PEG

a-g, n = 1; h = 1 to 3;
i, r-u (independently selected) = 0 or 1; o = 1;
q, p, v-y = 0; j-m (independently selected) = 0 or 1;
R' = Gal-PEG

FIG. 40J

162/498

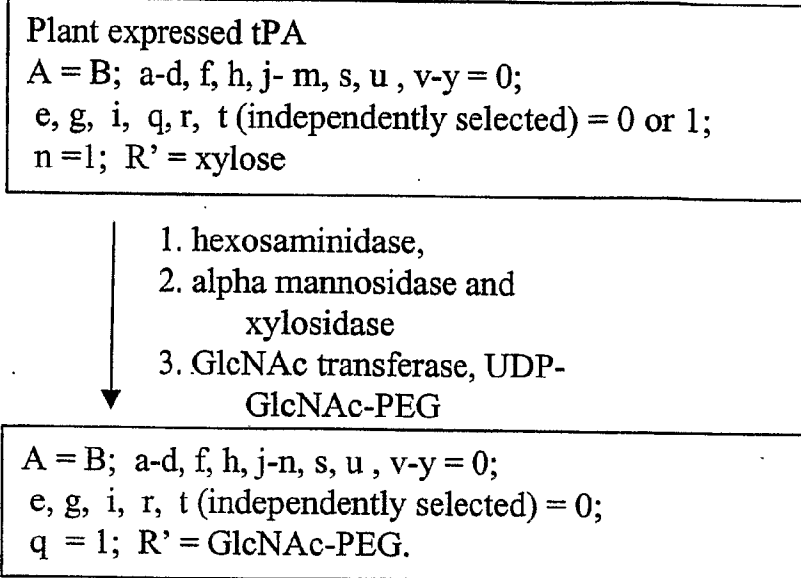
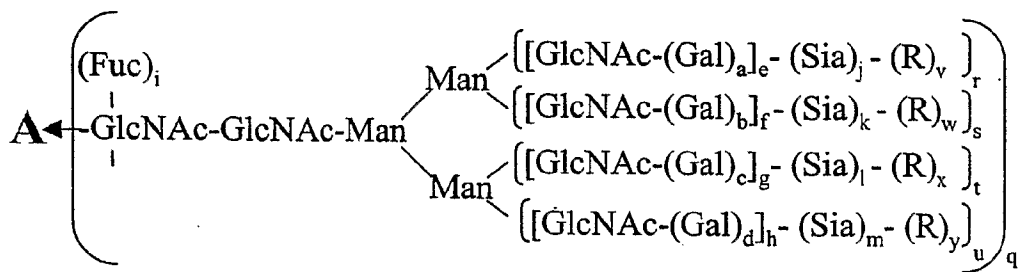
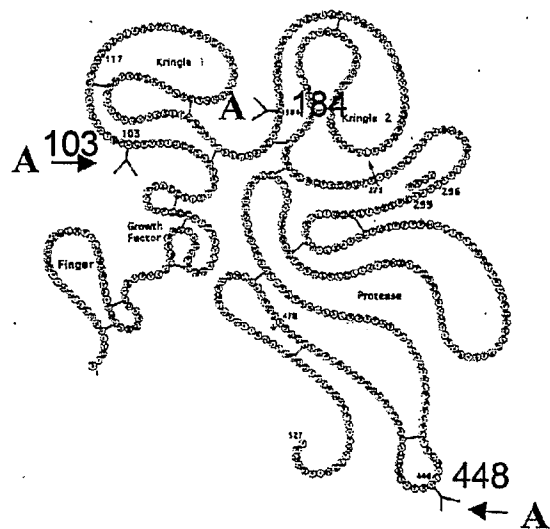


FIG. 40K

163/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40L

164/498

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 40M

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40N

165/498

NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

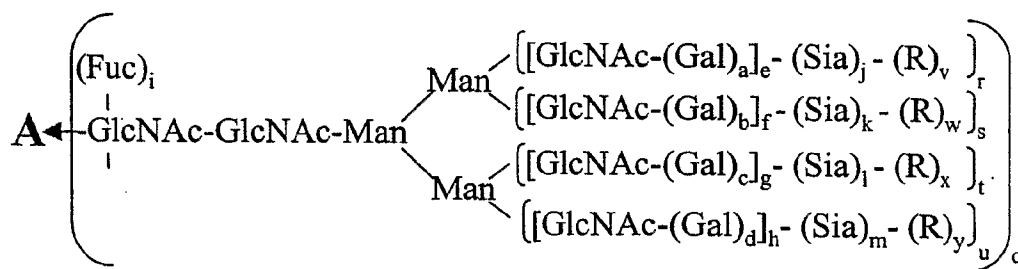
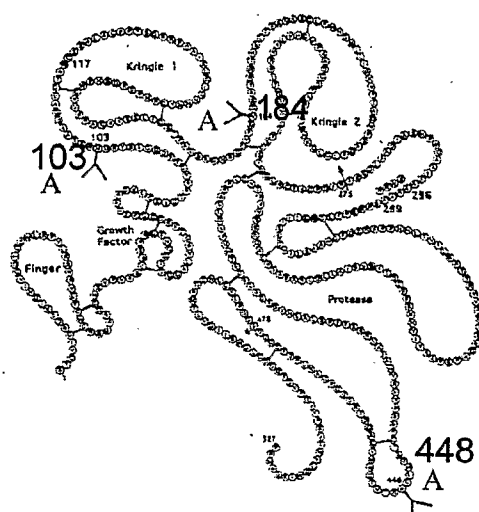
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 400

166/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40P

167/498

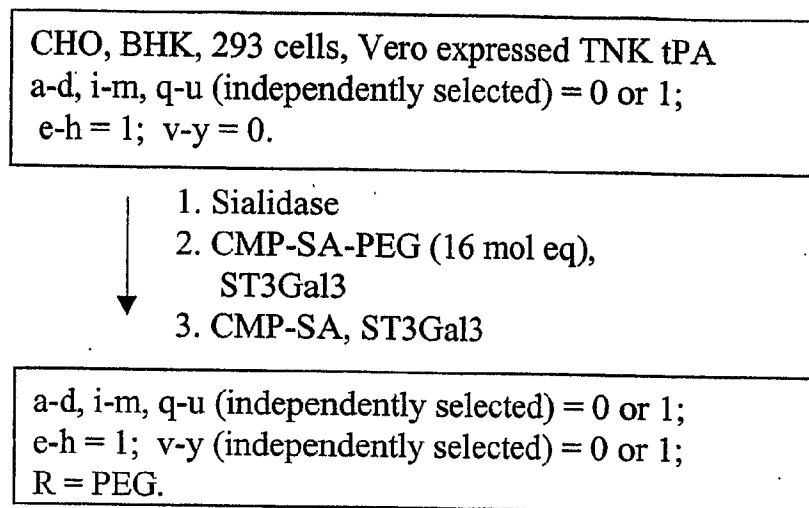


FIG. 40Q

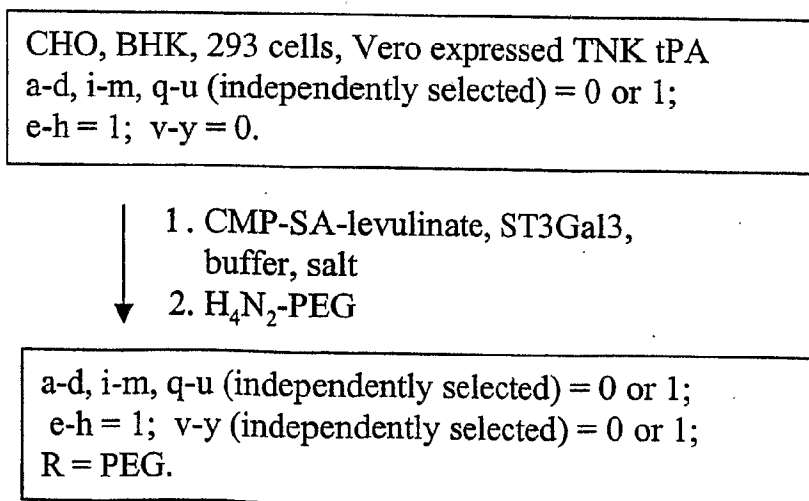


FIG. 40R

168/498

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

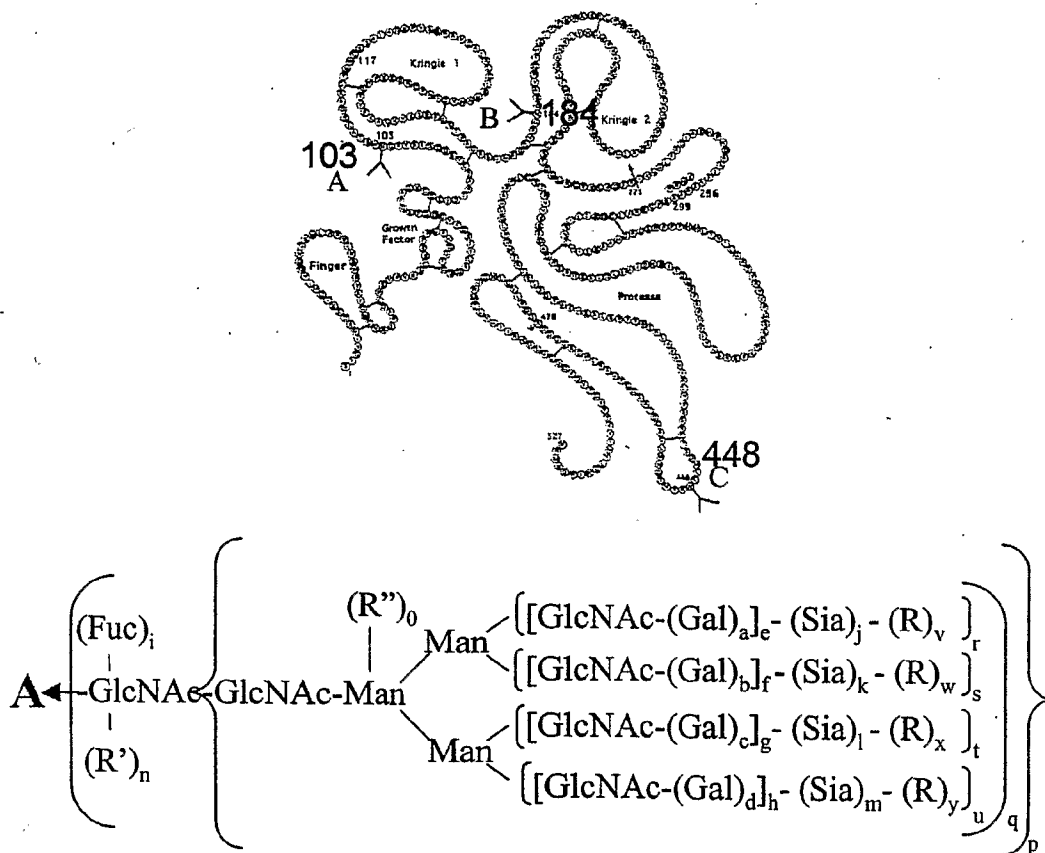


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 40S

169/498



a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 40T

170/498

Insect cell expressed TNK tPA

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 40U

Yeast expressed TNK tPA

a-m = 0; q-y (independently selected) = 0 to 1; p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal-PEG

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 40V

171/498

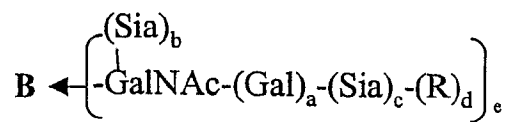
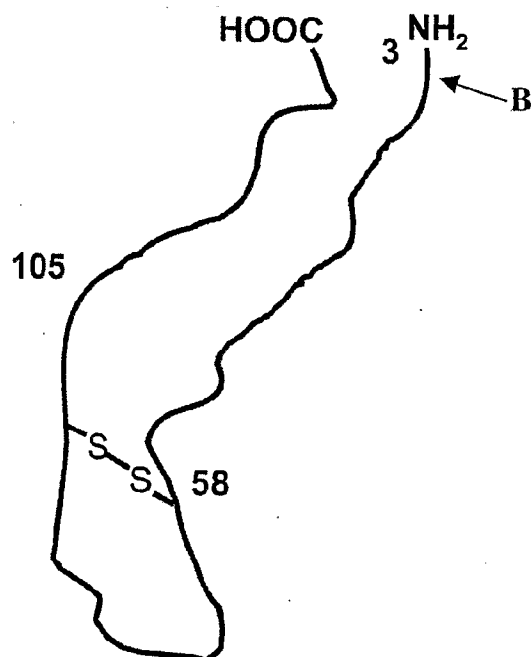
CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, anti-TNF
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;
n = 0; v-y (independently selected) = 0 or 1;
R = linker-anti-TNF IG chimera protein.

FIG. 40W

172/498



a-c, e (independently selected) = 0 or 1;
d = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 41A

173/498

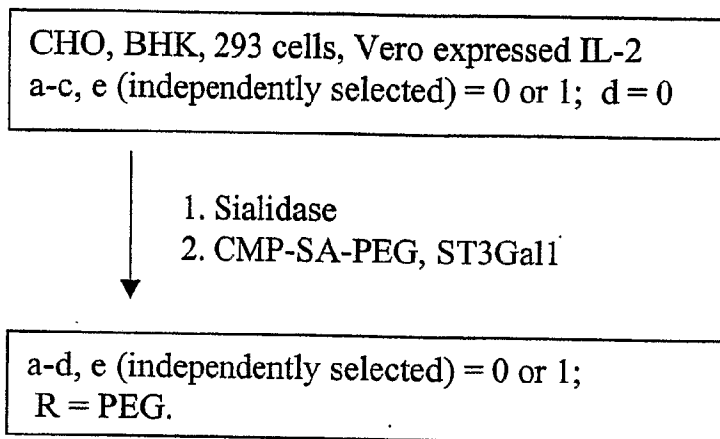


FIG. 41B

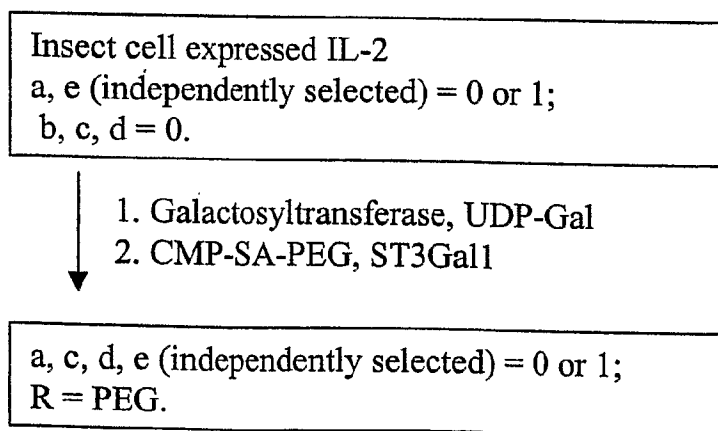


FIG. 41C

174/498

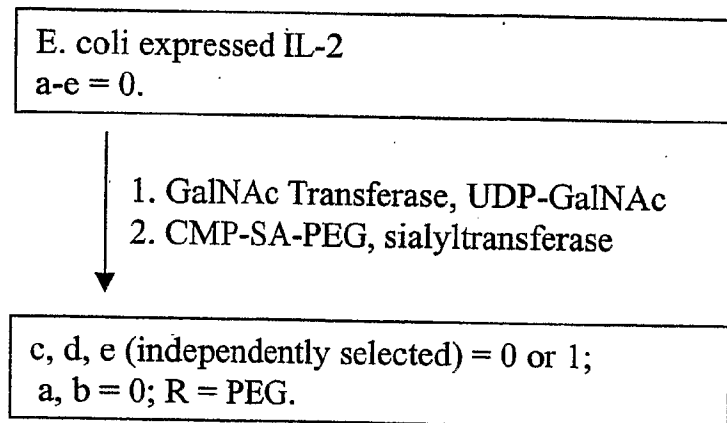


FIG. 41D

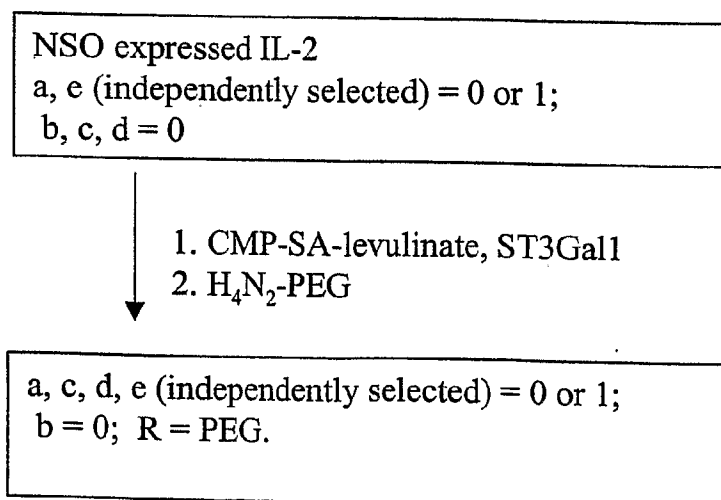


FIG. 41E

175/498

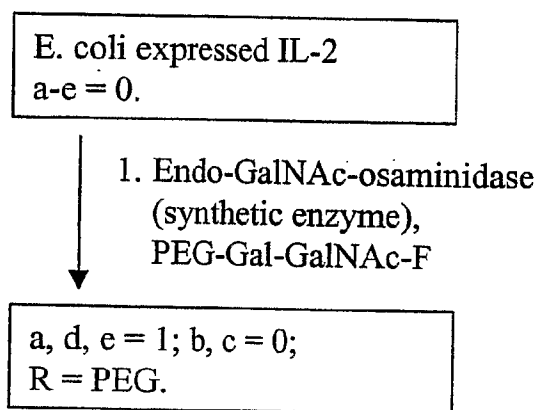


FIG. 41F

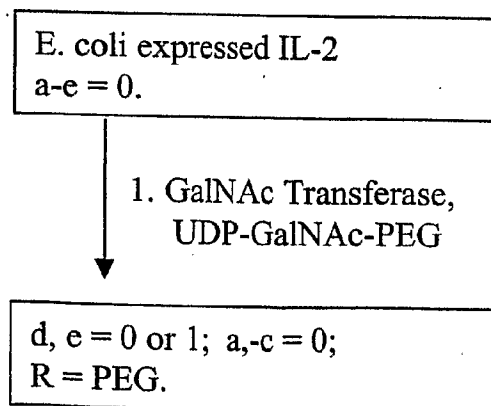
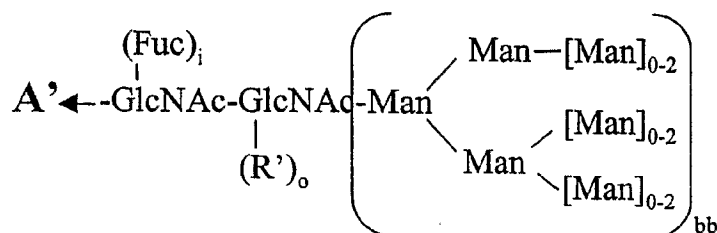
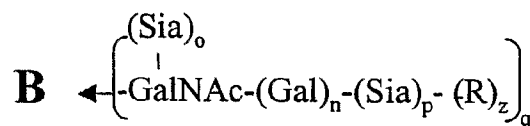
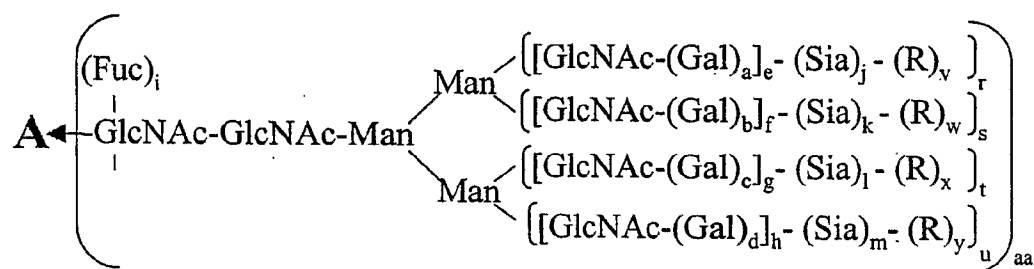


FIG. 41G

176/498

2 peptides
 A and A' - N-linked sites
 B - O-linked sites



Alternate structure
 for some N-linked
 structures of A.

a-d, i, n-u (independently selected) = 0 or 1.
 aa, bb (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 20.
 v-z = 0; R = polymer, glycoconjugate.

FIG. 42A

177/498

CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
2. CMP-SA-PEG, ST3Gal3
3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42C

178/498

CHO, BHK, 293s cells, Vero, MDCK, HEKC
expressed Factor VIII.
e-h = 1 to 4;
aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;
v-z = 0.

↓
1. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;
z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42D

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.
e-h = 1 to 4;
aa, bb, a-d, j-m, i, n-u (independently selected) 0 or 1;
v-z = 0.

↓
1. CMP-SA-PEG, ST3Gal1

e-h = 1 to 4;
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;
z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42E

179/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.



1. CMP-SA-PEG, α 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

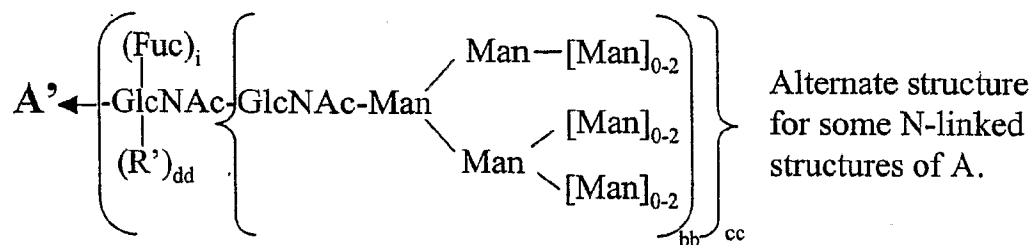
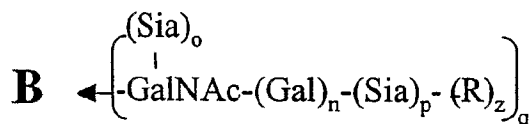
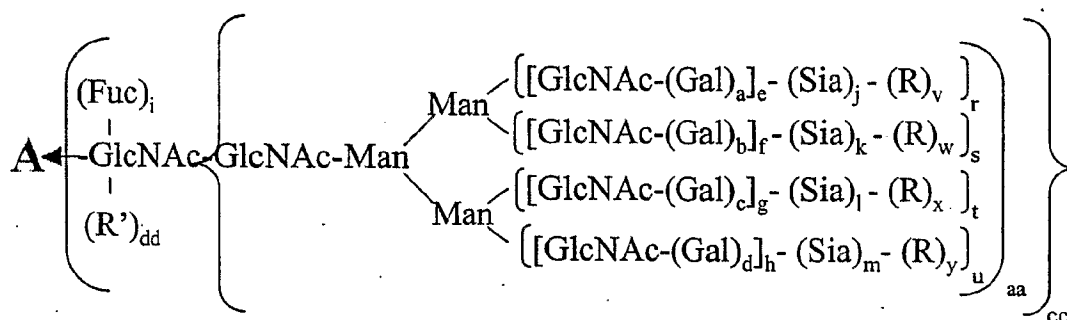
when j-m (independently selected) is 2;

R = PEG.

FIG. 42F

180/498

2 peptides

A or A' - N-linked sites**B** - O-linked sites

a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 42G

181/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓ 1. CMP-SA-levulinate, ST3Gal3,
2. H₄N₂-PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;

dd, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42H

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓ 1. endo-H
2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 42I

182/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC

expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
 2. endo-H
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 42J

CHO, BHK, 293S cells, Vero, MDCK, HEKC

expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT 1 & 2, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0; R = PEG.

FIG. 42K

183/498

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

1. mannosidases
- ↓ 2. GNT-1, 2, 4 & 5; UDP-GlcNAc
- ↓ 3. galactosyltransferase, UDP-Gal
4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;

dd, v-z = 0.

FIG. 42L

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓ 1. mannosidases
- ↓ 2. GNT-1, UDP-GlcNAc-PEG

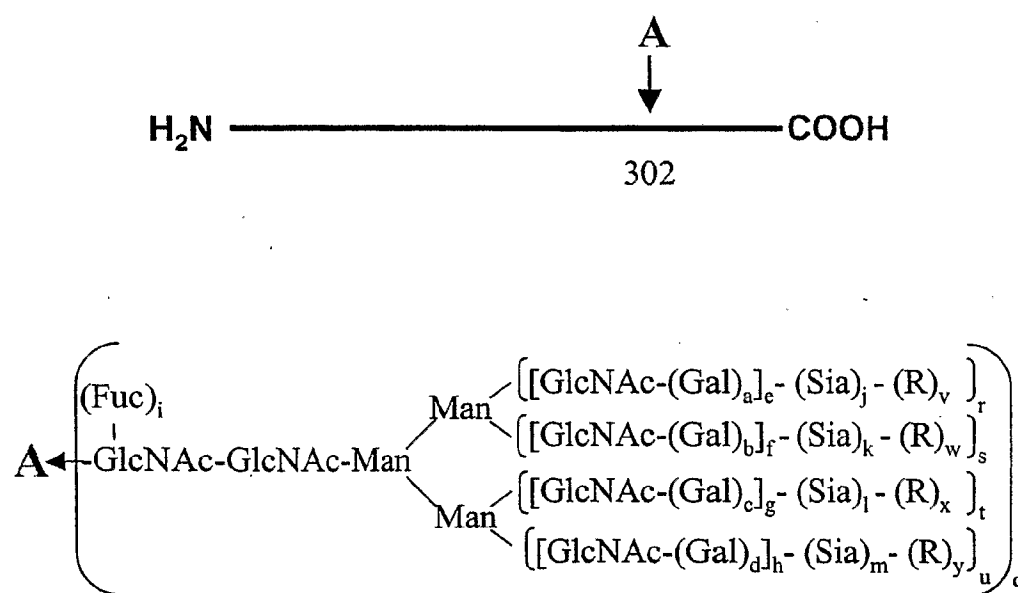
e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0.

FIG. 42M

184/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 43A

185/498

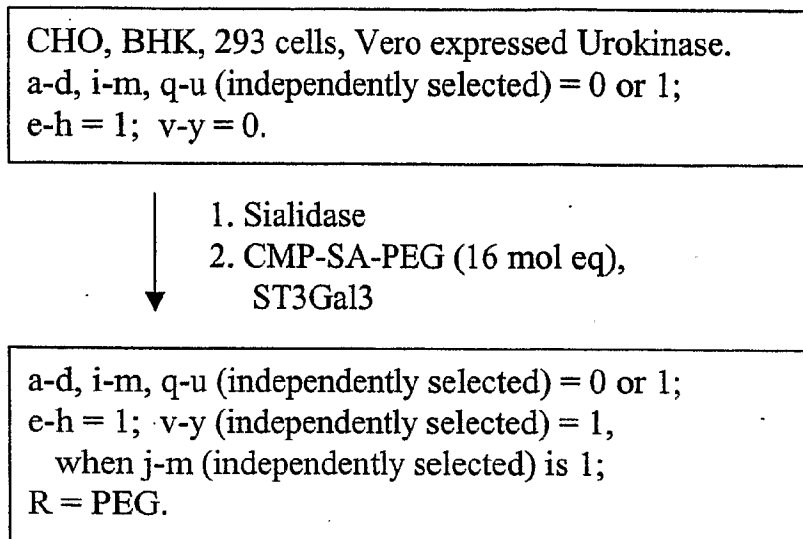


FIG. 43B

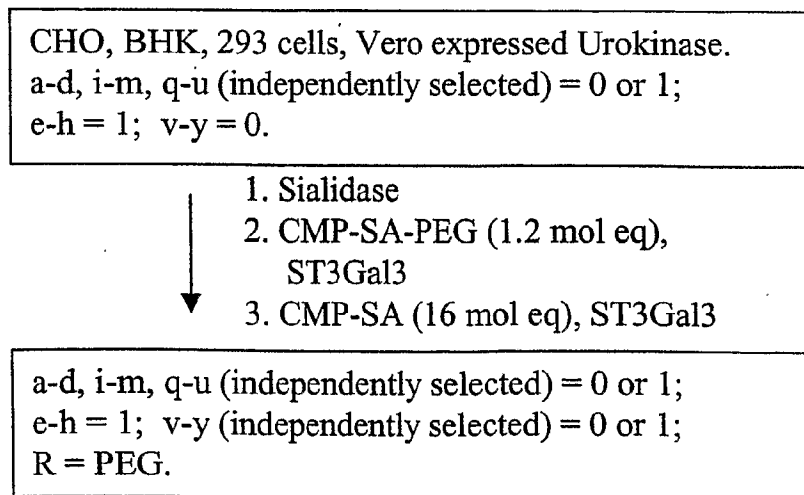


FIG. 43C

186/498

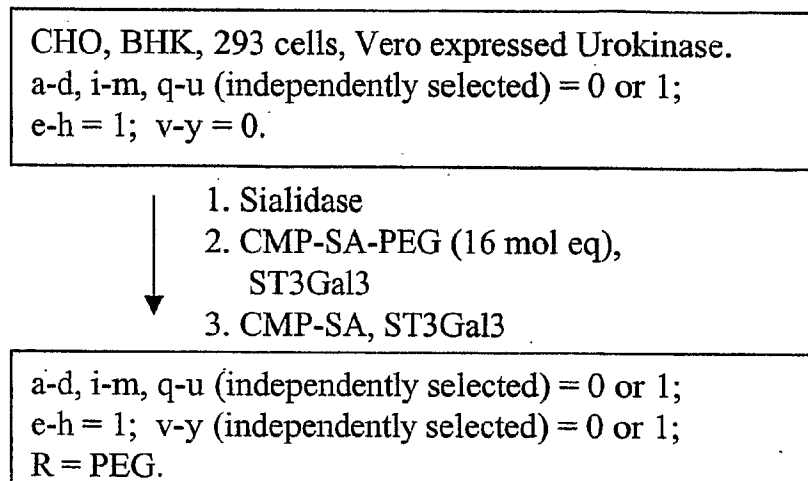


FIG. 43D

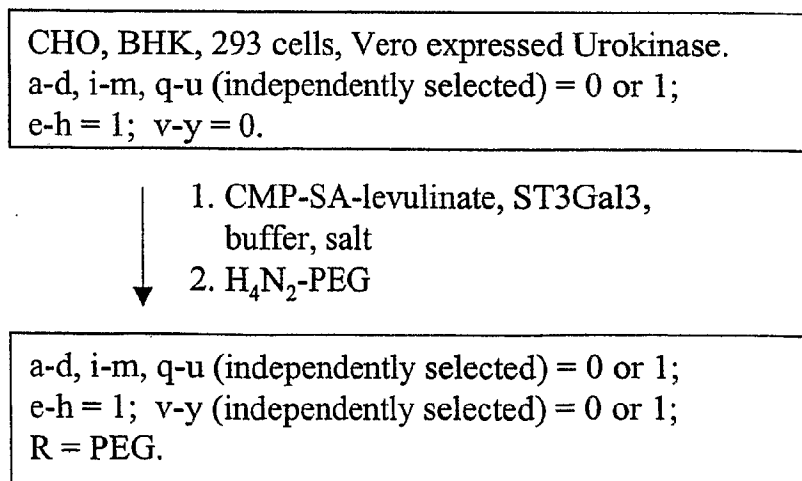


FIG. 43E

187/498

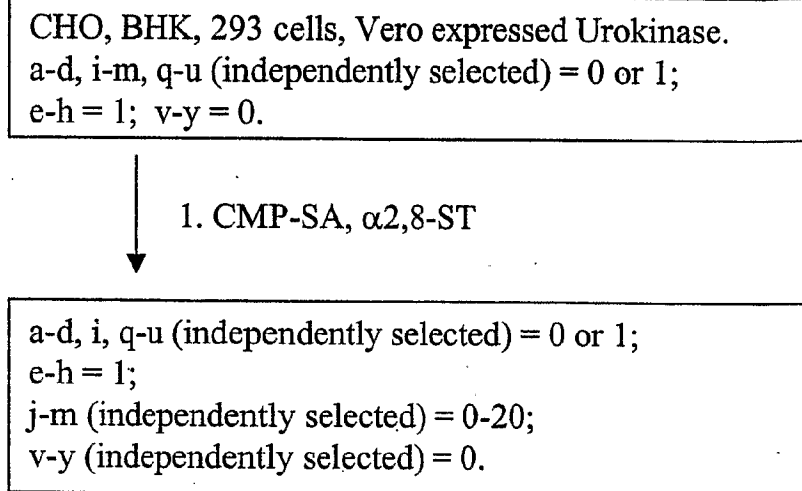
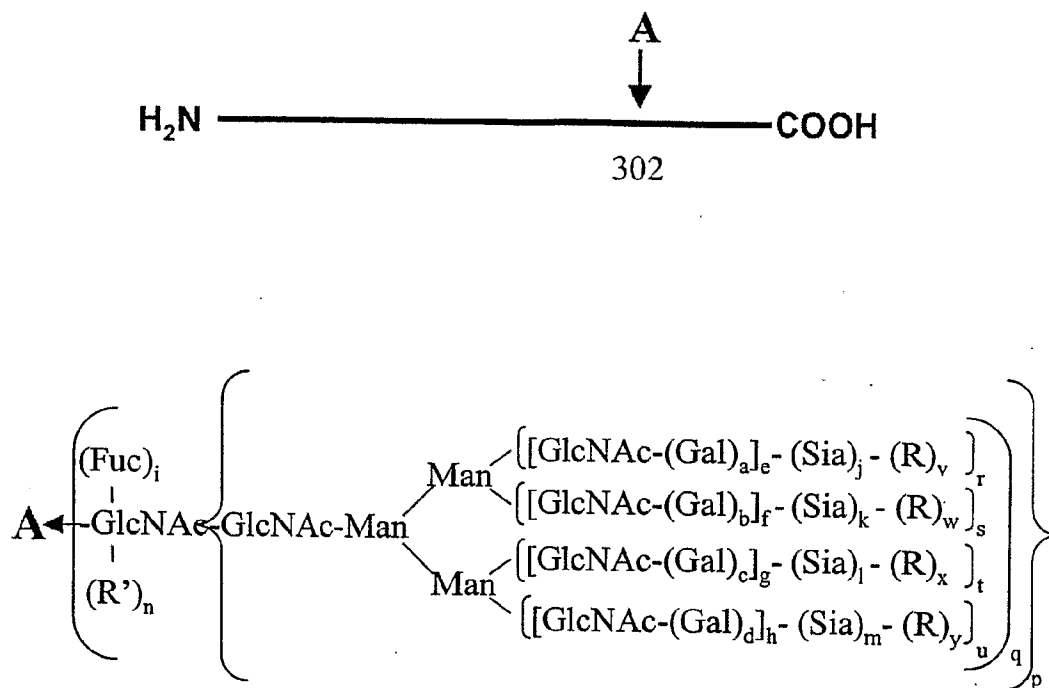


FIG. 43F

188/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 43G

189/498

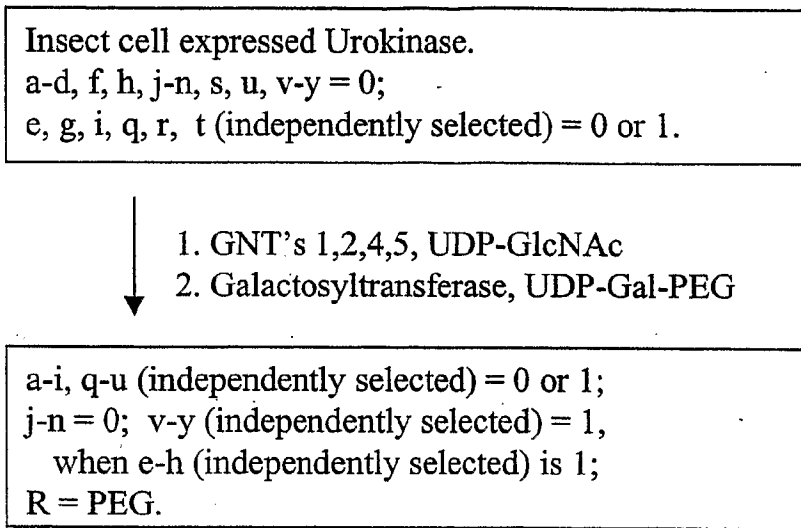


FIG. 43H

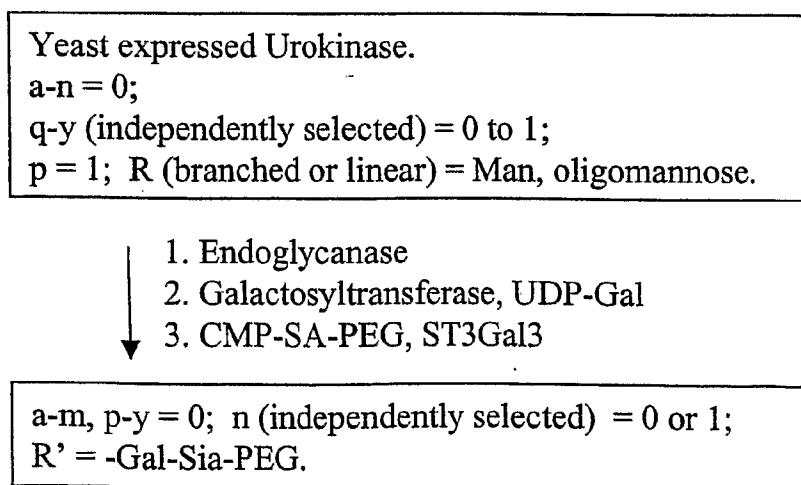


FIG. 43I

190/498

CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated Urokinase produced in CHO.
 - ↓ 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;

p = 1; n = 0;

v-y (independently selected) = 0 or 1;

R = linker-Urokinase.

FIG. 43J

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0; n = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase
 2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

n = 0; e-h = 1; Sia = Sia;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 43K

191/498

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.



1. sulfohydrolase, hexosaminidase

2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

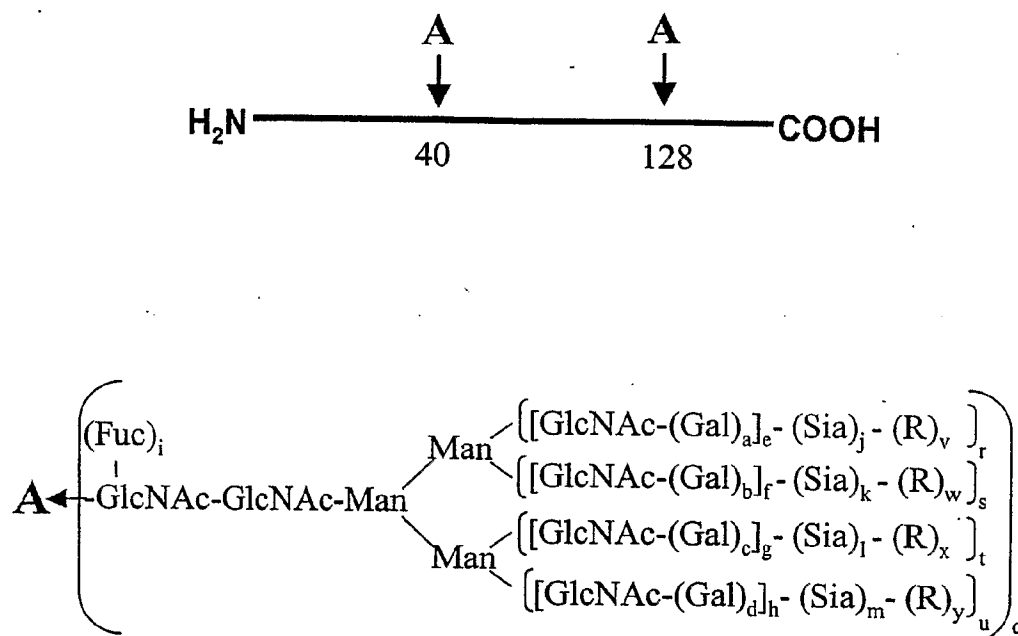
e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 43L

192/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

193/498

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 44C

194/498

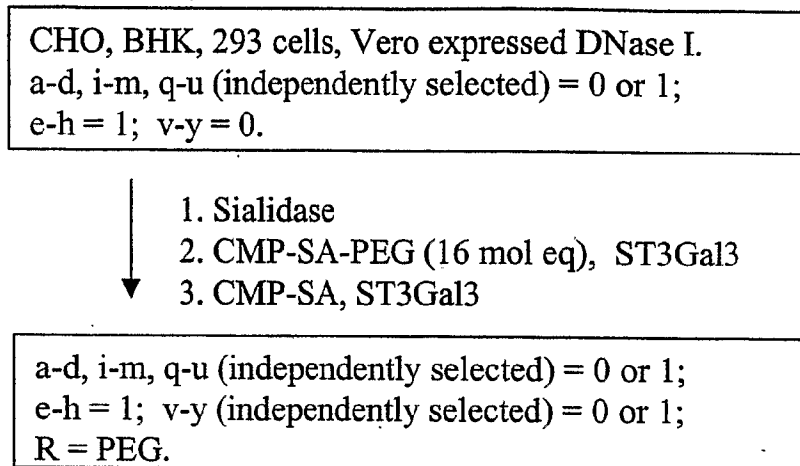


FIG. 44D

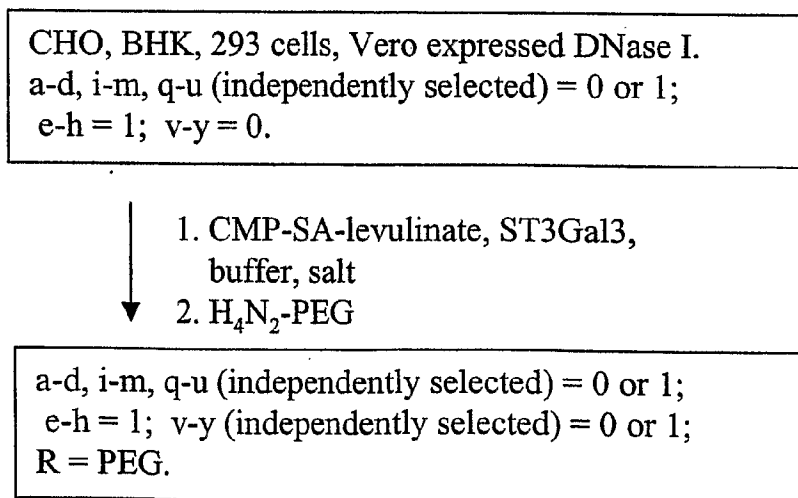


FIG. 44E

195/498

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

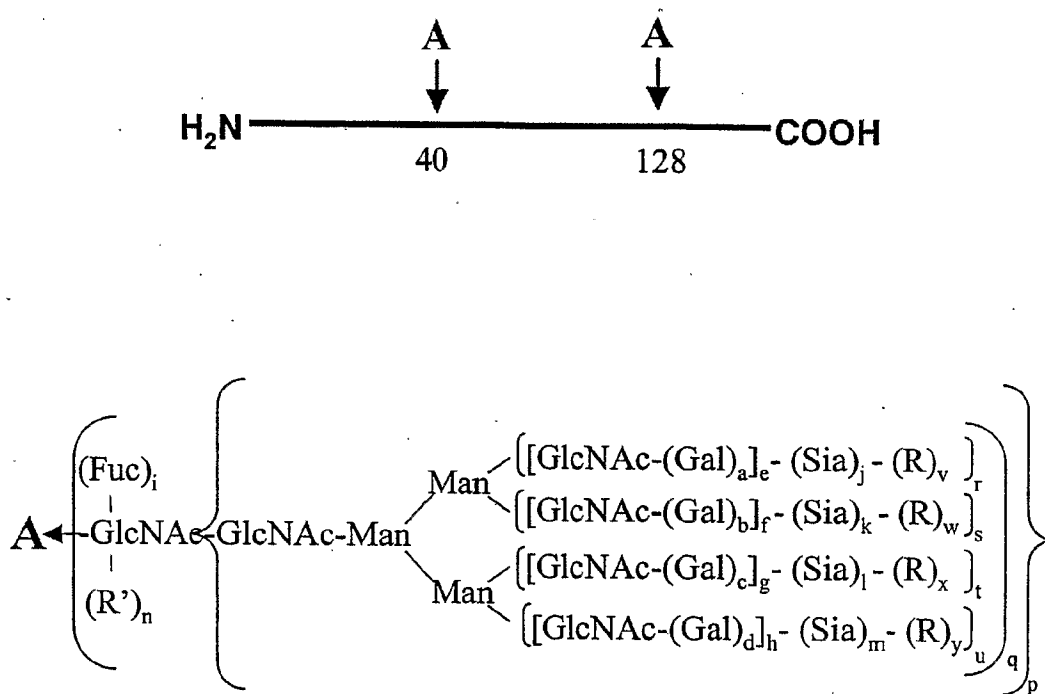


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 44F

196/498



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 44G

197/498

Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 44H

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 44I

198/498

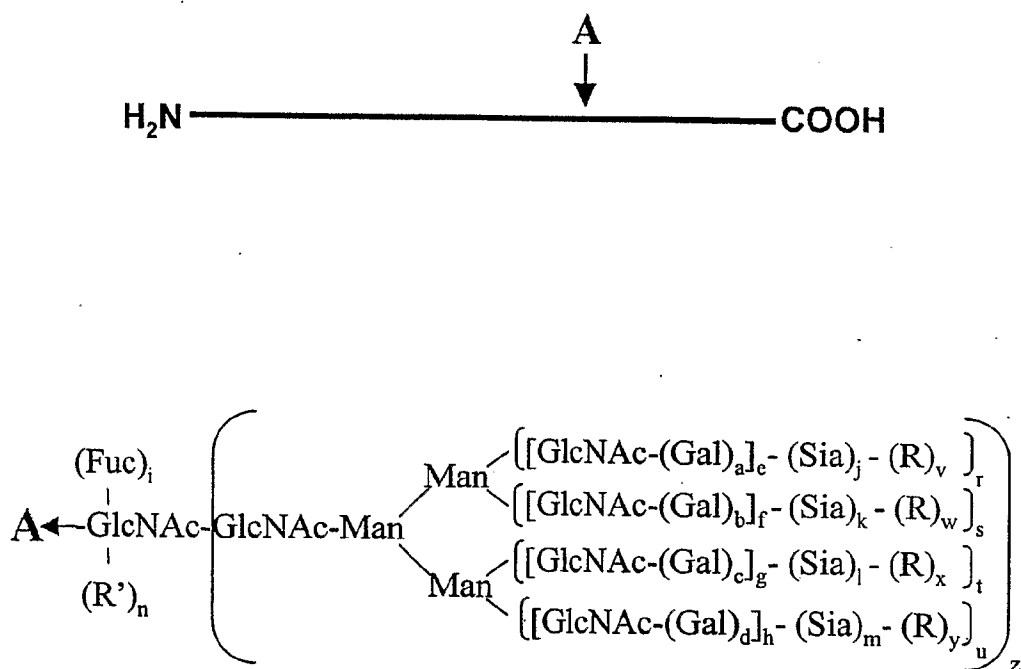
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker- alpha-1-Proteinase inhibitor.

FIG. 44J

199/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 45A

200/498

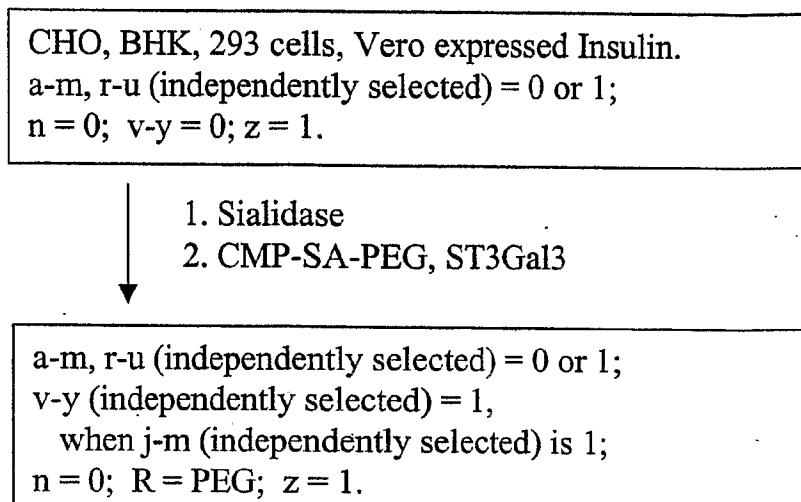


FIG. 45B

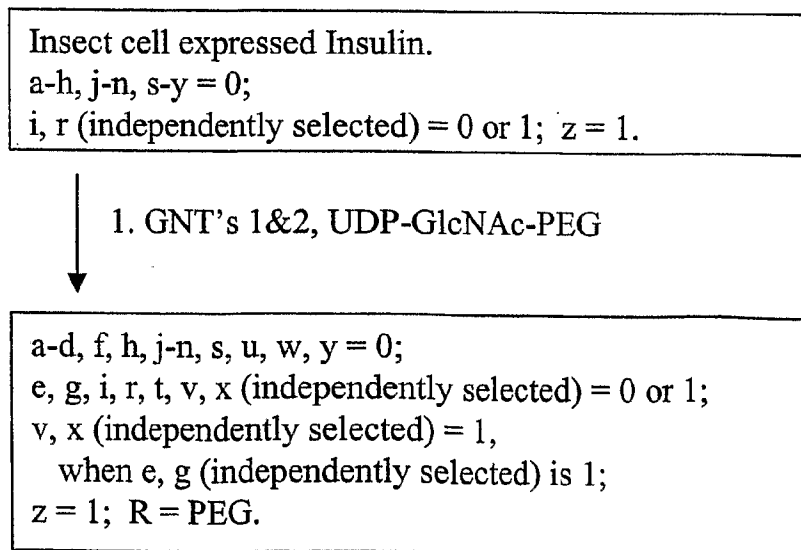


FIG. 45C

201/498

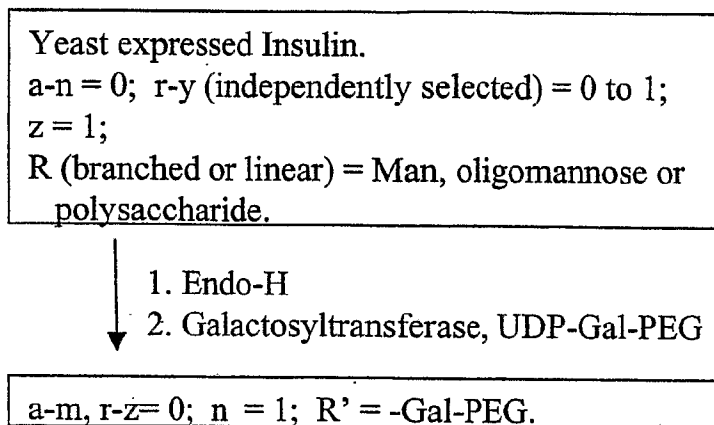


FIG. 45D

203/498

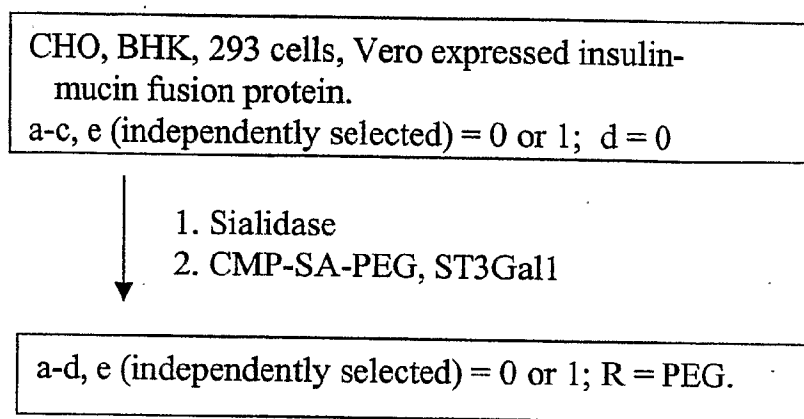


FIG. 45F

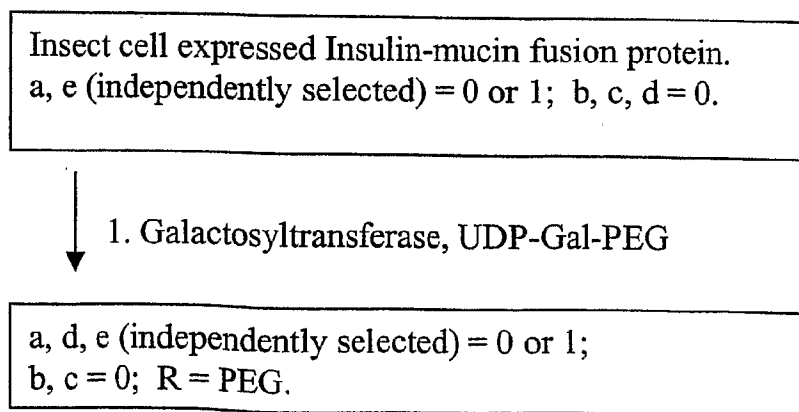


FIG. 45G

204/498

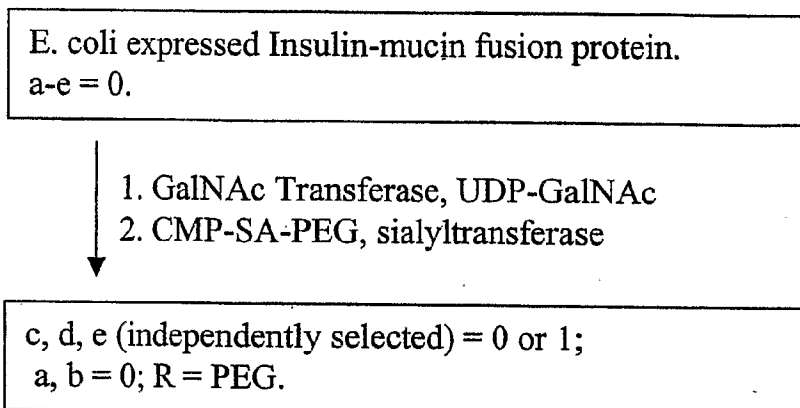
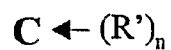
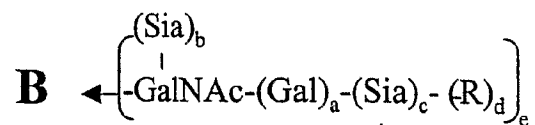
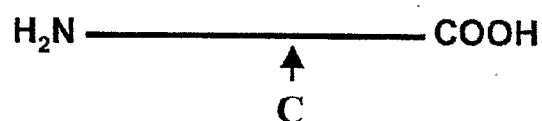
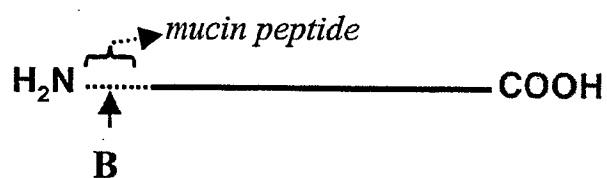
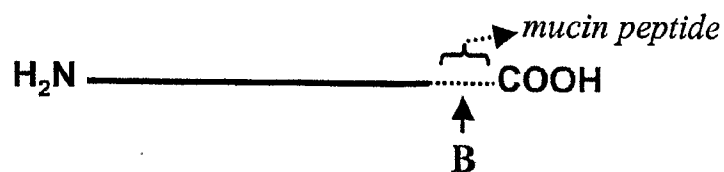


FIG. 45H

205/498



a-c, e (independently selected) = 0 or 1;
 d = 0; R = modifying group, mannose,
 oligo-mannose.

FIG. 45I

206/498

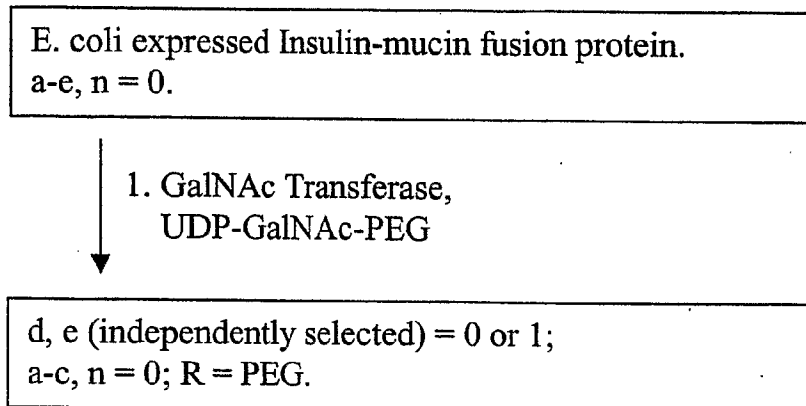


FIG. 45J

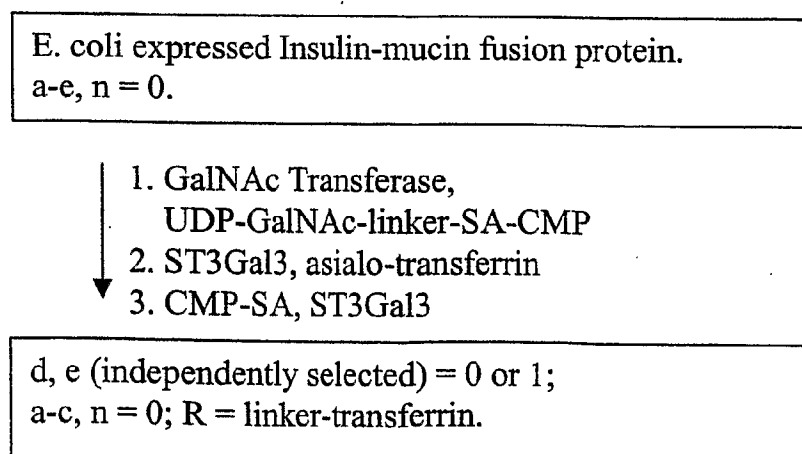


FIG. 45K

207/498

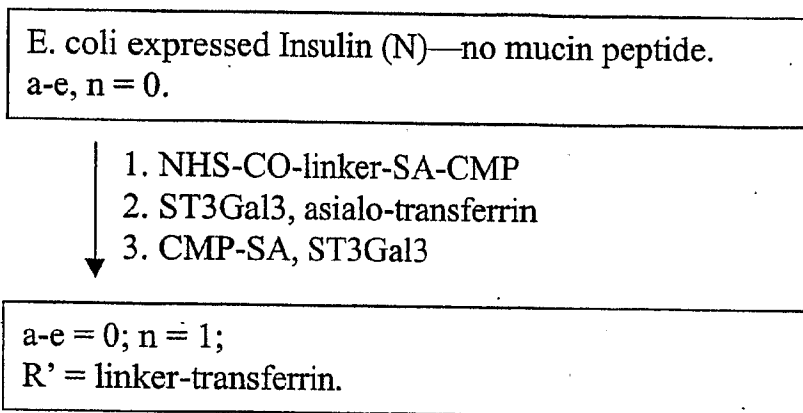
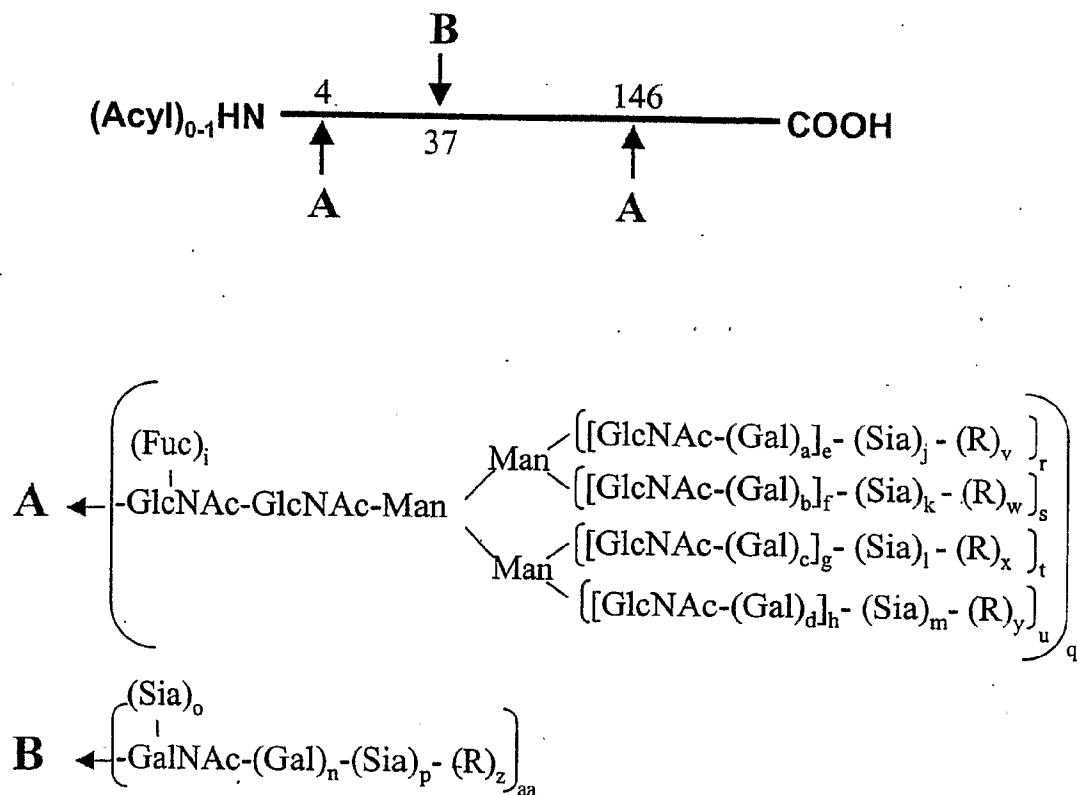


FIG. 45L

208/498



a-d, i, n-u, aa (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer, glycoconjugate.

FIG. 46A

209/498

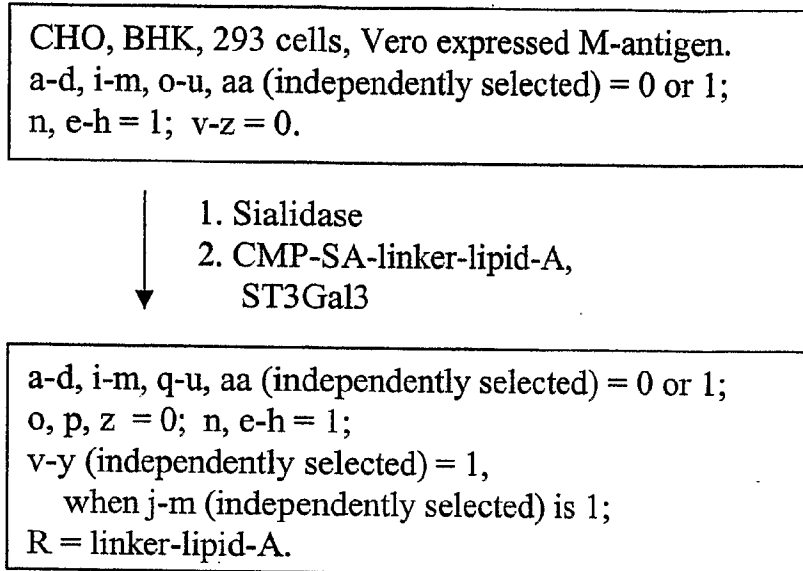


FIG. 46B

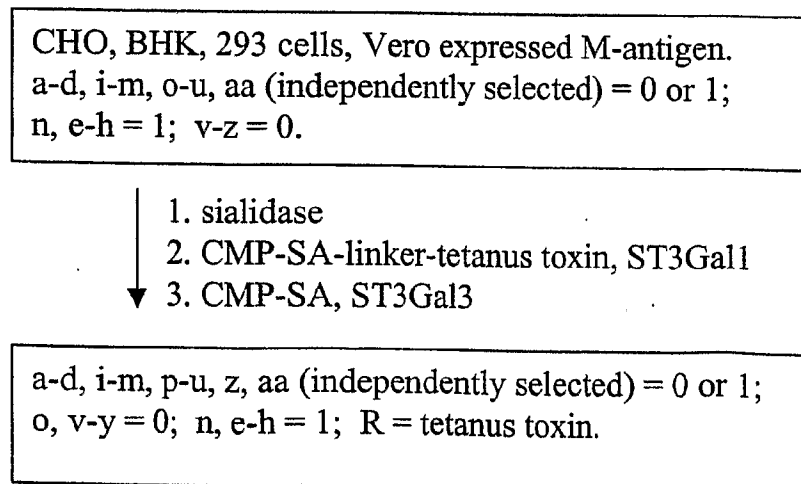


FIG. 46C

210/498

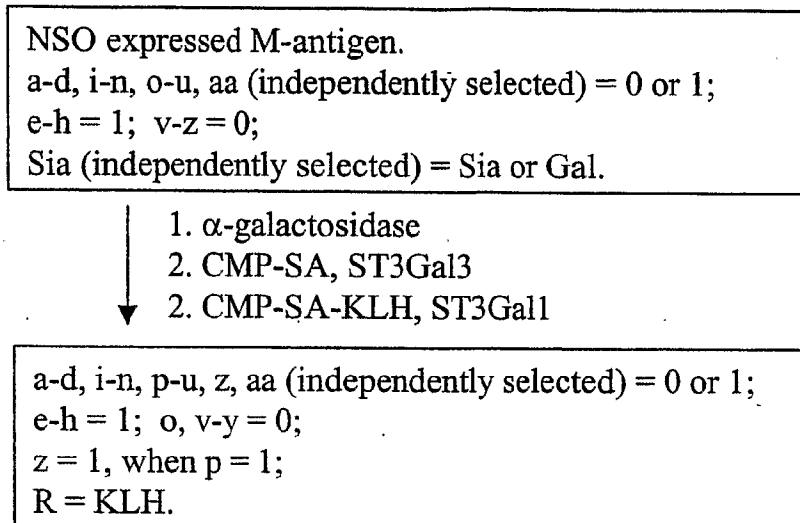


FIG. 46D

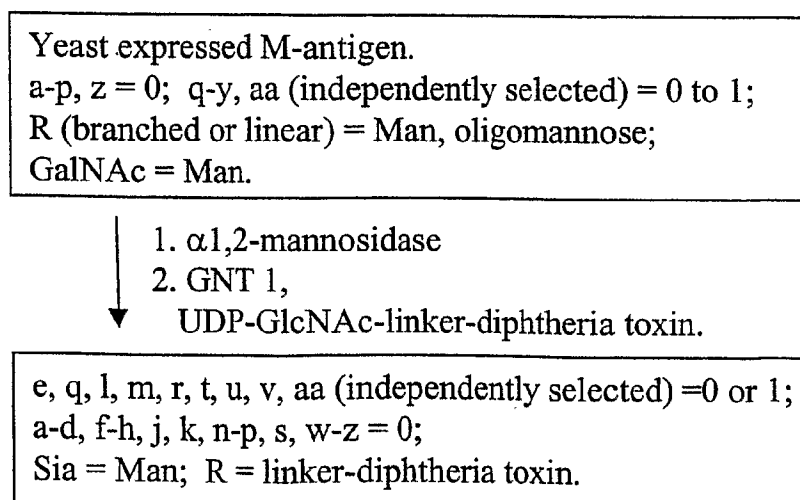


FIG. 46E

211/498

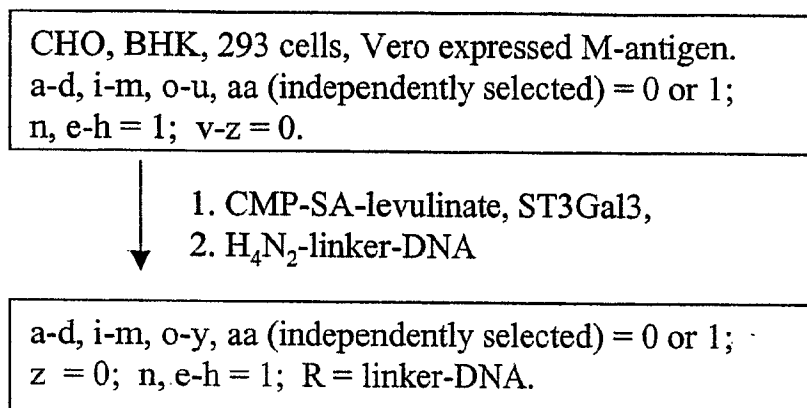


FIG. 46F

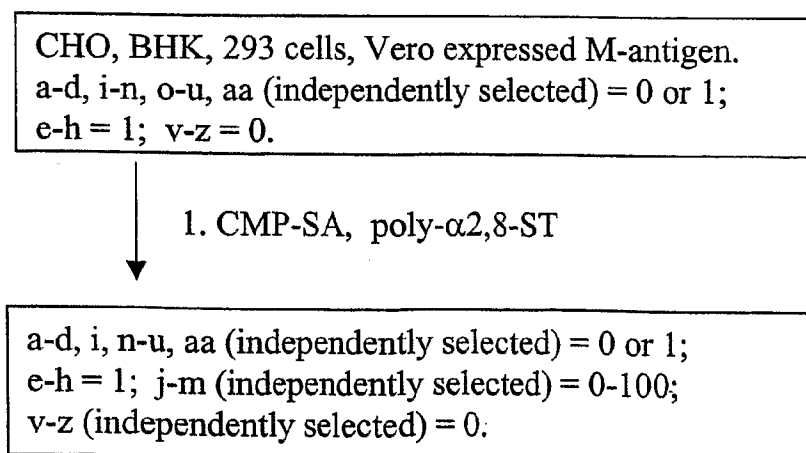
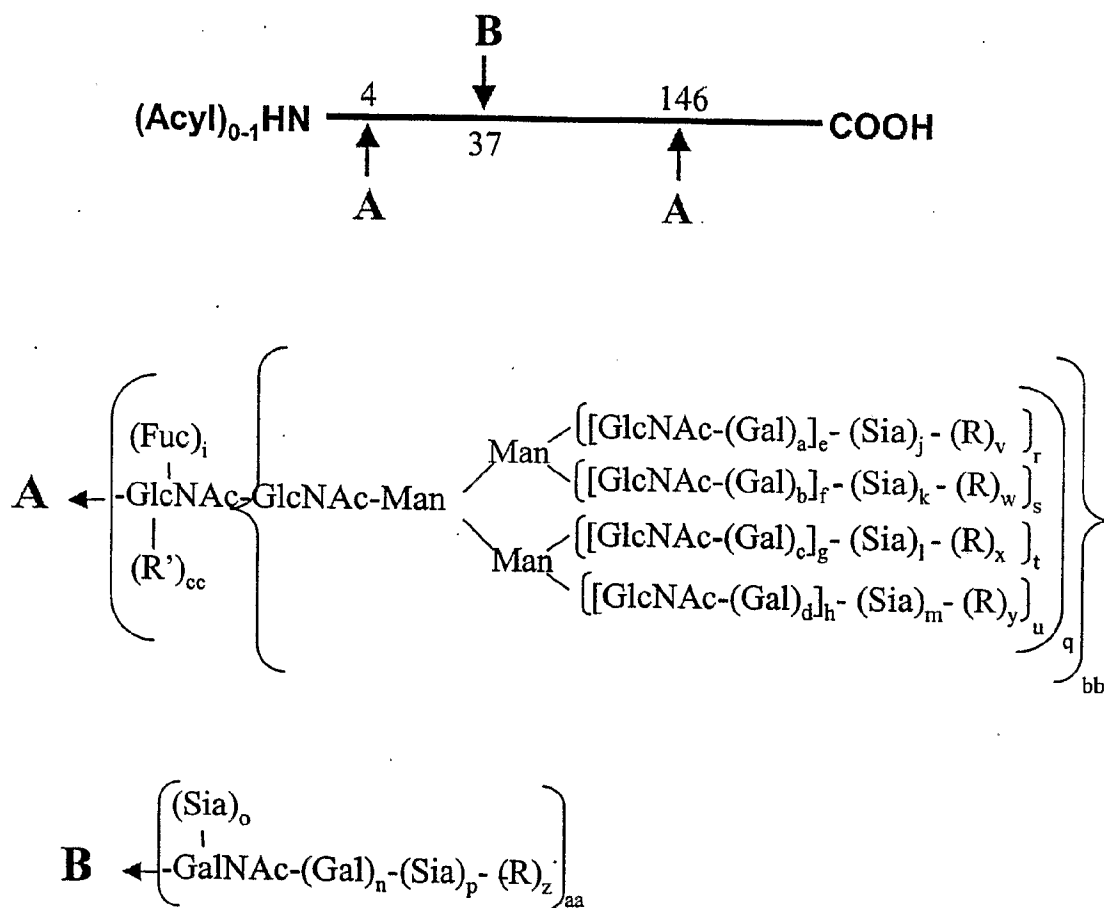


FIG. 46G

212/498



a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46H

213/498

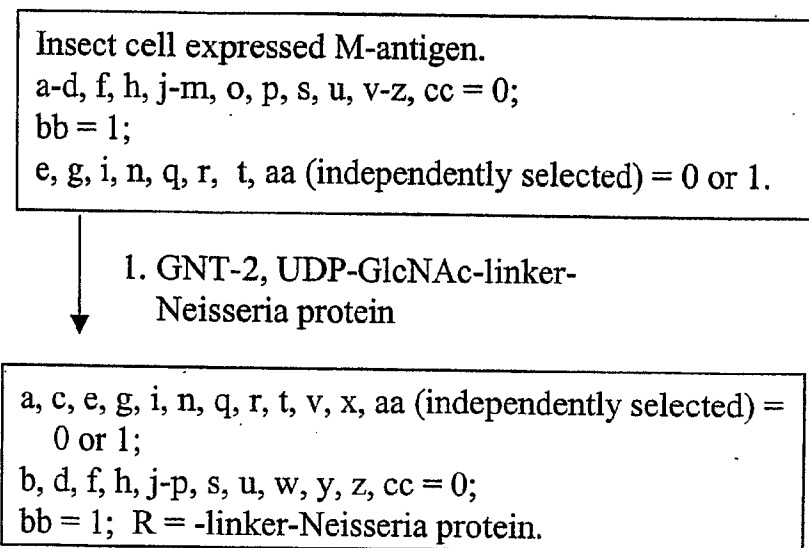


FIG. 46I

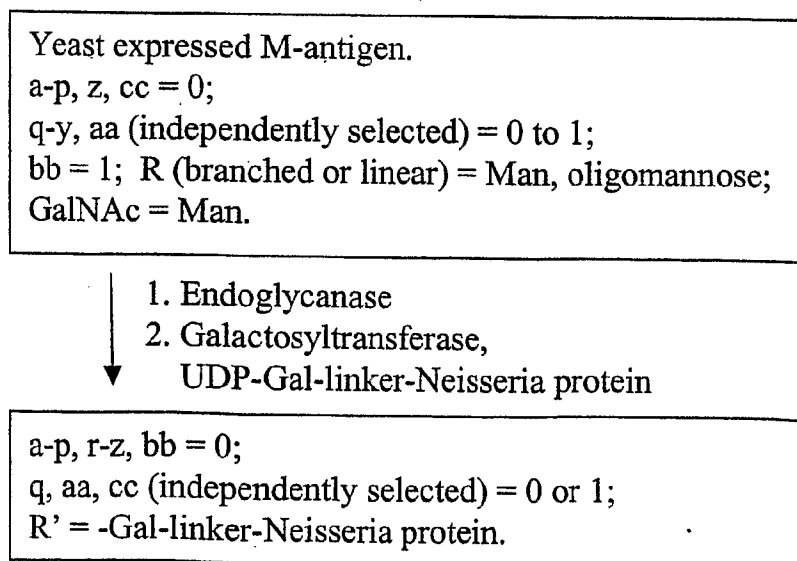


FIG. 46J

214/498


Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

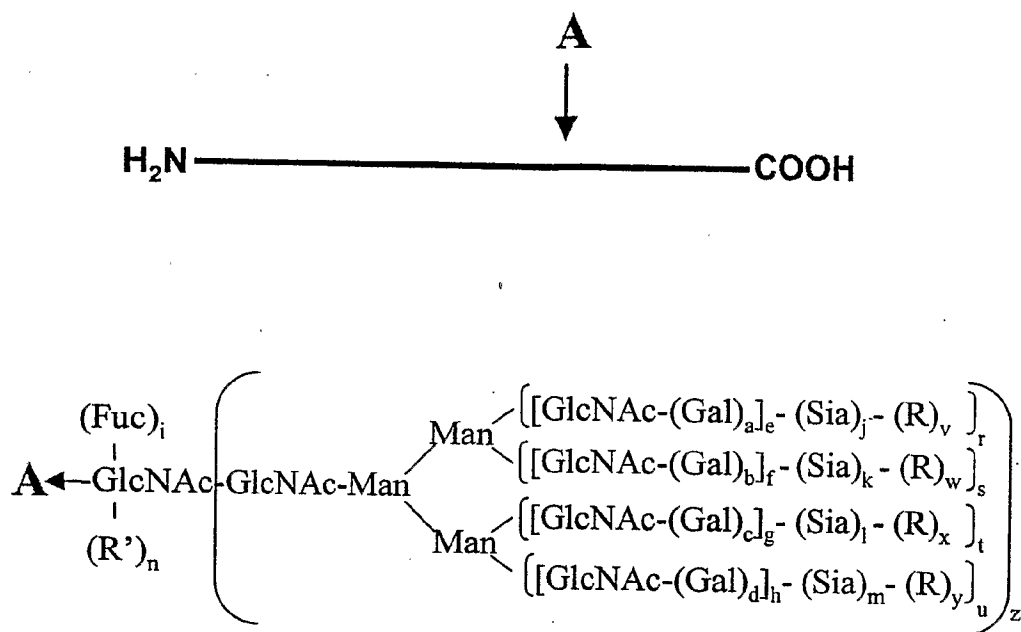
GalNAc = Man.

- 
1. mannosidases
 2. GNT 1 & 2, UDP-GlcNAc
 3. UDP-Gal, Galactosyltransferase,
 4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;
b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 46K

215/498



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 47A

216/498

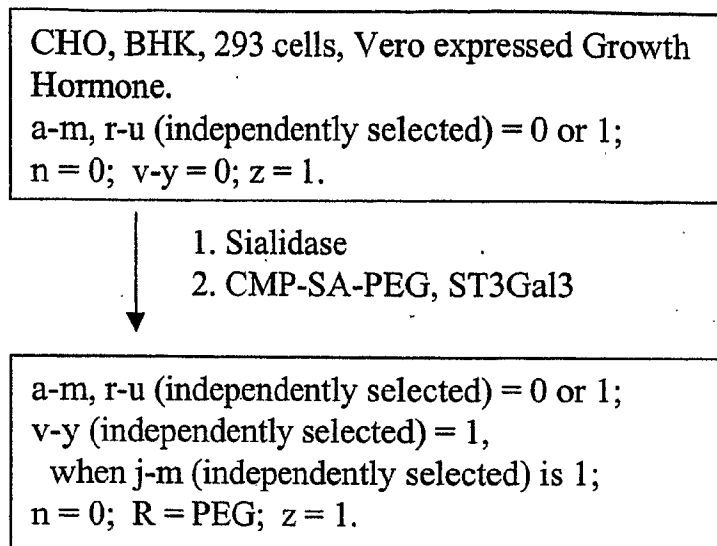


FIG. 47B

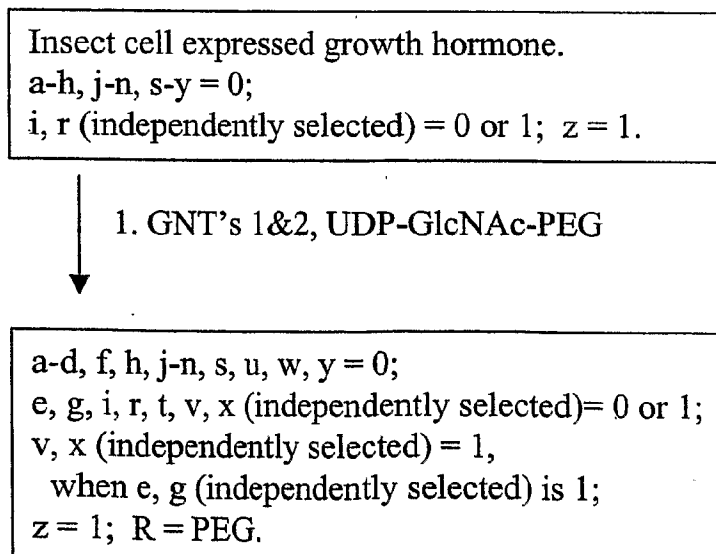


FIG. 47C

217/498

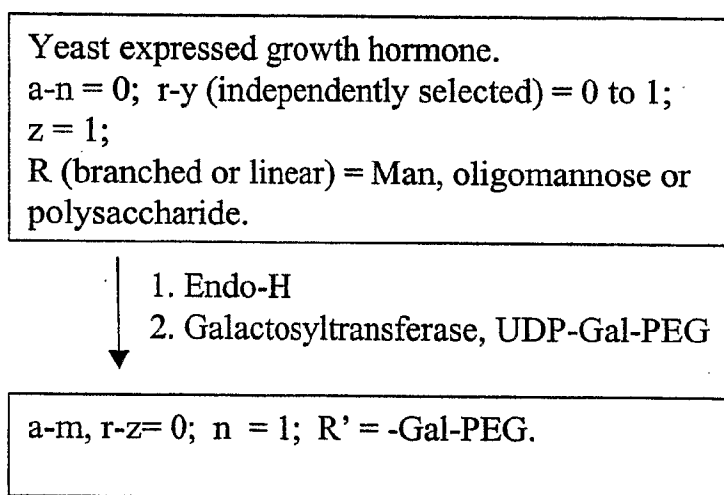


FIG. 47D

219/498

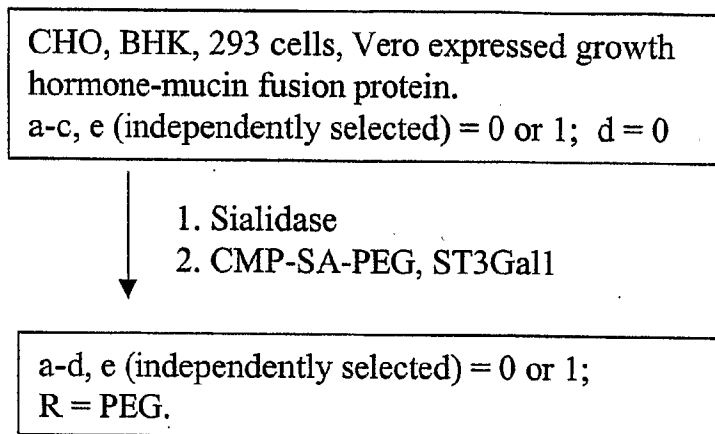


FIG. 47F

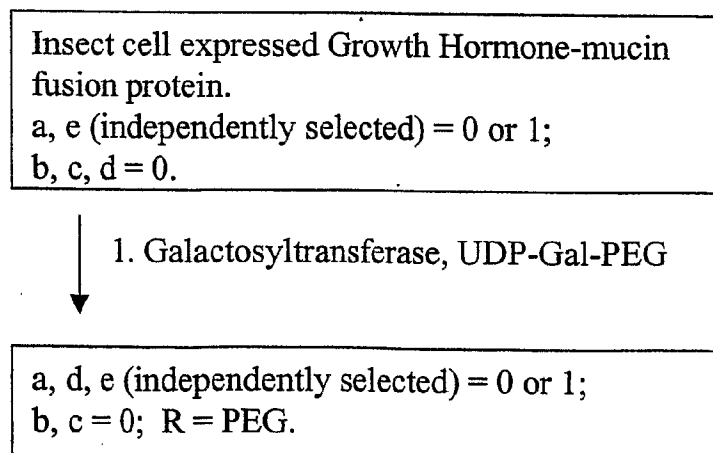


FIG. 47G

220/498

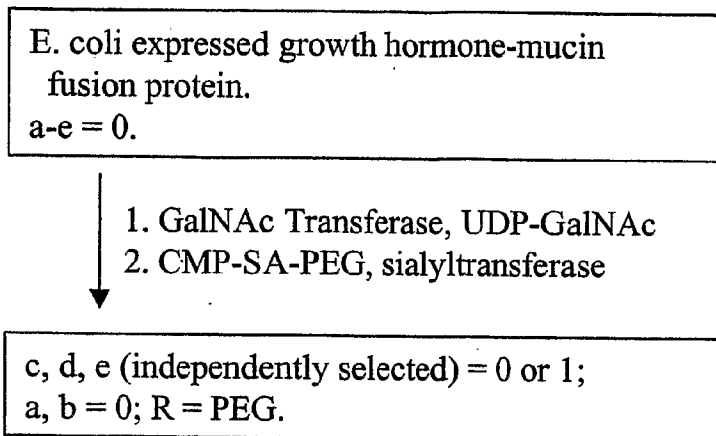


FIG. 47H

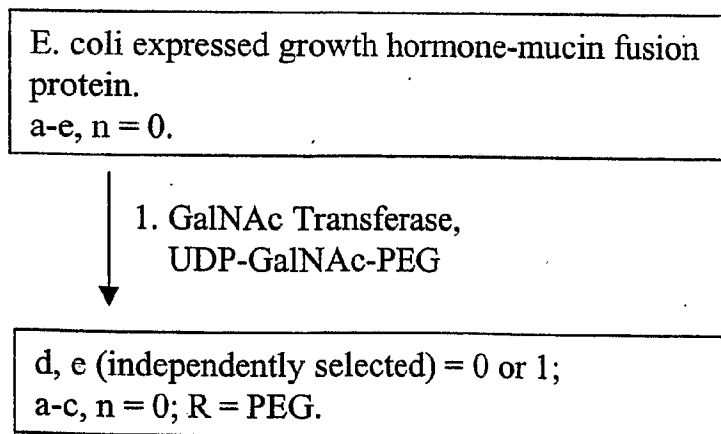


FIG. 47I

221/498

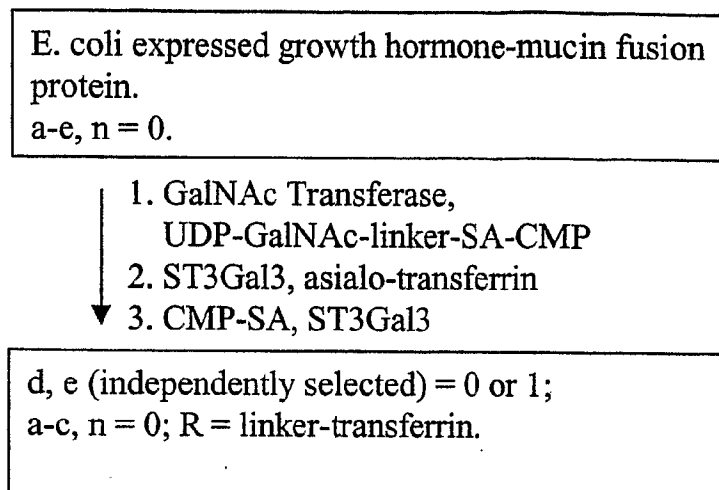


FIG. 47J

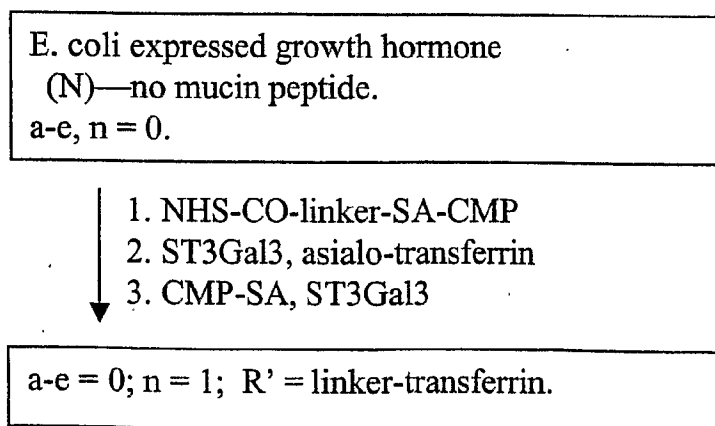
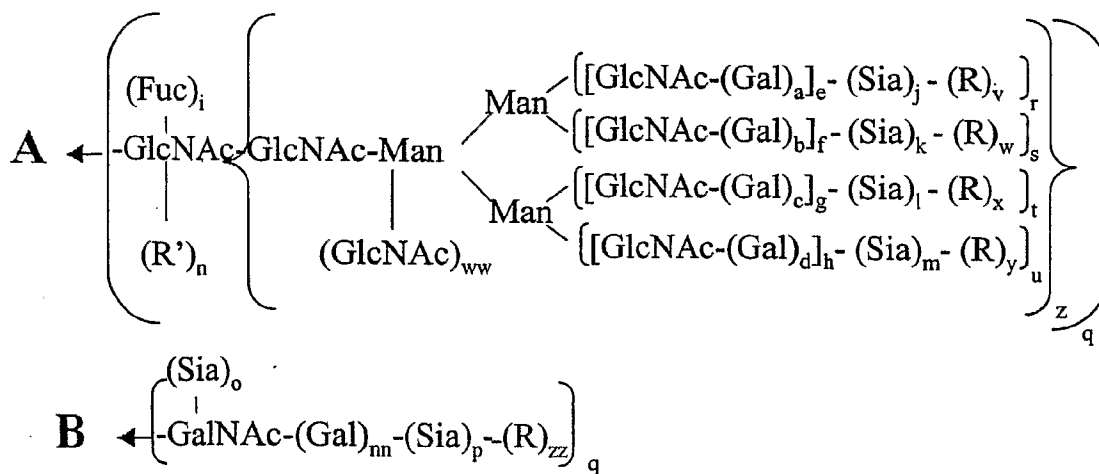
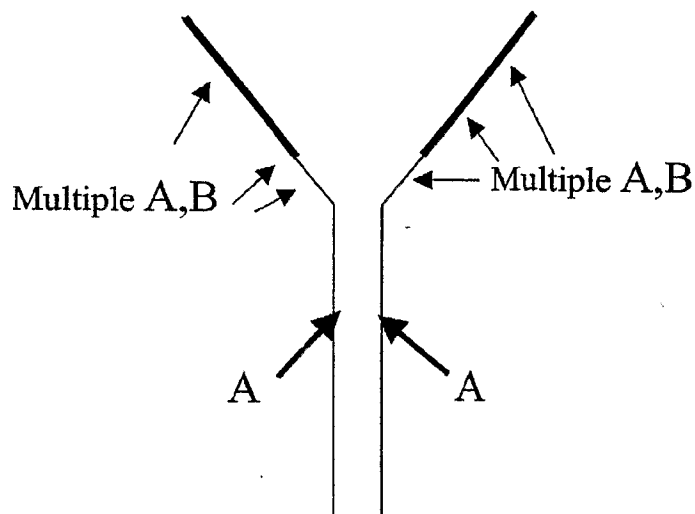


FIG. 47K

222/498



a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

223/498

CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
 2. galactosyltransferase, UPD-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 48C

224/498

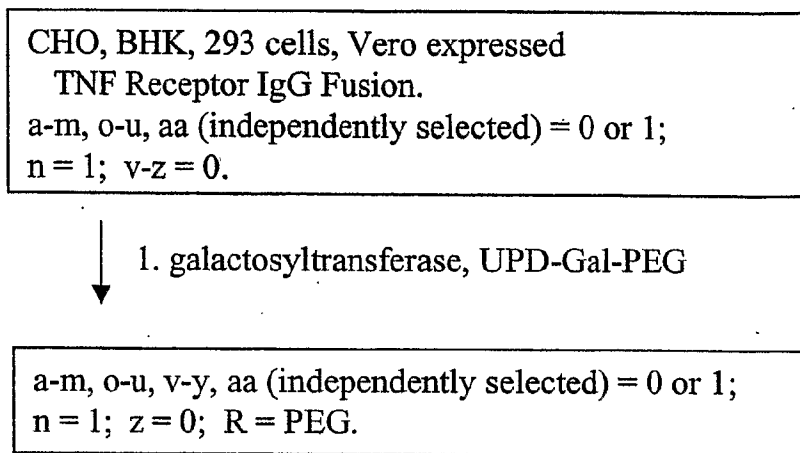


FIG. 48D

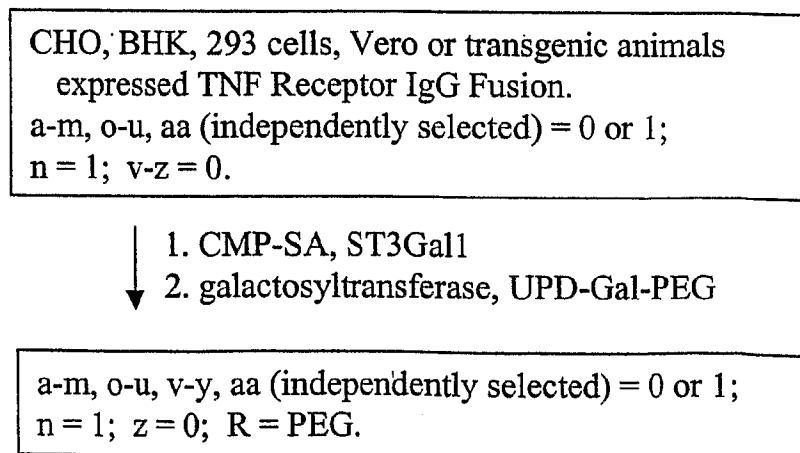


FIG. 48E

225/498

CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-levulinate, ST3Gal1
2. H₄N₂-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48F

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.

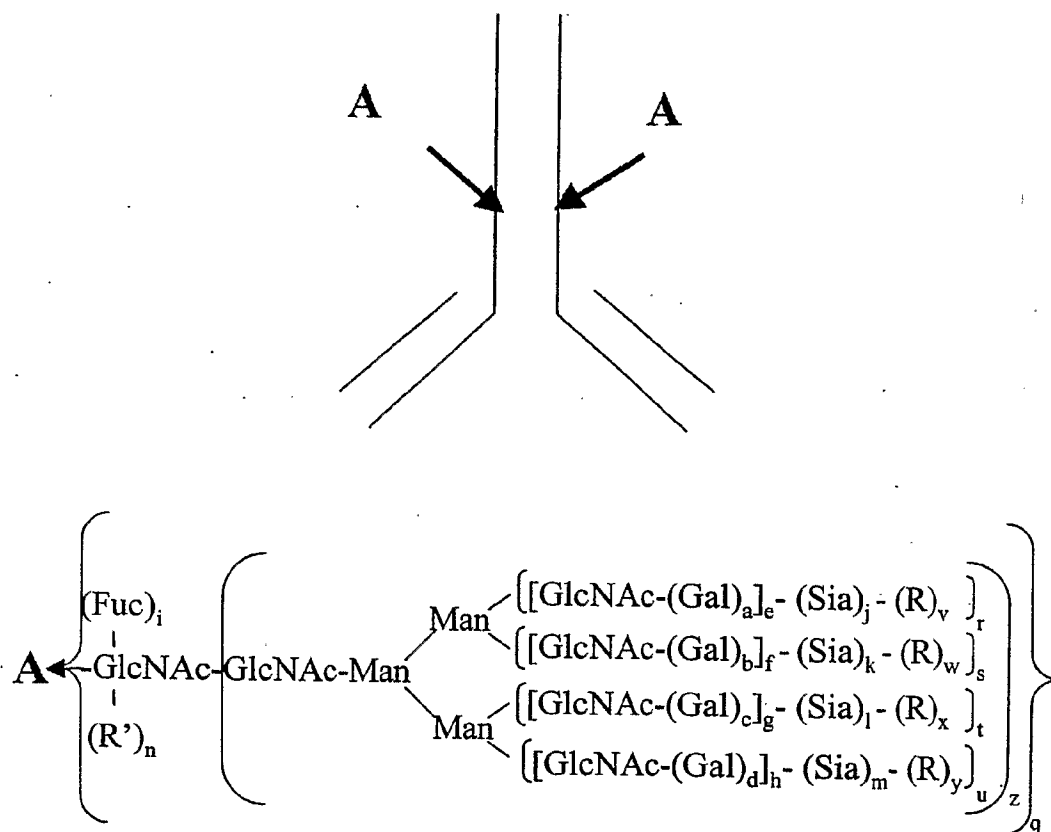
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-PEG, α 2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;
n = 1; j-m, p (independently selected) = 0 to 2;
v-z (independently selected) = 1,
when j-m, p (independently selected) is 2;
R = PEG.

FIG. 48G

226/498



a-d, i, l, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

 $j-k$ (independently selected) = 0 or 1.

$M = 0$ to 20.

$$n, v-y=0; z=0 \text{ or } 1;$$

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

227/498

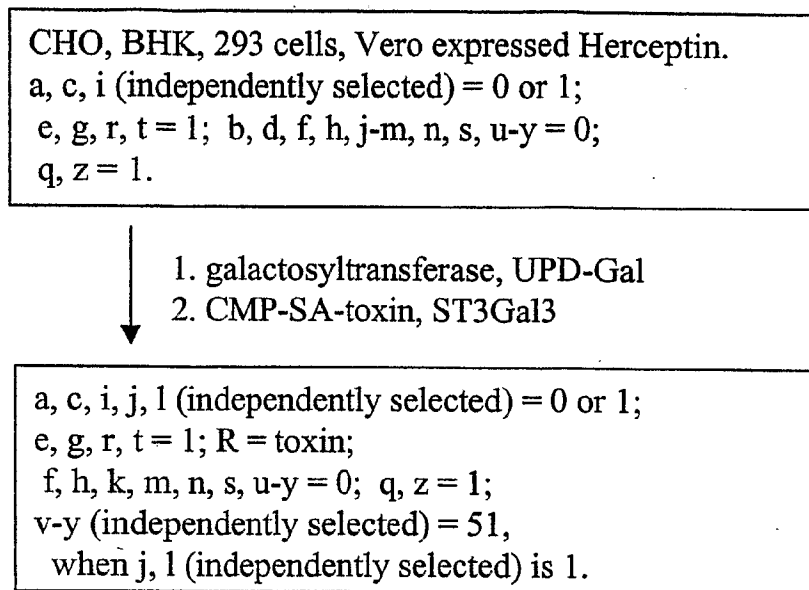


FIG. 49B

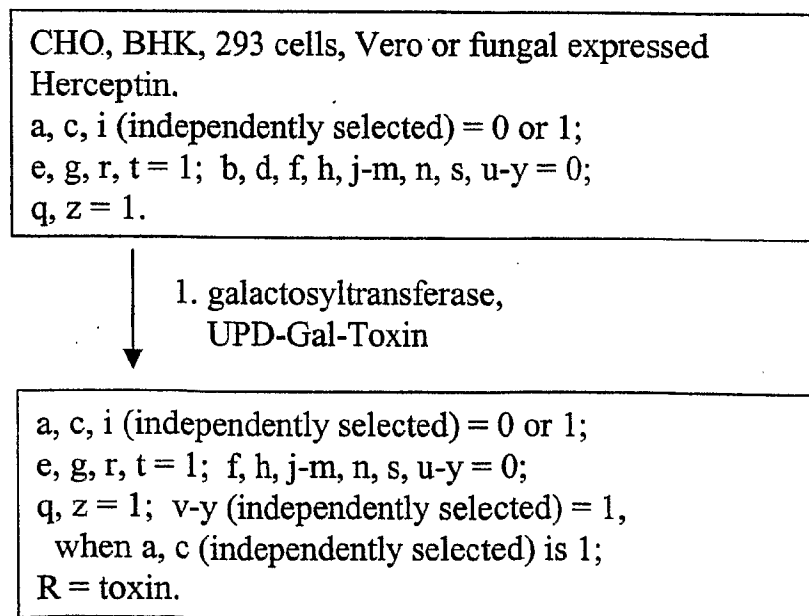


FIG. 49C

228/498

Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

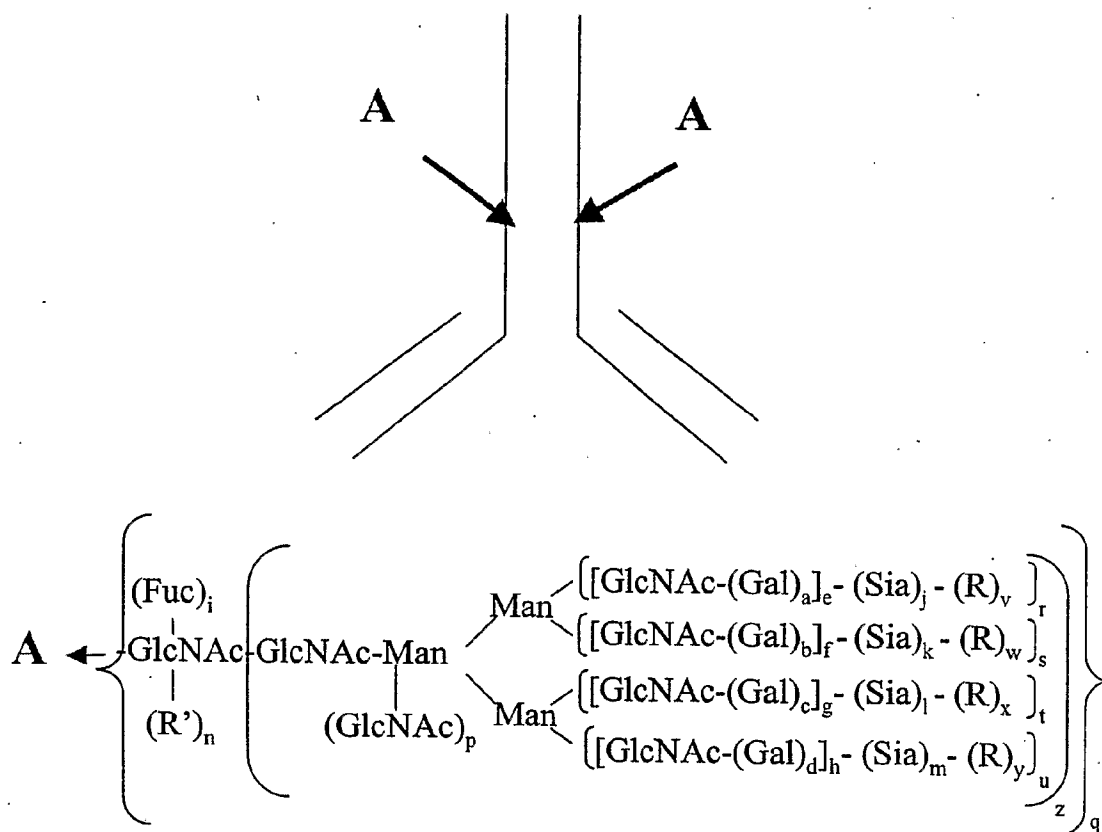
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - ▼ 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z= 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D

229/498



a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 50A

230/498

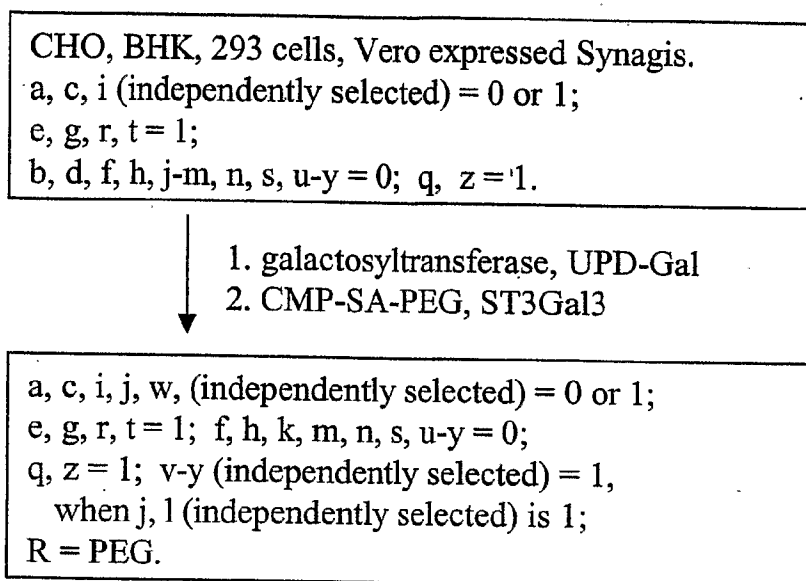


FIG. 50B

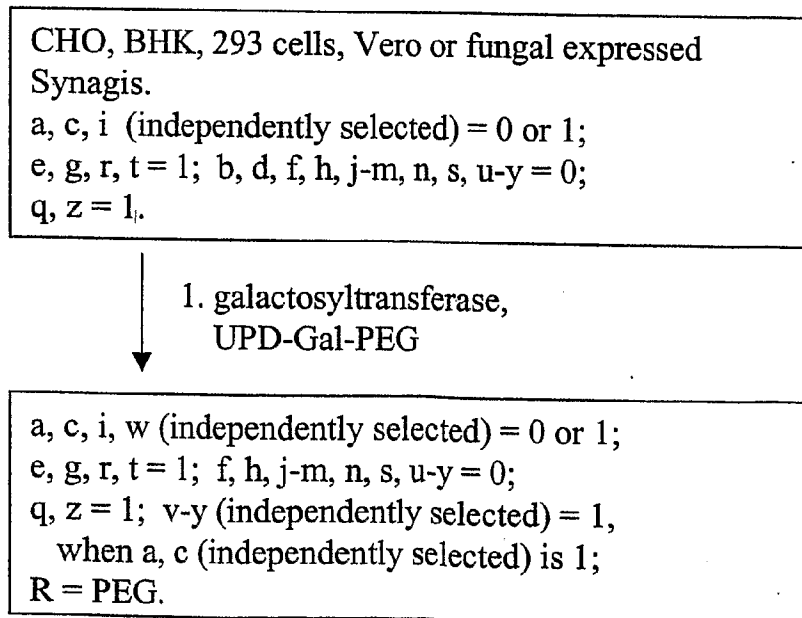


FIG. 50C

231/498

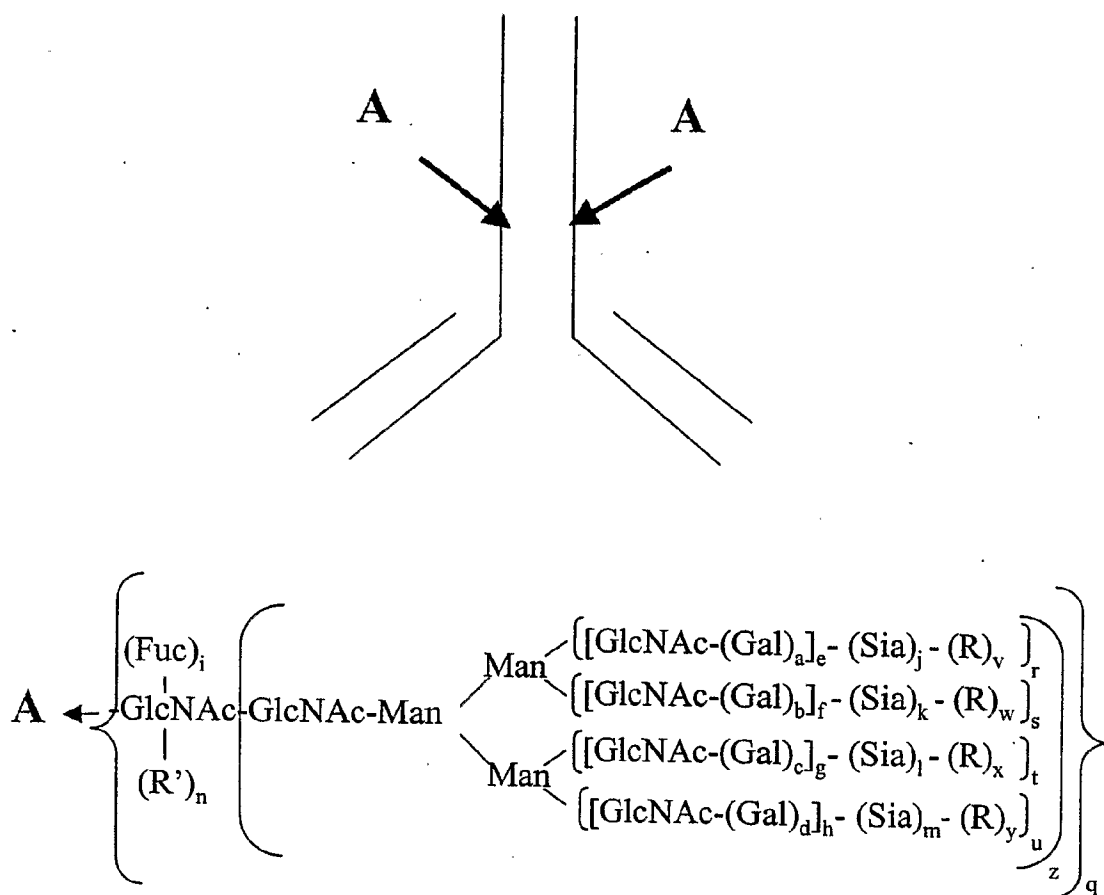
Fungi expressed Synagis.
e, g, i, r, t (independently selected) = 0 or 1;
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal
3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 50D

232/498



a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51A

233/498

CHO, BHK, 293 cells, Vero expressed Remicade.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when j, l (independently selected) is 1;
 R = PEG.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed
 Remicade.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.



1. galactosyltransferase,
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when a, c (independently selected) is 1;
 R = PEG.

FIG. 51C

234/498

Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

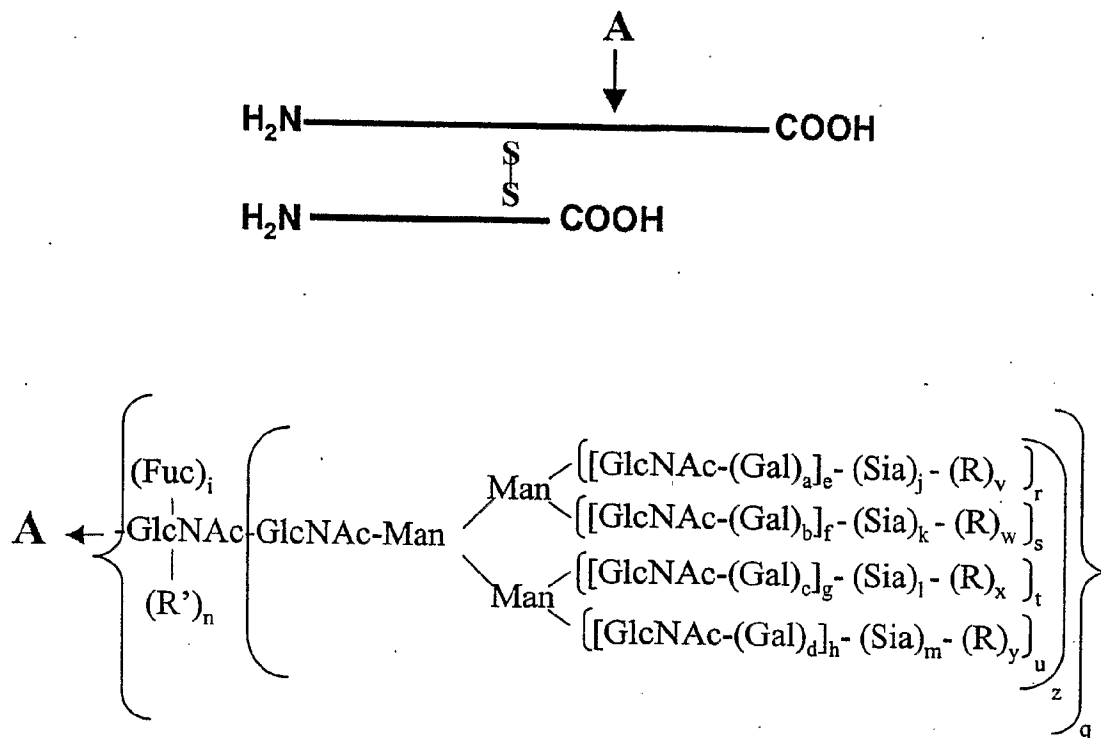
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

235/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 52A

236/498

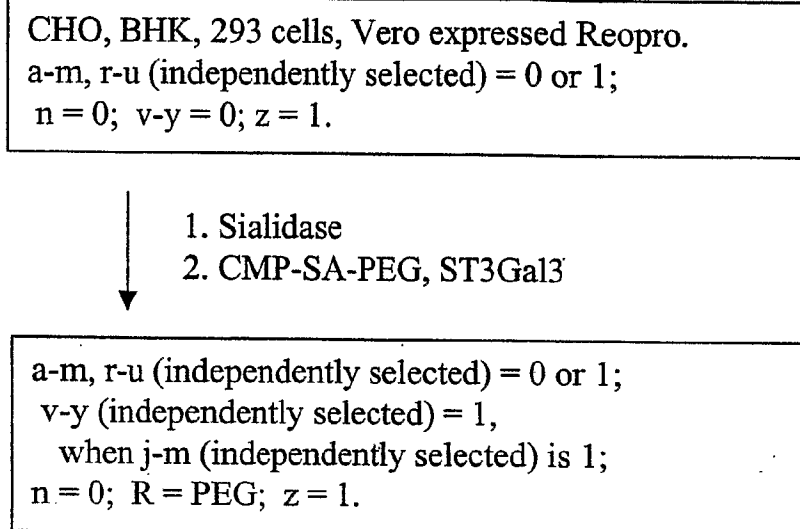


FIG. 52B

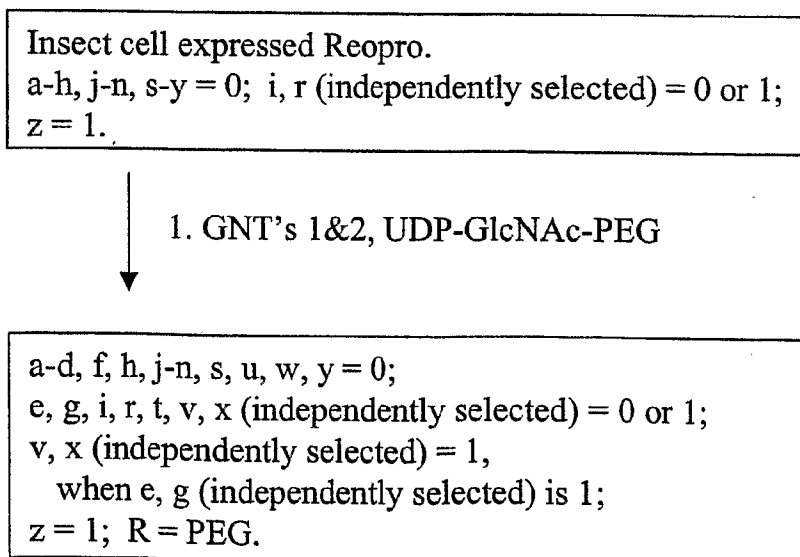


FIG. 52C

237/498

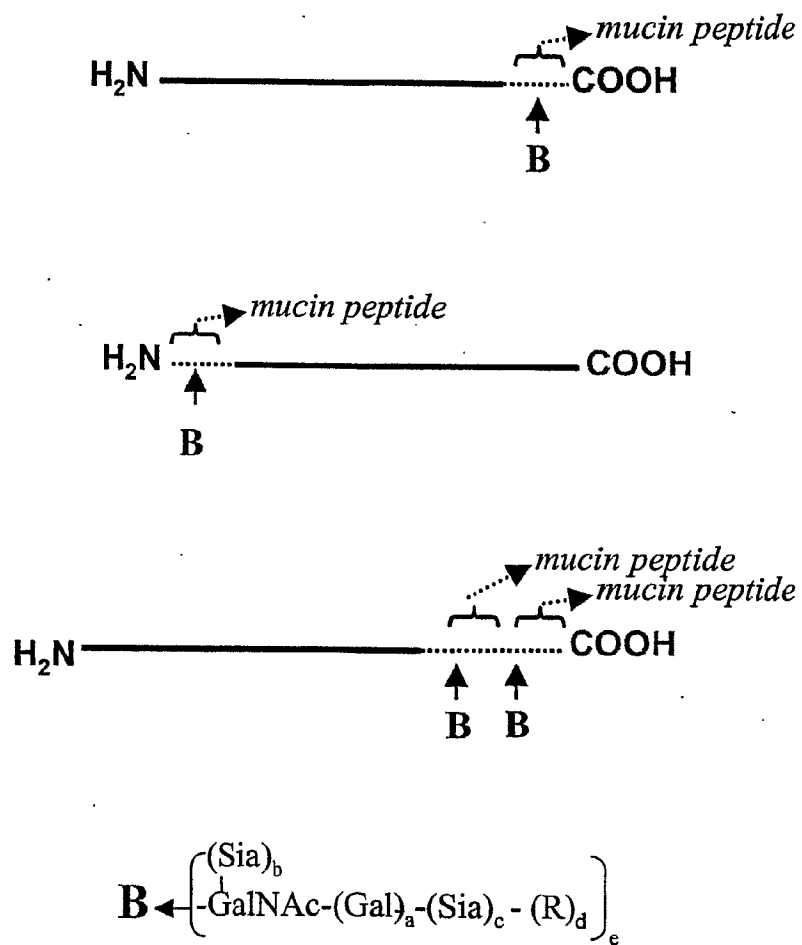
Yeast expressed Reopro.
a-n = 0; r-y (independently selected) = 0 to 1;
z = 1;
R (branched or linear) = Man, oligomannose or
polysaccharide.

1. Endo-H
2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 52D

238/498



a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 52E

239/498

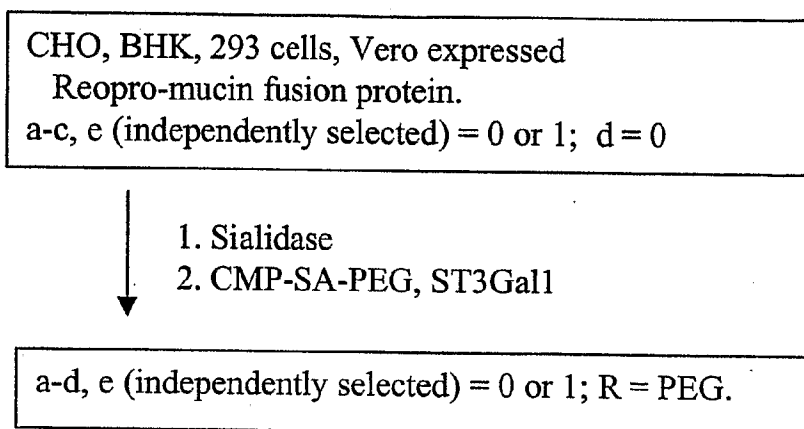


FIG. 52F

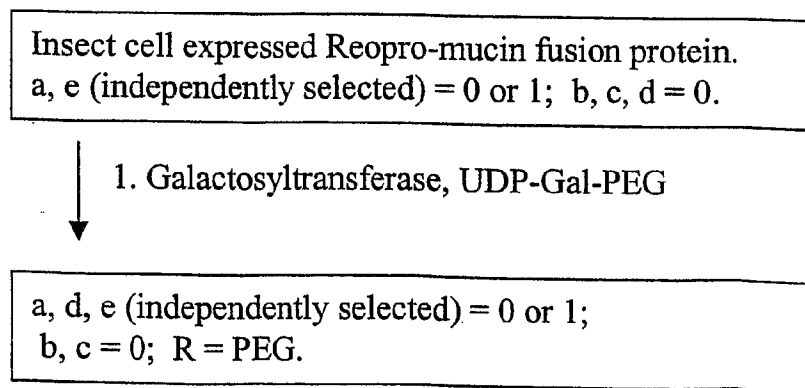


FIG. 52G

240/498

E. coli expressed Reopro-mucin fusion protein.
a-e = 0.

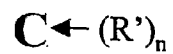
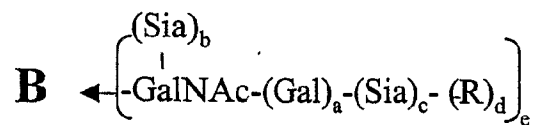
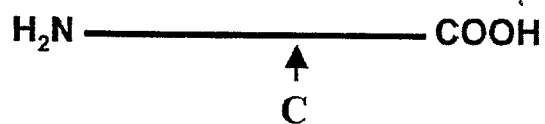
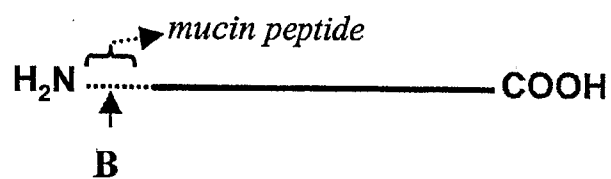
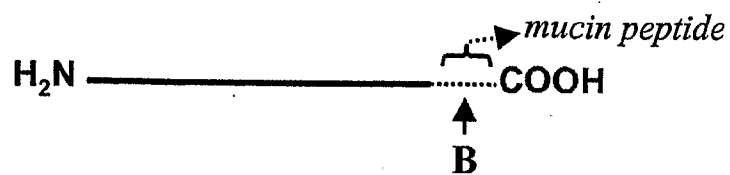


1. GalNAc Transferase, UDP-GalNAc
2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;
a, b = 0; R = PEG.

FIG. 52H

241/498



a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 52I

242/498

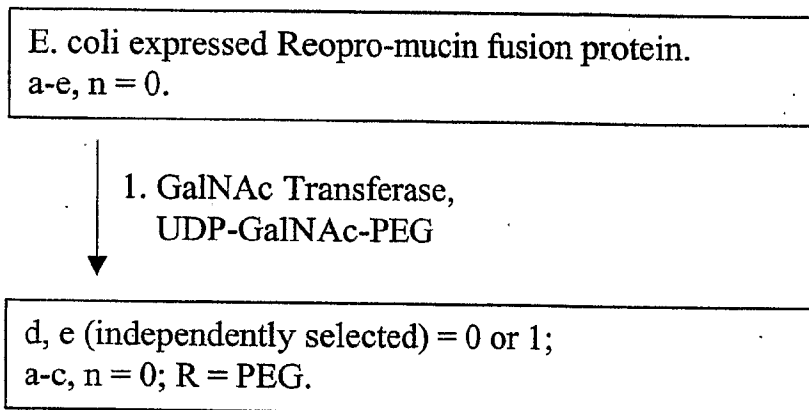


FIG. 52J

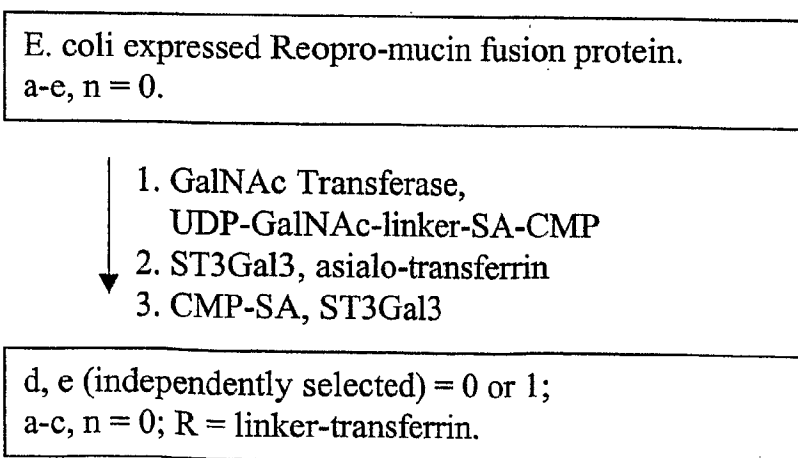


FIG. 52K

243/498

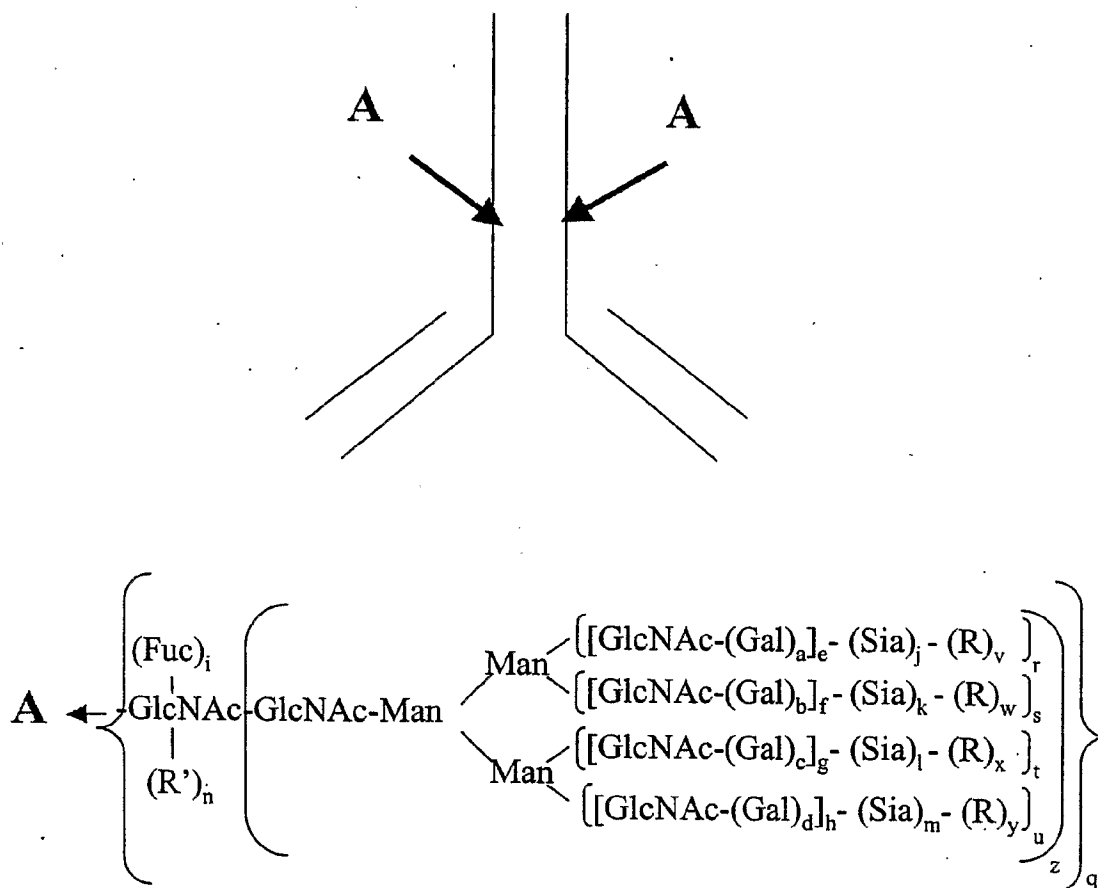
E. coli expressed Reopro(N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 3. CMP-SA, ST3Gal3
- ↓

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 52L

244/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 53A

245/498

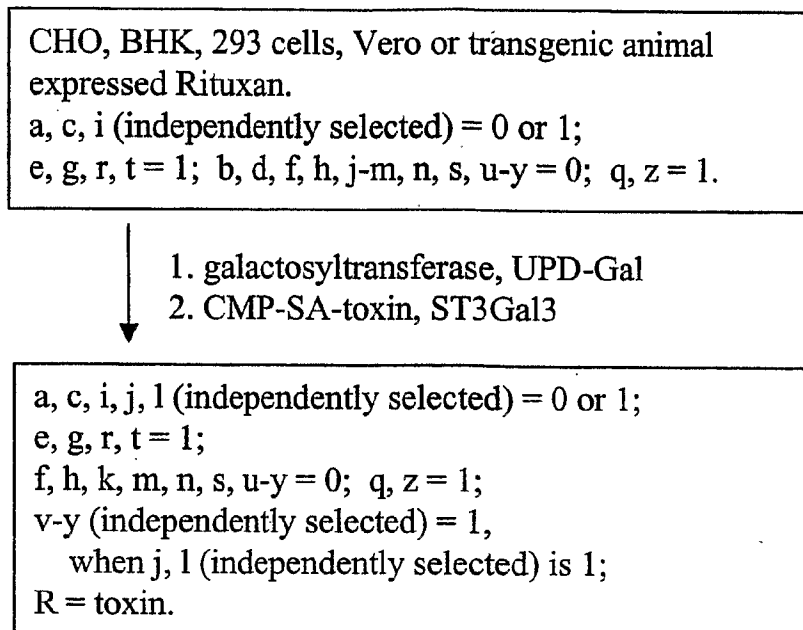


FIG. 53B

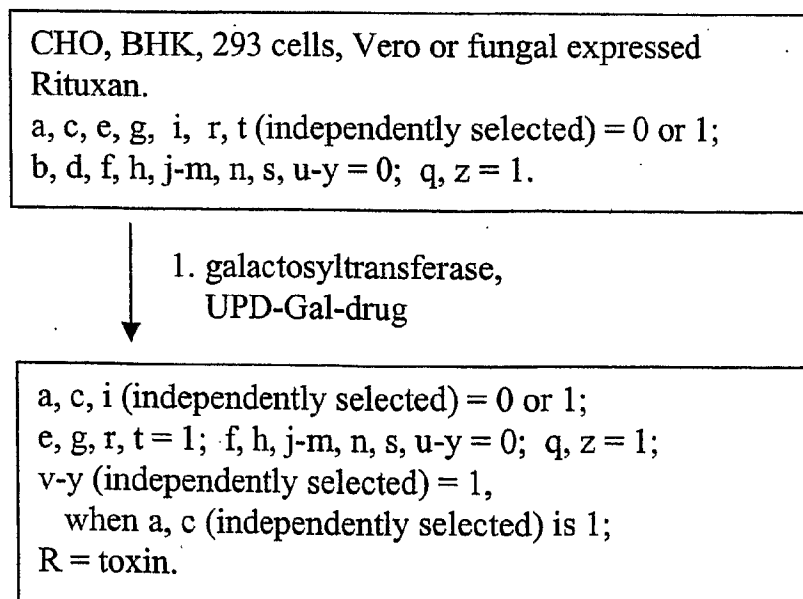


FIG. 53C

246/498

Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

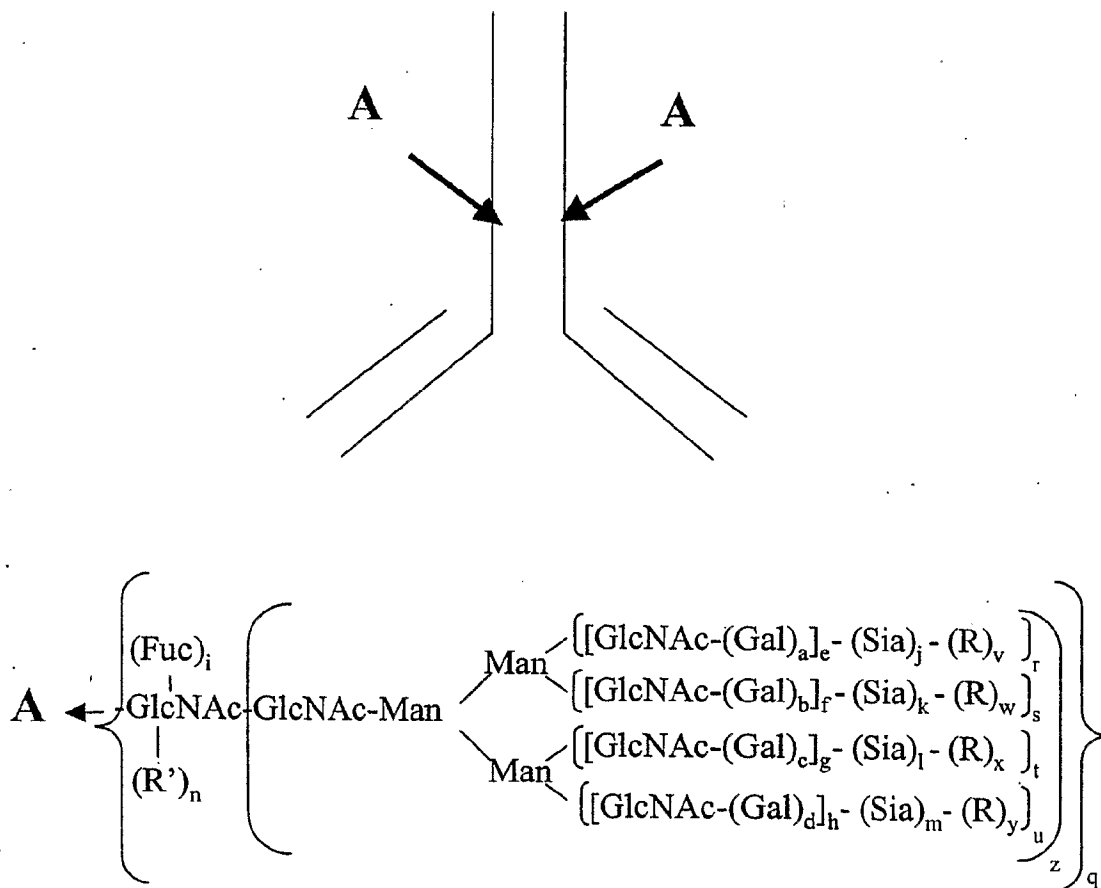
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - ↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 53D

247/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 53E

248/498

CHO, BHK, 293 cells, Vero or transgenic animal
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.



1. galactosyltransferase, UDP-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when j, l (independently selected) is 1;
R = PEG.

FIG. 53F

Fungi, yeast or CHO expressed Rituxan.

e, g, i, r, t, v, x (independently selected) = 0 or 1;
a-d, f, h, j-m, n, s, u, w, y = 0; q, z = 1;
R (independently selected) = mannose, oligomannose,
polymannose.

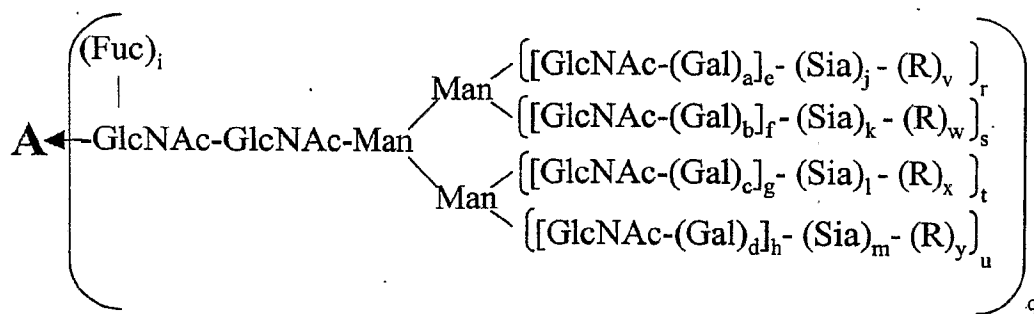
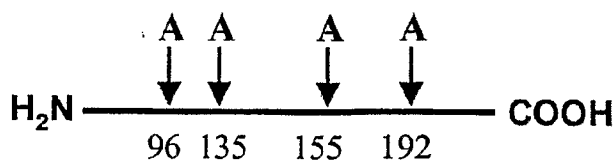


1. mannosidases (alpha and beta)
2. GNT-I,II, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal-radioisotope

a-m, r-z = 0; q, n = 1;
R' = -Gal-radioisotope complex.

FIG. 53G

249/498



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = mannose, polymer.

FIG. 54A

250/498

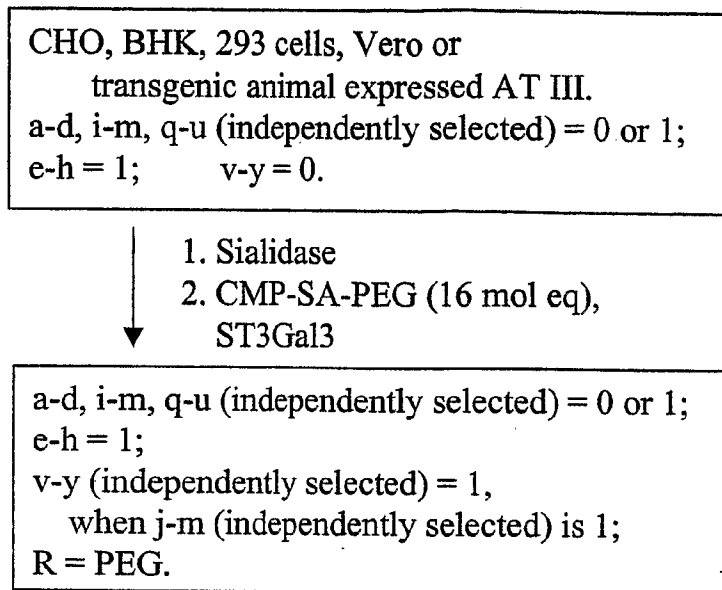


FIG. 54B

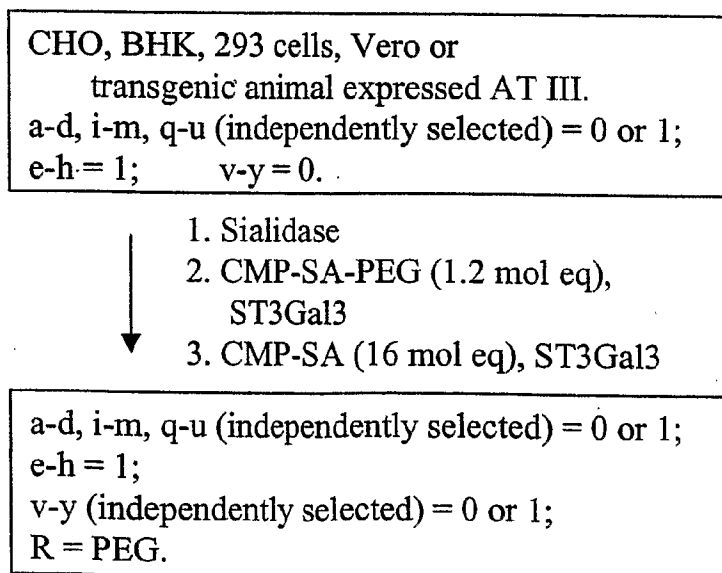


FIG. 54C

251/498

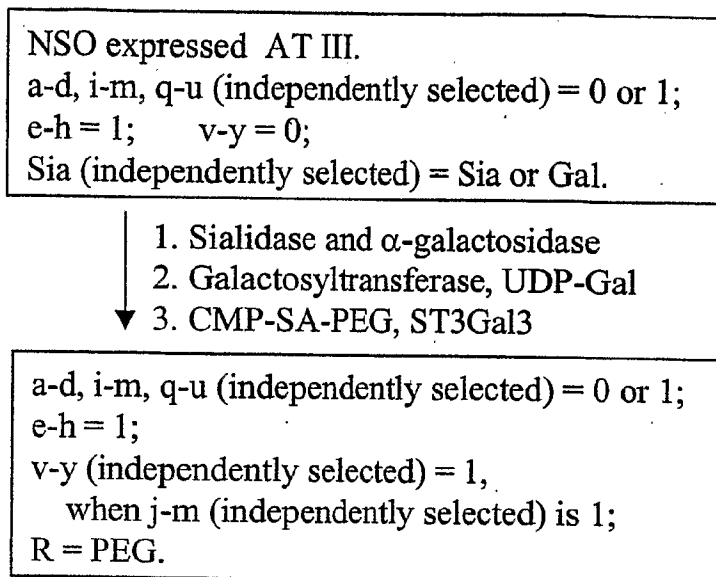


FIG. 54D

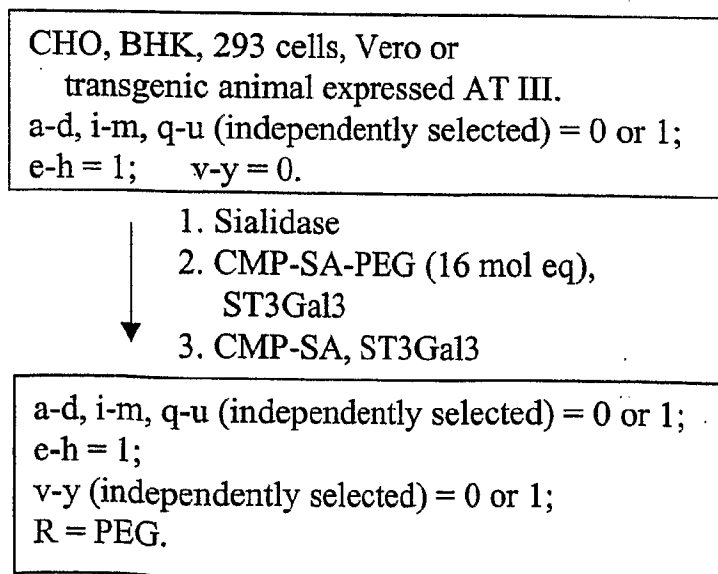


FIG. 54E

252/498

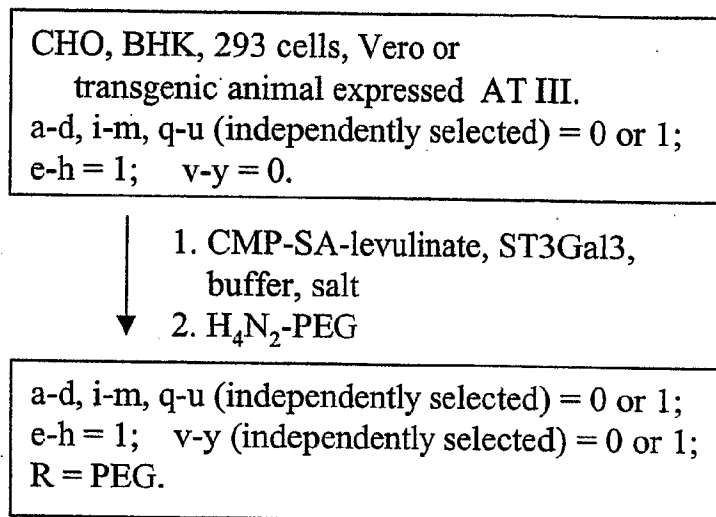


FIG. 54F

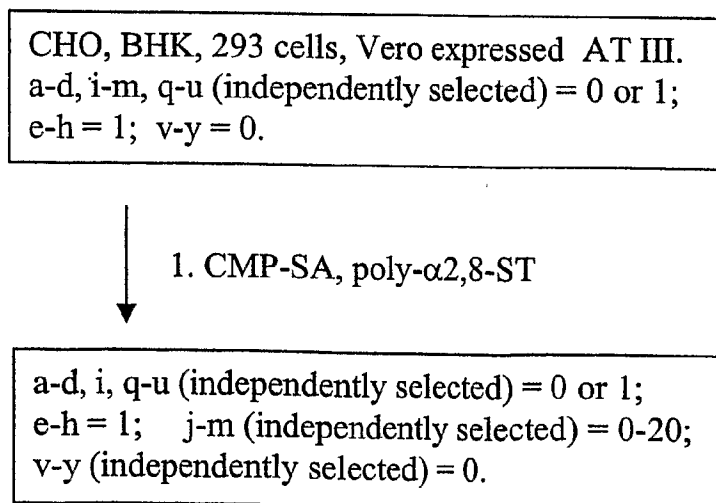
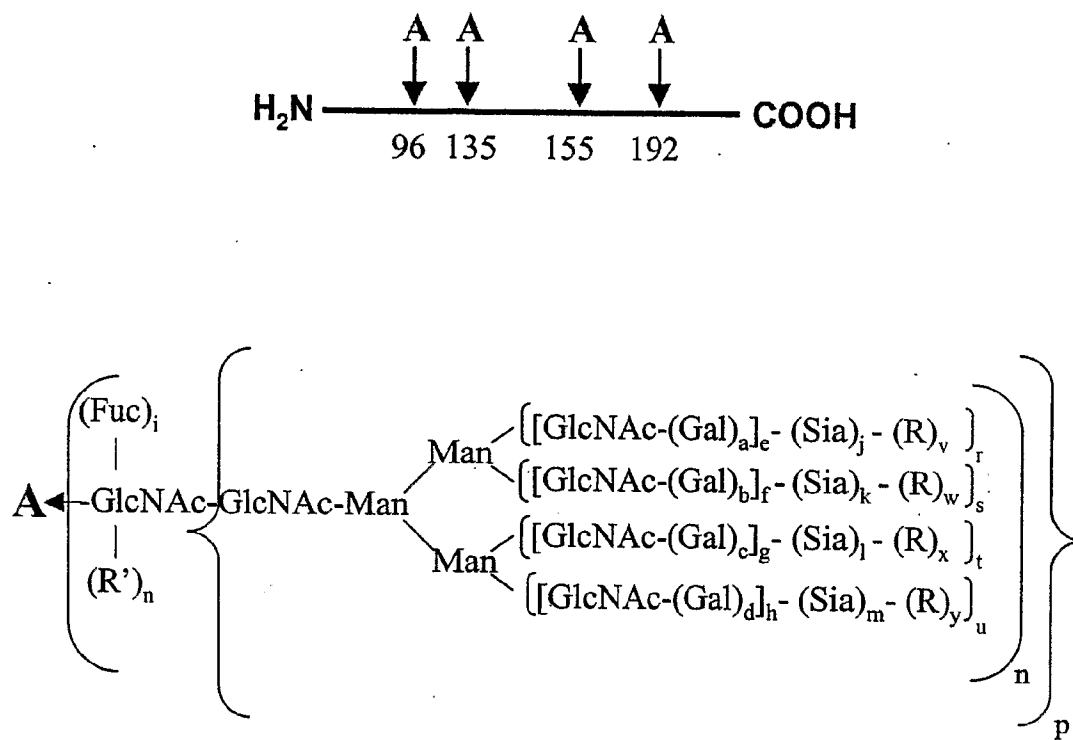


FIG. 54G

253/498



a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100.

R = polymer, linker, mannose.

R' = H, sugar, glycoconjugate.

FIG. 54H

254/498

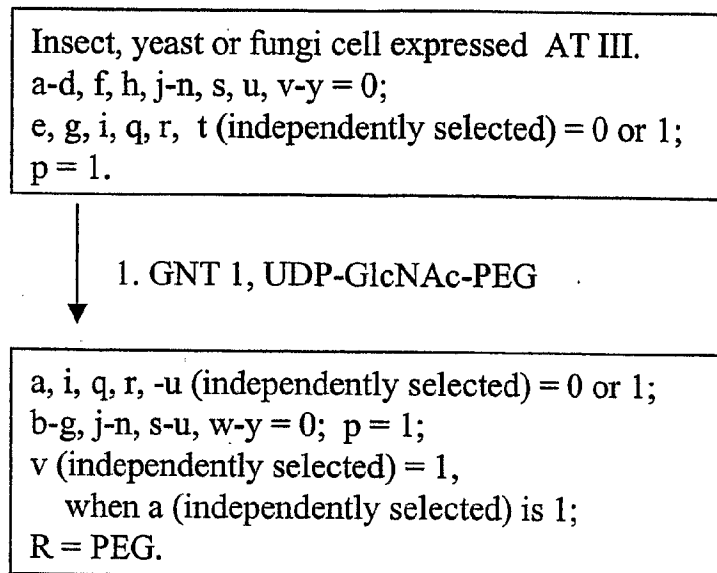


FIG. 54I

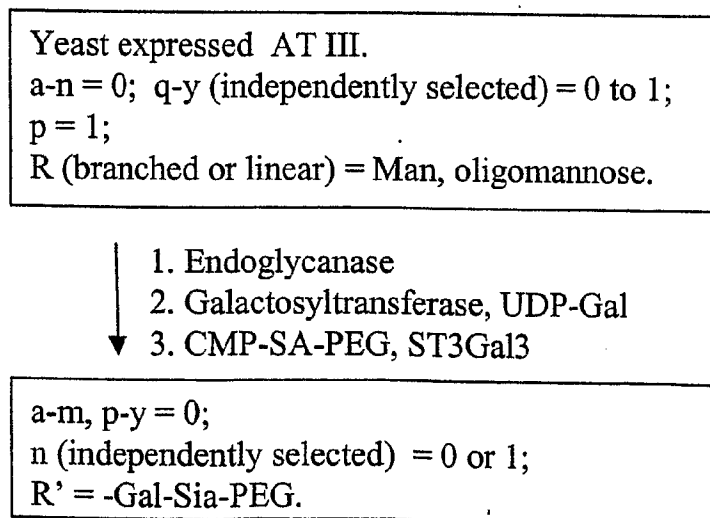


FIG. 54J

255/498

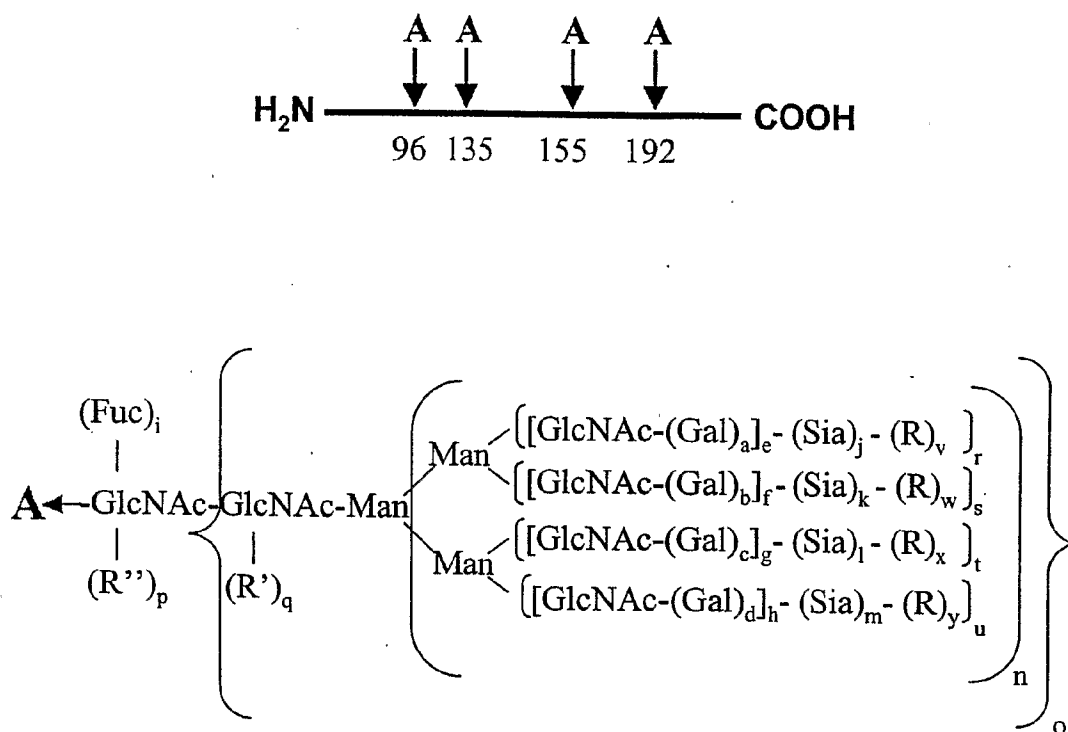
CHO, BHK, 293 cells, Vero expressed AT III.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin
treated with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 54K

256/498



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer.

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 54L

257/498

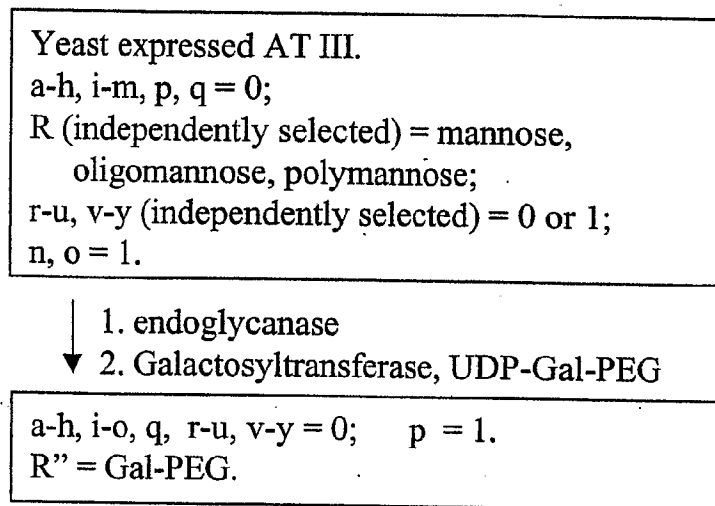


FIG. 54M

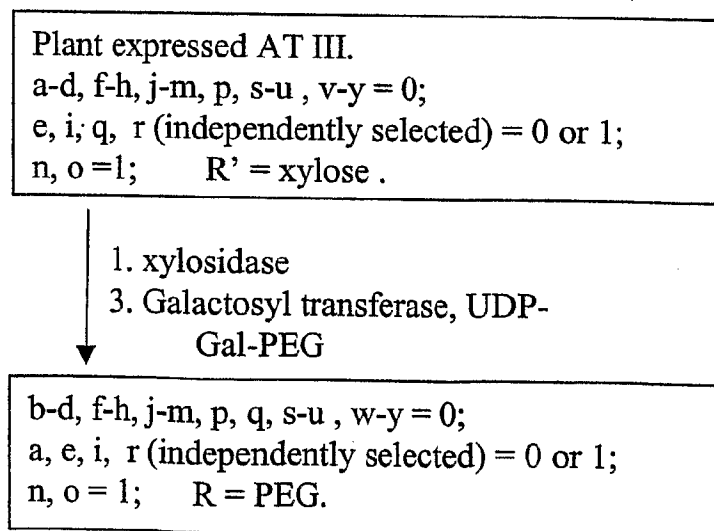


FIG. 54N

258/498

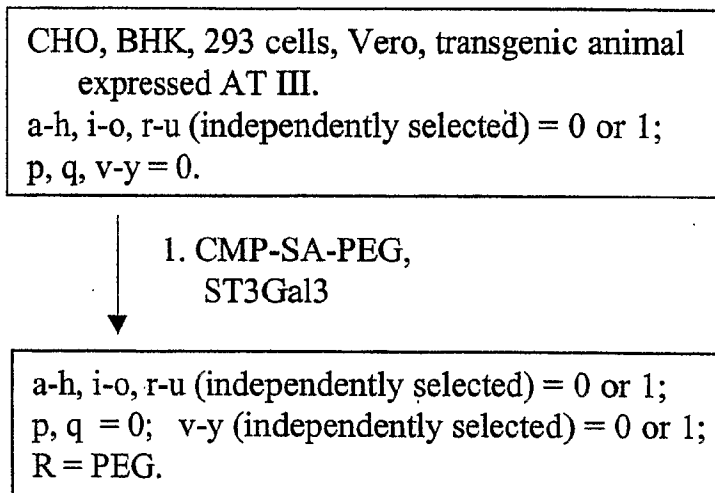
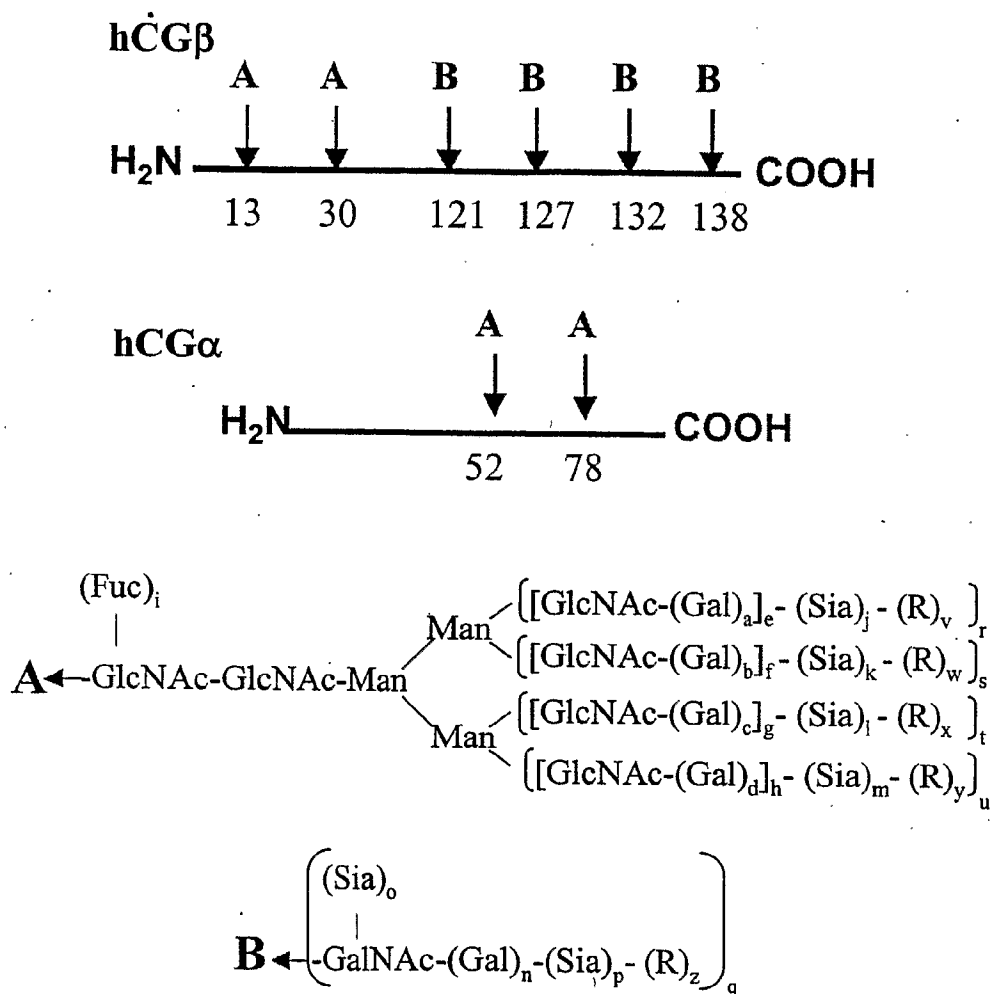


FIG. 540

259/498



a-d, i, n-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 4.
 j-m (independently selected) = 0 to 20.
 v-z = 0; R = polymer

FIG. 55A

260/498

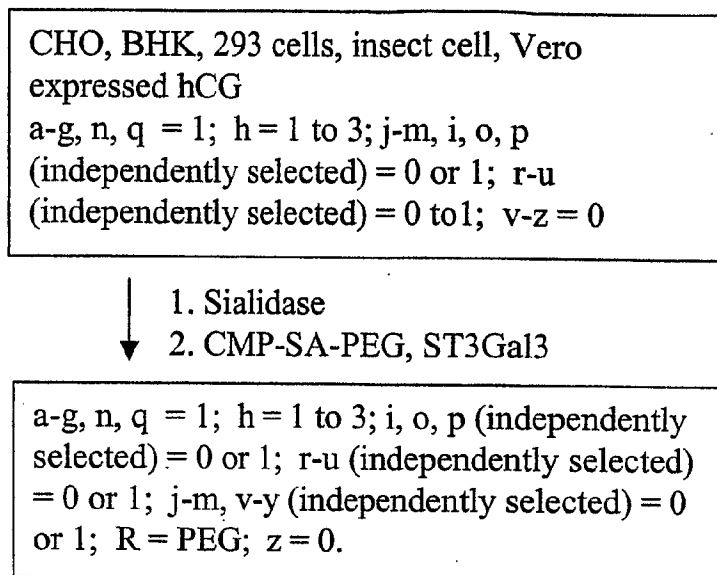


FIG. 55B

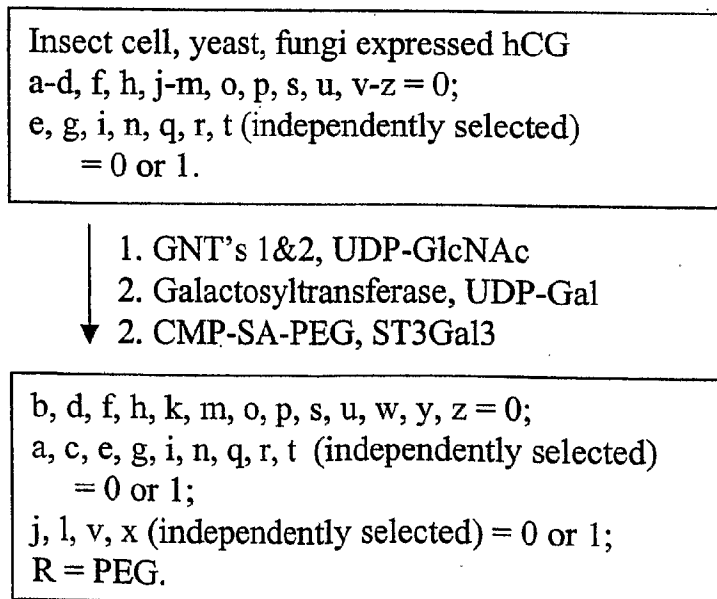


FIG. 55C

261/498

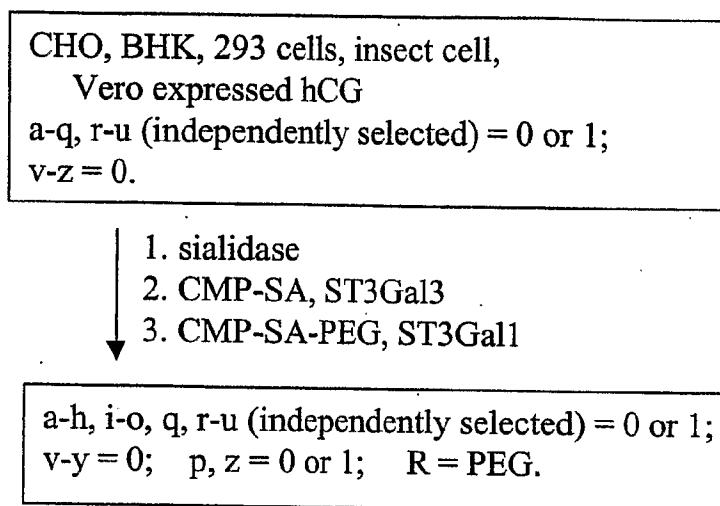


FIG. 55D

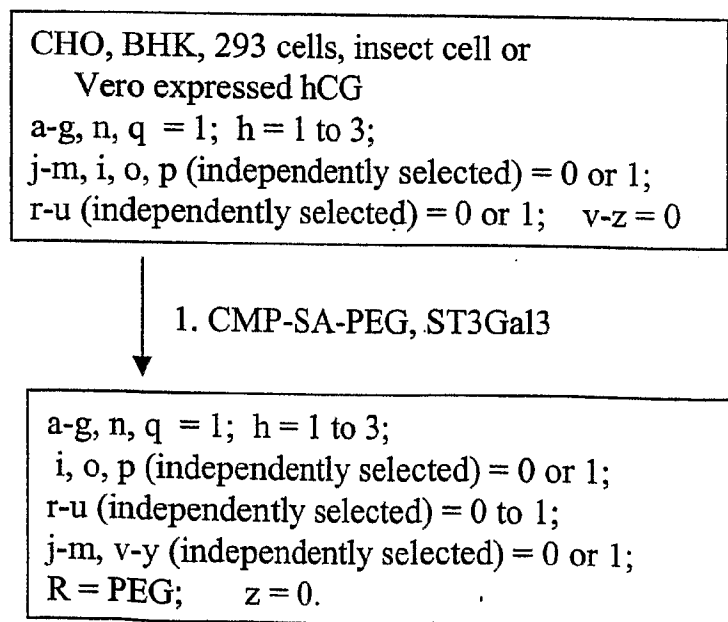


FIG. 55E

262/498

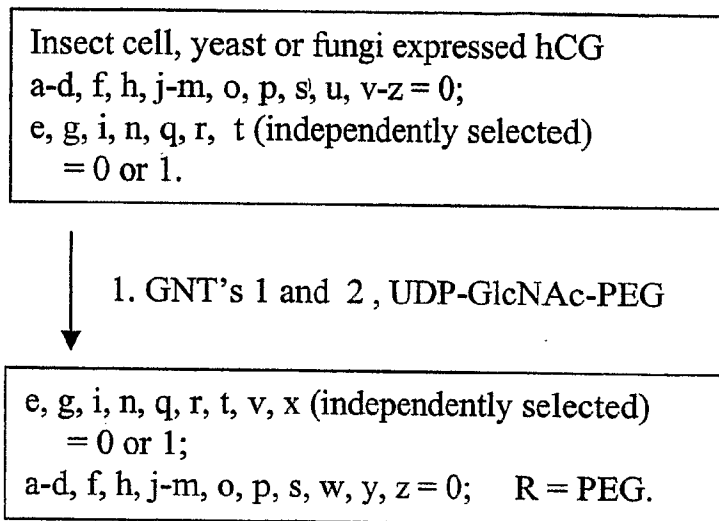


FIG. 55F

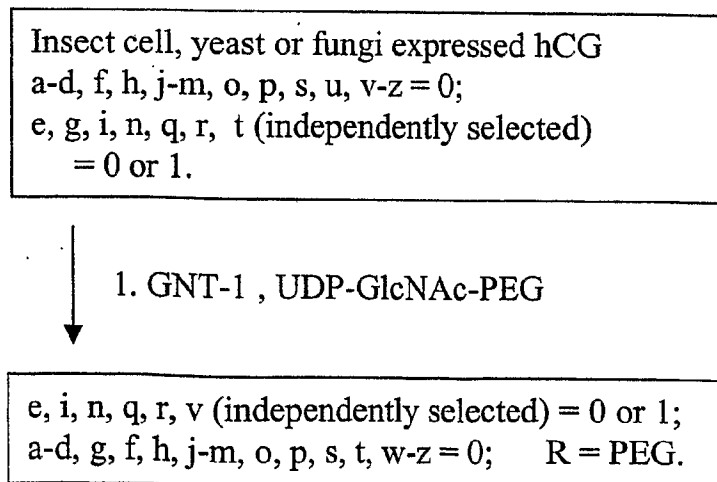


FIG. 55G

263/498

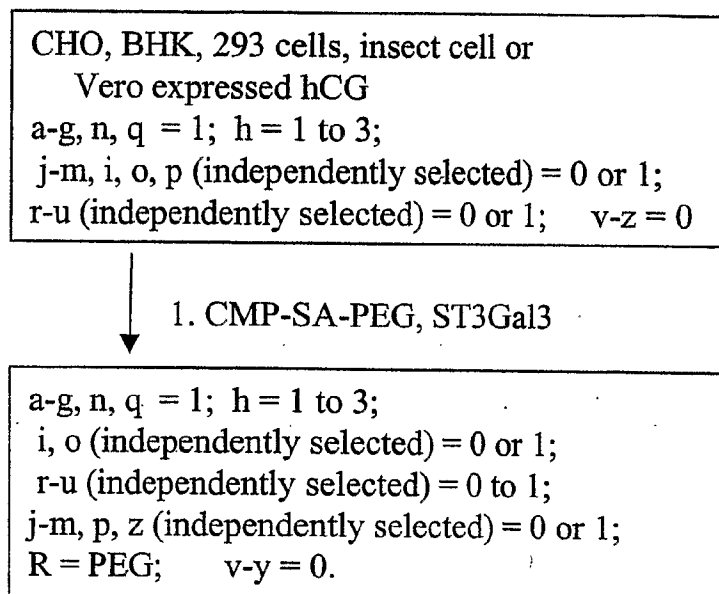


FIG. 55H

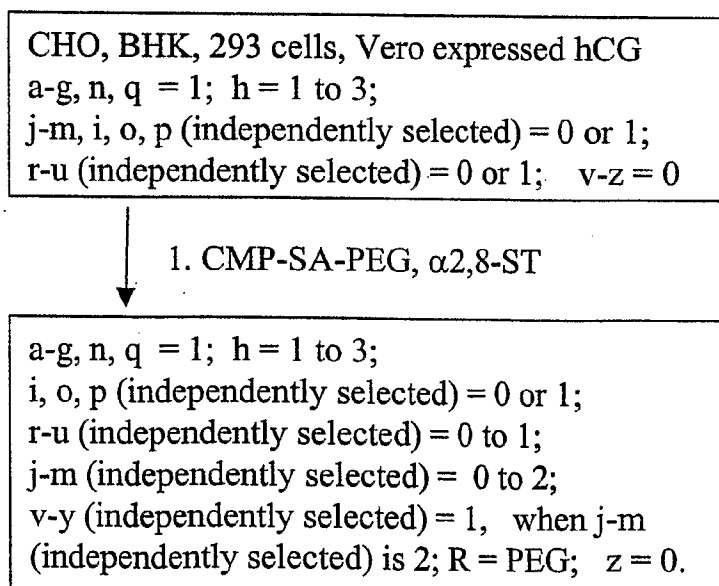


FIG. 55I

264/498

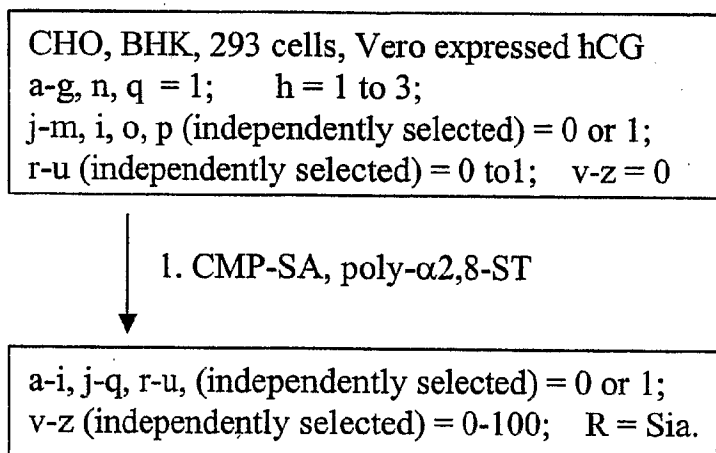
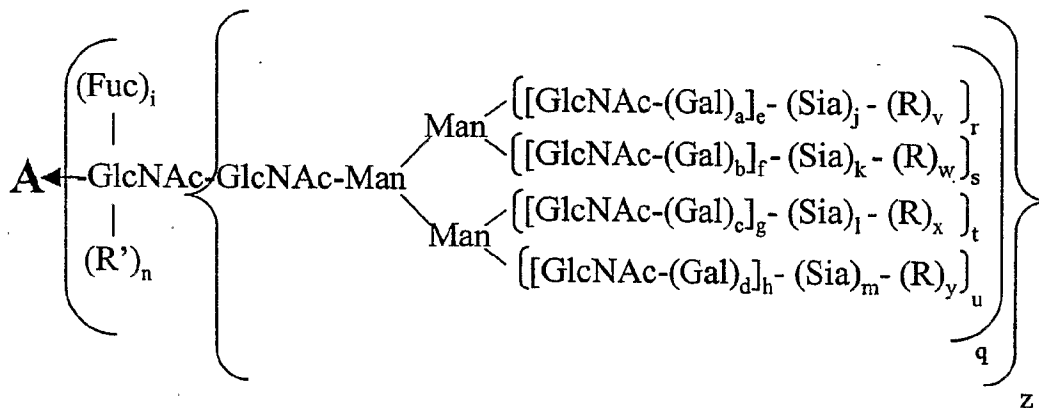
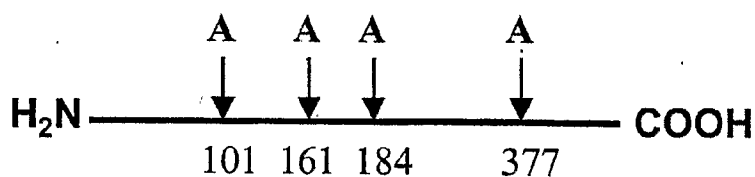


FIG. 55J

265/498



a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 56A

266/498

CHO, BHK, 293 cells, insect cells, Vero expressed
and secreted alpha-galactosidase
a-h, i-m, q-u (independently selected) = 0 or 1;
z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1; and when z = 0 and q = 1,
then n (independently selected) = 0 or 1;
R' = Gal-PEG-transferrin.

FIG. 56B

CHO, BHK, 293 cells, Insect cells,
Vero expressed and secreted alpha-galactosidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1; n, v-y
= 0; and when a-n = 0, then r-u (independently selected) = 0
or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
2. CMP-SA-linker-Mannose-6-phosphate
ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1;
n = 0; z = 1; R = mannose-6-phosphate; and when a-n
= 0, then r-u (independently selected) = 0 or 1;
v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 56C

267/498

NSO expressed alpha-galactosidase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0;
 Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-linker-mannose-6-phosphate
sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;
 v-y (independently selected) = 1, when j-m (independently
 selected) is 1; R = mannose-6 phosphate

FIG. 56D

CHO, BHK, 293 cells, Insect cells, Vero expressed and
 secreted alpha-galactosidase
 a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
 n, v-y = 0; and when a-n = 0, then r-u (independently
 selected) = 0 or 1; v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
 2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0; z
 = 1; R = PEG; and when a-n = 0, then r-u (independently
 selected) = 0 or 1; v-y = 0-100; R = mannose or mannose
 with mannose-6-phosphate.

FIG. 56E

268/498

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate;
v-y (independently selected) = 0 or 1;
R = mannose-linker-ApoE.

FIG. 56F

CHO, BHK, 293 cells, Insect cells, Vero, yeast,
fungi expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H
2. galactosyltransferase,
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;
R' = galactose-linker-alpha2-macroglobulin.

FIG. 56G

269/498

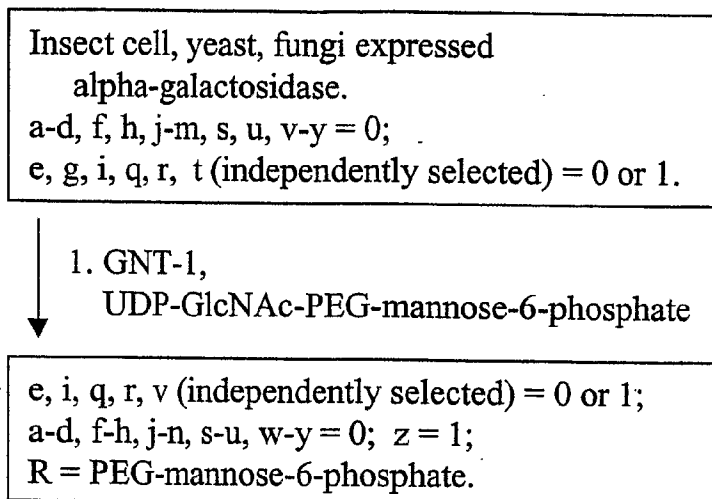


FIG. 56H

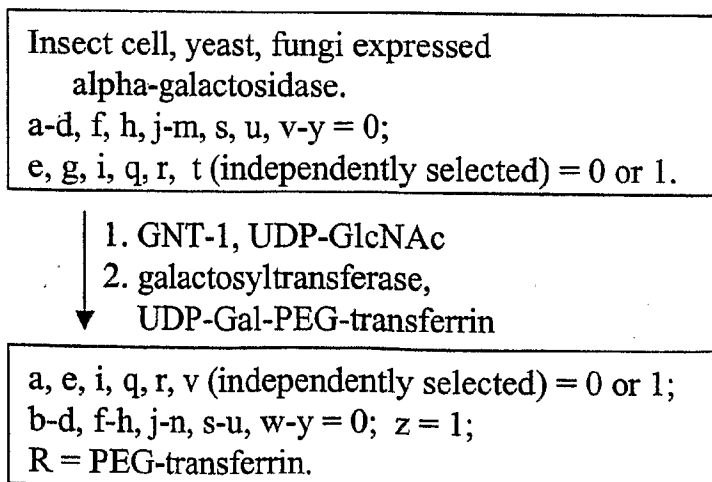


FIG. 56I

270/498

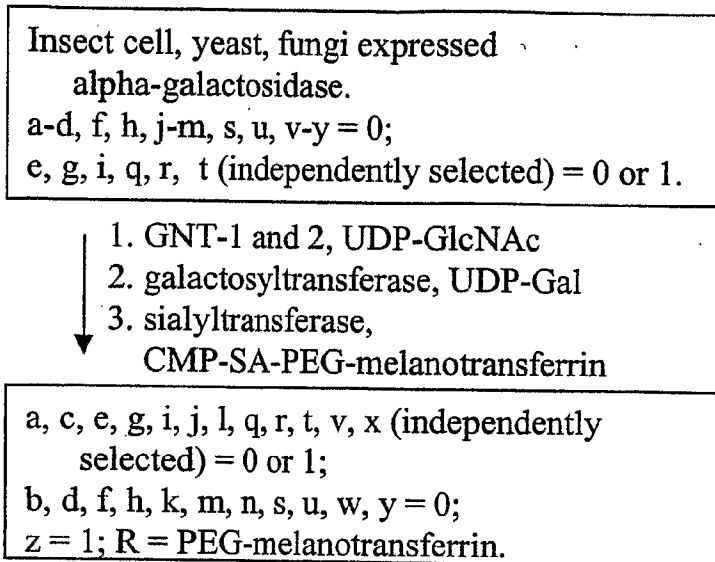
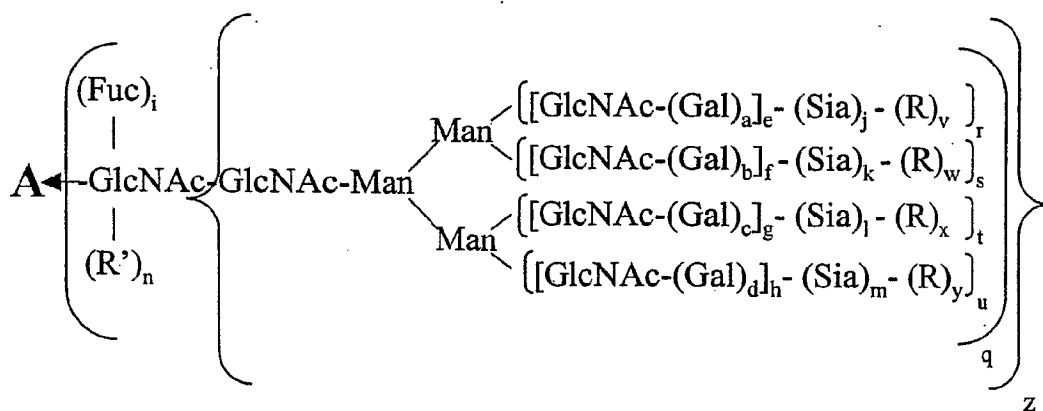
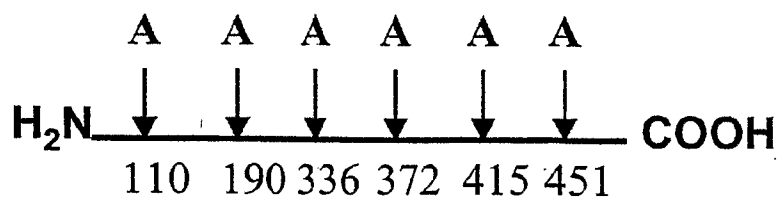


FIG. 56J

271/498



a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

$$v-y = 0 \text{ to } 100;$$

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 57A

272/498

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Endo-H
↓
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1; and when z = 0 and q = 1, then n
(independently selected) = 0 or 1; R' = Gal-PEG-transferrin.

FIG. 57B

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
↓
2. CMP-SA-linker-Mannose-6-phosphate ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;
z = 1; R = mannose-6-phosphate; and when a-n = 0,
then r-u (independently selected) = 0 or 1;
v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 57C

273/498

NSO expressed alpha-iduronidase.

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;
v-y = 0; Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ↓ 3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = mannose-6 phosphate

FIG. 57D

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
 2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;
z = 1; R = PEG; and when a-n = 0, then r-u
(independently selected) = 0 or 1; v-y = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 57E

274/498

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-iduronidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1; j-m (independently
selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate;
v-y (independently selected) = 0 or 1;
R = mannose-linker-ApoE.

FIG. 57F

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-iduronidase.
a-i, v-y = 0; q (independently selected) = 0 or 1;
z = 1; r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H
2. galactosyltransferase,
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;
R' = galactose-linker-alpha2-macroglobulin.

FIG. 57G

275/498

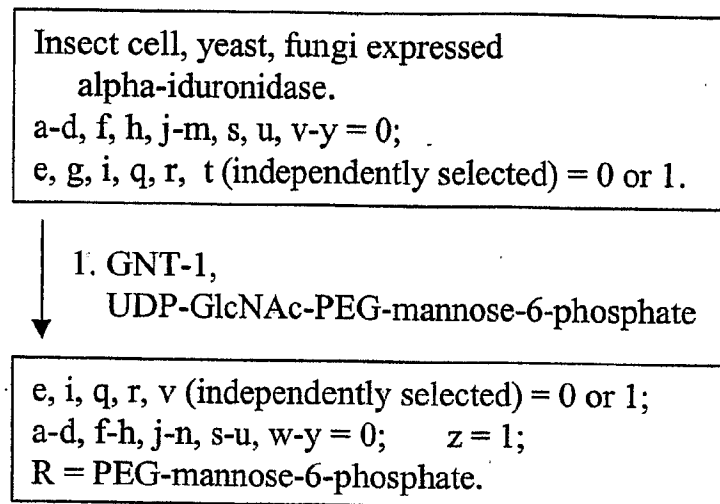


FIG. 57H

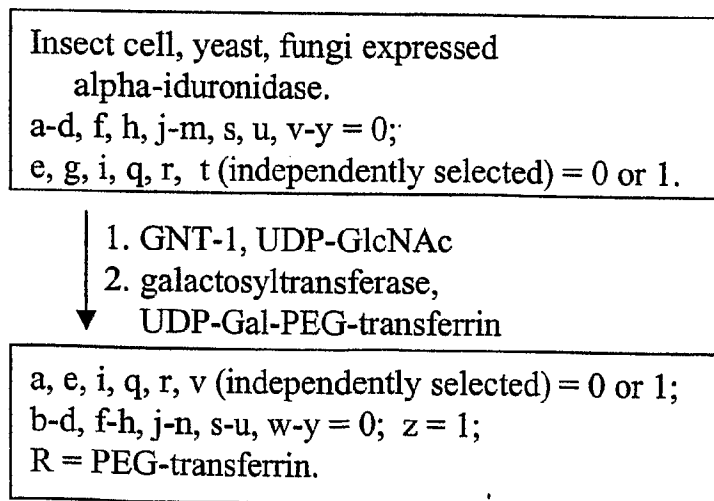


FIG. 57I

276/498

Insect cell, yeast, fungi expressed
alpha-iduronidase.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.

- ↓ 1. GNT-1 and 2, UDP-GlcNAc
2. galactosyltransferase, UDP-Gal
3. sialyltransferase,
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x

(independently selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0; z = 1;

R = PEG-melanotransferrin.

FIG. 57J

277/498

FIG. 58A

ACCCCCCTGGGCCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT
GCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTG
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA
GCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT
CCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTGCGCCG
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT
TTCCAGCGCCGGGCAGGAGGGGTCTGGTTGCCTCCCATCTGCAGAG
CTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG
A

FIG. 58B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
Leu Ala Gln Pro

278/498

FIG. 59A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA
AGAATATAGTTATCAAGTTAAGTAAAATGTCAATAGCCTTTTAATTTA
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAACATTAACTTTAT
ACTTTTAAATTAAATGTATAGAATAGAGATATACATAGGATATGTAAA
TAGATACACAGTGTATATGTGATTAAAATATAATGGGAGATTCAATC
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA
AAGAGTGTATAAAGAAAGCAAAAAGAGAAGTAGAAAGTAACACAGG
GGCATTGGAAGAAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGG
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTCTTTTCTCC
TGCTTGAAGGACAGACATGACTTTGGATTTCCCCAGGAGGAGTTTGG
CAACCAGTTCCAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGA
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT
GGGATGAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAG
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTGT
GCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCTTTTTCTTTGTCA
ACAAACTTGCAAGAAAGTTTAAGAAGTAAGGAATGAAAACCTGGTTCA
ACATGGAAATGATTTTCATTGATTCGTATGCCAGCTCACCTTTTTATG
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTAG
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT
ATCTATTTAAATATTTTTAAAATATTATTTAATTAACTATTTATAAAC
AACTTATTTTTGTTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTGTGTTGTT
CATTGAACTTTTGCTATGGAACCTTTGTAAGTTGTTTATTCTTTAAAATG
AAATTCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA
CTTCATTTGTCCATCAATATTATATTCAAGATATAAGTAAAAATAAAC
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC
TAACAAATACAATTCTGCTCTCTTGTGTATTTGATTTTTGTATGAAAA
AACTAAAAATGGTAATCATACTTAATTATCAGTTATGGTAAATGGT
ATGAAGAGAAGAAGGAACG

279/498

FIG. 59B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser
Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr
Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu
Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu
Arg Ser Lys Glu

FIG. 59C

ATGGCCCTCCTGTTCCCTCTACTGGCAGCCCTAGTGATGACCAGCTAT
AGCCCTGTTGGATCTCTGGGCTGTGATCTGCCTCAGAACCATGGCCTA
CTTAGCAGGAACACCTTGGTGCTTCTGCACCAAATGAGGAGAATCTCC
CCTTTCTTGTGTCTCAAGGACAGAAGAGACTTCAGGTTCCCCCAGGAG
ATGGTAAAAGGGAGCCAGTTGCAGAAGGCCCATGTCATGTCTGTCTCT
CCATGAGATGCTGCAGCAGATCTTCAGCCTCTTCCACACAGAGCGCTC
CTCTGCTGCCTGGAACATGACCCTCCTAGACCAACTCCCACTGGACT
TCATCAGCAACTGCAACACCTGGAGACCTGCTTGCTGCAGGTAGTGG
GAGAAGGAGAATCTGCTGGGGCAATTAGCAGCCCTGCACTGACCTTG
AGGAGGTACTTCCAGGGAATCCGTGTCTACCTGAAAGAGAAGAAATA
CAGCGACTGTGCCTGGGAAGTTGTCAGAATGGAAATCATGAAATCCT
TGTTCTTATCAACAAACATGCAAGAAAGACTGAGAAGTAAAGATAGA
GACCTGGGCTCATCTTGA

FIG. 59D

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr Ser Pro Val
Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr
Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu Lys Asp
Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser Gln Leu Gln Lys
Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His
Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr
Gly Leu His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe
Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Val
Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met Gln Glu Arg
Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser

280/498

FIG. 60A

ATGACCAACAAGTGTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC
ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCCCTACAAAGA
AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG
GCTTGAATATTGCCTCAAGGACAGGATGAACTTTGACATCCCTGAGG
AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGCATTGACC
ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA
TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA
TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC
TGGAGAAAGAAGATTTTACCAGGGGAAACTCATGAGCAGTCTGCAC
CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA
GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA
ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT
CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTTCAAGCATTCTTC
AACCAGCAGATGCTGTTTAAAGTGACTGATGGCTAATGTACTGCAAAT
GAAAGGACACTAGAAGATTTTGAATTTTATTAAATTATGAGTTATT
TTTATTTAT TTAAATTTTATTTTGGAAAATAAATTATTTTGGTGC

FIG. 60B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala
Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp
Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu
Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp
Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile
Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

281/498

FIG. 61A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT
CCTGCACCGGCGCCGGCGCGCCAACGCGTTCCTGGAGGAGCTGCGGC
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA
GAATGGGGGGCTCCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCT
GCCTCCCTGCCTTCGAGGGGCCGGAACGTGTGAGACGCACAAGGATGAC
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG
TGACCACACGGGCACCAAGCGCTCCTGTGCGGTGCCACGAGGGGTACT
CTCTGCTGGCAGACGGGGTGTCTGTCACACCCACAGTTGAATATCCA
TGTGGAAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAACCCCA
AGGCCGAATTGTGGGGGGGCAAGGTGTGCCCCAAAGGGGAGTGTCCA
TGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACACGACATC
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTGGTG
CCCCTCTGCCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC
GTGCGCTTCTCATTTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGG
CGCCACGGCCCTGGAGCTCATGGTGCTCAACGTGCCCCGGCTGATGA
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT
ATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCACATGCCACCCACTACCGGG
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA
ACCGTGGGCCACTTTGGGGGTGTACACCAGGGTCTCCAGTACATCGA
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCAGGAGTCCTCC
TGCGAGCCCCATTTCCC

282/498

FIG. 61B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

283/498

FIG. 62A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC
CATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTT
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA
TTCAGGTAAATTGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAAT
GTATGGAAGAAAAGTGTAGTTTTGAAGAACCACGAGAAGTTTTTGAA
AACACTGAAAAGACAACCTGAATTTTGGAAGCAGTATGTTGATGGAGA
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGA
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT
GAGGGATATCGACTTGCAGAAAACCAGAAGTCCTGTGAACCAGCAGT
GCCATTTCCATGTGGAAGAGTTTCTGTTTCACAACTTCTAAGCTCAC
CCGTGCTGAGGCTGTTTTTCCTGATGTGGACTATGTAAATCCTACTGA
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA
GGCTCTATCGTTAATGAAAAATGGATTGTAAGTCTGCTGCCCACTGTGTT
GAAACTGGTGTAAAATTACAGTTGTTCGCAGGTGAACATAATATTGA
GGAGACAGAACATACAGAGCAAAAGCGAAATGTGATTTCGAGCAATT
ATTCCTCACCACAACCTACAATGCAGCTATTAATAAGTACAACCATGA
CATTGCCCTTCTGGAACTGGACGAACCCTTAGTGCTAAACAGCTACG
TTACACCTATTTGCATTGCTGACAAGGAATACACGAACATCTTCCTCA
AATTTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTTGAC
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG
ATAGTGGGGGACCCCATGTTACTGAAGTGGAAGGGACCAGTTTCTTA
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAATA
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAA
AAACAAAGCTCACTTAATGAAAGATGGATTTCCAAGGTTAATTCATT
GGAATTGAAAATTAACAG

284/498

FIG. 62B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

285/498

FIG. 63A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCA
GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCC
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAG
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG
GGGGGTTTCAAAGTGGAAGAACACACGGCGTGCCACTGCAGTACTTG
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT
GTGAGATAAACTCTCCTTTTCTTACCATAACCACTTTGACACGCTTC
AAGGATATACTGCAGCTTTACTGCCTTCCTCCTTATCCTACAGTACAA
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAGCTTG
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 63B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

286/498

FIG. 63C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCCC
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG
ATTGTACTGTGCGAGGCCTGGGGCCCAGCTACTGCTCCTTTGGTGAAA
TGAAAGAATAA

FIG. 63D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

287/498

FIG. 64A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT
GCACCGCCGAGCTTCCCGGGATGAGGGCCCCCGGTGTGGTCACCCGG
CGCGCCCCAGGTGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG
GTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTCG
CTCCCTCTGGGCCTCCCAGTCCTGGGCGCCCCACCACGCCTCATCTGT
GACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGAT
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG
CTGTGCGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGCGAGCCCAGAAGG
AAGCCATCTCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA
ATCACTGCTGACACTTTCCGCAAACCTCTTCCGAGTCTACTCCAATTC
CTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC
GTCGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC
AACTCTGAGATCTAAGGATGTCACAGGGCCAACCTGAGGGGCCAGAG
CAGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC
AGGACACGCTTTGGAGGCGATTTACCTGTTTTTCGCACCTACCATCAGG
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCTCTGG
CTCTCATGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGA
ACTGAAACCACCAAAAAAAAAAAAAA

288/498

FIG. 64B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu Leu Ser
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

FIG. 65

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

289/498

FIG. 66A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT
CTCTGCACCCGCCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGC
ATGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGA
GAACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAT
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCCTTG
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA
ACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG
TCCAGGAGTGA

FIG. 66B

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

290/498

FIG. 67A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG
GGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGA
AAACCTTAAGAAATATTTTAATGCAGGTCATTCAGATGTAGCGGATA
ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAAC
TTTTAAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT
GAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTG
AACTGTCGCCAGCAGCTAAAACAGGGAAGCGAAAAAGGAGTCAGAT
GCTGTTTCGAGGTCGAAGAGCATCCCAGTAA

FIG. 67B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

291/498

FIG. 68A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC
CAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT
GACCACCGGCAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC
ACTGTCAACTTCGGGGACACCGAAGAGGGCCAAGAAACAGATCAACG
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAG
GAGCTTGACAGAGACACAGTTTTTGTCTCTGGTGAATTACATCTTCTT
AAAGGCCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG
AAGCGTTTAGGCATGTTTAAACATCCAGCACTGTAAGAAGCTGTCCAG
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC
CACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGC
CAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAA
GAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG
CTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAG
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC
TGCTGGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCCGA
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATAC
CAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAT
AACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC
CTGGATGACATTAAAGAAGGGTTGAGCTGG

292/498

FIG. 68B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val
Phe Ala LeuVal Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys
Phe Leu Glu Asn Glu AspArg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val
Val Asn Pro Thr Gln Lys

293/498

FIG. 69A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTTT
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCA
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCGTGGGCATCAGGT
GCCCCGCCCTGCATCCCTAAAAGCTTTCGGCTACAGCTCGGTGGTGTGT
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCGACCTTTCCT
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG
GCCTGCTACTGACCCTGCAGCCAGAACAGAAAGTTCCAGAAAGTGAAG
GGATTTGGAGGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC
CTGTACCCCCCTGCCCAAATTTGCTACTTAAATCGTACTTCTCTGAA
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCCA
GTTGCACAACCTTCAGCCTCCAGAGGAAGATACCAAGCTCAAGATAC
CCCTGATTCACCGAGCCCTGCAGTTGGCCCAGCGTCCCGTTTCACTCC
TTGCCAGCCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG
GTGAATGGGAAGGGGTCACTCAAGGGACAGCCCGGAGACATCTACC
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG
AGCACAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTCACCCCT
GAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCCTACCCTCGCC
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACGC
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCT
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA
ACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGG
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC
CACAGCATCATCACGAACCTCCTGTACCATGTGGTCGGCTGGACCGAC
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA
CTTTGTCGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTTA
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC
TGAGGGCTCCCAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC
TGGACGCAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTCTG
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG
CTGTGGGCTTCCTGGAGACAATCTCACCTGGCTACTCCATTACACCT
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGG
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG
TGACTAAAGAGGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

294/498

FIG. 69A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCCCTCTAGGTGGT
GCCCAGGGCTGGAGGCCCCCTAGAAAAAGATCAGTAAGCCCCAGTGTC
CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT
TGGAAACT

FIG. 69B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser
Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser
Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys
Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr
Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly
Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu
Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser
Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser
Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu
Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile
Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu
His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp
Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg
Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val
Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro
Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser
Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu
Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr
Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu
Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn
Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

295/498

FIG. 70A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCGATTTCAGAA
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAAACGCA
GATGATATACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA
GCAACCGGGTGGAAATATTGCTGGTGCAACAGTGGCAGGGCACAGTGC
CACTCAGTGCCTGTCAAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTTCGTGTGCCAGTG
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCA
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCAC
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG
GCCTGGGGAACCACTACTGCAGAAACCCAGATCGAGACTCAAA
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCT
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCAGTCGGGTGC
CTCCTGCCTCCCGTGGAATTCATGATCCTGATAGGCAAGGTTTACAC
AGCACAGAACCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATT
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG
GAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCT
TTGCCAAGCACAGGAGGTCGCCGGGAGAGCGGTTCTGTGCGGGGGC
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT
TGCGCTGCTGCAGCTGAAATCGGATTTCGTCCCGCTGTGCCCAGGAGA
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG
CCGGA CTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC
CTTGTCTCCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTCAGACT
GTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAG
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCC
CAGGCAAACCTTGACGACGCCTGCCAGGGCGATTTCGGGAGGCCCCCT
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG
GTTACCAACTACCTAGACTGGATTTCGTGACAACATGCGACCGTGACC
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

296/498

FIG. 70B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg
Asp Asn Met Arg Pro

297/498

FIG. 71A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA
TGTACAGGATGCAACTCCTGTCTTGCATTGCACTAATTCTTGCACCTG
TCACAAACAGTGCACCTACTTCAAGTTGACAAAGAAAACAAAGAAA
ACACAGCTACAACCTGGAGCATTACTGCTGGATTTACAGATGATTTTG
AATGGAATTAATAATTACAAGAATCCCAAACCTCACCAGGATGCTCAC
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC
AGTGTCTAGAAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA
GCTCAAAGCAAAAACCTTCACTTAAGACCCAGGGACTTAATCAGCAA
TATCAACGTAATAGTTCTGGAACATAAGGGATCTGAAACAACATTCA
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA
TTAAGTGCTTCCCACTTAAACATATCAGGCCTTCTATTTATTTATTTA
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG
TAACTATTATTCTTAATCTTAAACATAAATATGGATCTTTTATGAT
TCTTTTTGTAAAGCCCTAGGGGCTCTAAAATGGTTTACCTTATTTATCC
CAAAAATATTTATTATTATGTTGAATGTTAAATATAGTATCTATGTAG
ATTGGTTAGTAAACCTATTTAATAAATTTGATAAATATAAAAAAAAAA
AAACAAAAAAAAAAAA

FIG. 71B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
Gln Ser Ile Ile Ser Thr Leu Thr

298/498

FIG. 72A-1

ATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTTCGATTCT
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGTCA
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG
ATTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT
GTACAAAAAGACTCTGTTTGTAGAATTACGGATCACCTTTTCAACAT
CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCC
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT
TCCCATCCTGTGCTCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCT
TCTGAGGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGGAGAAAG
AAGATGATAAAGTCTTCCCTGGTGGAAAGCCATACATATGTCTGGCAG
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG
CCTCATTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG
AAAAGACACAGACCTTGCACAAATTTATACTACTTTTTGCTGTATTTG
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATGCA
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA
GTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCAT
CGCCAGGCGTCCTTGGAAATCTCGCCAATAACTTTCCTTACTGCTCAA
ACACTCTTGATGGACCTTGGACAGTTTCTACTGTTTTTGTATATCTCTT
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG
ATGATGACAACCTCTCCTTTCCTTTATCCAAATTCGCTCAGTTGCCAAGA
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC
TGGGACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGAAGTTATAAA
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA
AAAAGTCCGATTTATGGCATAACAGATGAAACCTTTAAGACTCGTG
AAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG
AAGTTGGAGACACACTGTTGATTATATTTAAGAATCAAGCAAGCAGA
CCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCTTTGTAT
TCAAGGAGATTACCAAAGGTGTAAAACATTTGAAGGATTTTCCAAT
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAG
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC
TCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACAGATA
ATGTCAGACAAGAGGAATGTCATCCTGTTTTCTGTATTTGATGAGAAC
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTTCTCCCCAATCCA
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT
GCACAGCATCAATGGCTATGTTTTTGATAGTTTGCAGTTGTGAGTTTG
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTGGAGCACAGA
CTGACTTCCTTTCTGTCTTCTCTCTGGATATACCTTCAAACACAAAAT

299/498

FIG. 72A-2

GGTCTATGAAGACACACTCACCTATTCCCATTCTCAGGAGAACTGT
CTTCATGTGCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA
ACTCAGACTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT
AGTTGTGACAAGAACAACACTGGTGATTATTACGAGGACAGTTATGAAGA
TATTTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCCAAAAGCAATTT
AATGCCACCACAATTCCAGAAAATGACATAGAGAAGACTGACCCTTG
GTTTGCACACAGAACACCTATGCCTAAAATACAAAATGTCTCCTCTA
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT
CCTTATCTGATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCCC
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAACTGGGGGACAACTG
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTAGTACATCA
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT
GATAATACAAGTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT
AGTCAATTAGATACCACTCTATTTGGCAAAAAGTCATCTCCCCTTACT
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATAATGATTCAA
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA
AAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGGAAAAGA
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGTT
AGCATCTCTTTGTTAAAGACAAACAAAACCTTCCAATAATTCAGCAACT
AATAGAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAA
AAGTGACACCTTTGATTCATGACAGAATGCTTATGGACAAAAATGCT
ACAGCTTTGAGGCTAAATCATATGTCAAATAAACTACTTCATCAAA
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGCCCCATTCCACCA
GATGCACAAAATCCAGATATGTCGTTCTTTAAGATGCTATTCTTGCCA
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAAGTCTCTGAA
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG
AAAAATCTGTGGAAGGTCAGAATTTCTTGCTGAGAAAAACAAAGTG
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA
TGGTTTTTCCAAGCAGCAGAAACCTATTTCTTACTAACTTGGATAATT
TACATGAAAATAATACACACAATCAAGAAAAAAAATTCAGGAAGA
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC
AGATACATACAGTGACTGGCACTAAGAATTTTCATGAAGAACCTTTTC
TACTGAGCACTAGGCCAAAATGTAGAAGGTTTCATATGACGGGGCATA
TGCTCCAGTACTTCAAGATTTTAGGTCATTAAATGATTCAACAAATAG
AACAAAGAAACACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA
AACTTGGAAGGCTTGGGAAATCAAACCAGCAAATTGTAGAGAAATAT
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAATTTTG
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCACTA

FIG. 72A-3

300/498

GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCCCTCACAC
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAATAGA
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTA
TATATCTGACCAGGGTCCTATTCCAAGACAACCTCTTCTCATCTTCCAG
CAGCATCTTATAGAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT
TTCTTACAAGGAGCCAAAAAATAACCTTTCTTTAGCCATTCTAACC
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC
GAAACCAGACTTGCCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAAACTAGCAATG
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA
CAGAGGGAGCGATTAAGTGGAATGAAGCAAACAGACCTGGAAAAGT
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAAGACTCCCTCCAA
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC
AAAAGAAGAGTGGAATCCCAAGAGAAGTCACCAGAAAAAACAGCT
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAGCAAT
CATGCAATAGCAGCAATAAATGAGGGACAAAATAAGCCCGAAATAG
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA
AACCCACCAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAATC
AGAGCCCCCGCAGCTTTCAAAGAAAAACACGACACTATTTTATTGCTG
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAAGAAAGT
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT
GGAGAACTAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC
AGAAGTTGAAGATAATATCATGGTAACCTTCAGAAATCAGGCCTCTC
GTCCCTATTCTTCTATTCTAGCCTTATTTCTTATGAGGAAGATCAGAG
GCAAGGAGCAGAACCTAGAAAAAAGCTTTGTCAAGCCTAATGAAACCA
AACTTACTTTTGGAAAGTGCAACATCATATGGCACCCACTAAAGAT
GAGTTTGAAGTGCAGGCTGATTGGACCCCTTCTGGTCTGCCACACT
AACACACTGAACCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT
TGCTCTGTTTTTACCATCTTTGATGAGACCAAAGCTGGTACTTCACT
GAAAATATGGAAAGAACTGCAGGGCTCCCTGCAATATCCAGATGGA
AGATCCCCTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAACATCCATTCT
ATTCATTTCAGTGGACATGTGTTCACTGTACGAAAAAAGAGGAGTA
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGGAGACAGTGGA

FIG. 72A-4

301/498

AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGAATGCCTTATTGG
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA
TAAGTGTGAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG
CCAGACTTCATTATTCCGGATCAATCAATGCCTGGAGCACCAAGGAG
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTCAC
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA
CTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATG
TGGATTTCATCTGGGATAAAACACAATATTTTTTAACCCTCCAATTATTG
CTCGATACATCCGTTTGCACCCAACTCATTATAGCATTTCGCAGCACTC
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA
TCCTACTTTACCAATATGTTTGGCACCTGGTCTCCTTCAAAAGCTCGA
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA
CAGGAGTAACTACTCAGGGAGTAAAATCTCTGCTTACCAGCATGTAT
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC
TCTCTTTTTTTCAGAATGGCAAAGTAAAGGTTTTTTCAGGGAAATCAAGA
CTCCTTCACACCTGTGGTGAACCTCTCTAGACCCACCGTTACTGACTCG
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC
CACTGCAGCACCTGCCACTGCCGTACCTCTCCCTCCTCAGCTCCAGG
GCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGC
AGACACTGCCTTGAAGCCTCCTGAATTAACCTATCATCAGTCCCTGCATT
TCTTTGGTGGGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACTCTTA
CCTATTTTCTGCAGCTGCTCCCAGATTACTCCTTCCTTCCAATATAACT
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTCTTCCCTG
AAAAGTTAGGCCTCTCAGAGTCACCACTTCCCTCTGTTGTAGAAAACT
ATGTGATGAAACTTTGAAAAAGATATTTATGATGTTAACATTTTCAGGT
TAAGCCTCATACGTTTAAAATAAAACTCTCAGTTGTTTATTATCCTGA
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT
GGAGTCAAAAGGCAAATCATTTGGACAATCTGCAAAATGGAGAGAA
TACAATAACTACTACAGTAAAGTCTGTTTCTGCTTCCTTACACATAGA
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA
AACTAGCATTCTTAAACTGAGAATTATAGATGGGGTTCAAGAATCCC
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAATGTGC
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT
GACCAATAAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA
AAATGATGA

FIG. 72B-1

302/498

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe

FIG. 72B-2

303/498

Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn
Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln
Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp
Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu
Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu
Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr
Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu
Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu
Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly
Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn
Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly
Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly
Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu
Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp
Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser
Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser
Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala
Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg
Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro
Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu
Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly
Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp
Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile
Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln
Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg
Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys
Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val
Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe
Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu
Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn
Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu
Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile
Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile
Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro

FIG. 72B-3 304/498

Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu
Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr
Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser
Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro
Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu
Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys
Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu
Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu
Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile
Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu
Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg
Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp
Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val
Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro
Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg
Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro
Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu
Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu
Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr
Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro
Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly
Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys
Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr
Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu
His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr
Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln
Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly
Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile

FIG. 72B-4

305/498

Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr
His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr
Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln
Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr

306/498

FIG. 73A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG
GCGCGCCTGCTTCTCTGCGTCCTGGTCGTGAGCGACTCCAAAGGCAGC
AATGAAC TTCATCAAGTTCATCGAACTGTGACTGTCTAAATGGAGGA
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC
CCAAAGAAATTCGGAGGGGCAGCACTGTGAAATAGATAAGTCAAAAAC
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG
ACACCATGGGCGGGCCCTGCCTGCCCTGGA ACTCTGCCACTGTCCTTC
AGCAAACGTACCATGCCCACAGATCTGATGCTCTTCAGCTGGGCCTGG
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGCGACCCTGG
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTTCCAAGAGTGCATGGT
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT
TAAAATTTTCAGTGTGGCCAAAAGACTCTGAGGCCCGCTTTAAGATTA
TTGGGGGAGAAATTCACCACCATCGAGAACCAGCCCTGGTTTGCGGCC
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTCGCTCAA
GGCTTAACTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAC
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA
AGCTGATTTCCCACCGGGAGTGTGAGCAGCCCCACTACTACGGCTCTG
AAGTCACCACCAAAATGCTGTGTGCTGCTGACCCACAGTGGAAAACA
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA
GGGTCCCCAGGGAGGAAACGGGCACCAACCCGCTTTCTTGCTGGTTGTC
ATTTTTGCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA
AGAT

307/498

FIG. 73B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

308/498

FIG.74A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAATTGTCATCA
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGGCGCTGCTG
GCACTGGCGGCCCTACTGCAGGGGGGCCGTGTCCCTGAAGATCGCAGC
CTTCAACATCCAGACATTTGGGGGAGACCAAGATGTCCAATGCCACCCT
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTCGTGTA
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT
GTCAGGTTCTTCTCCCGGTTACAGAGGTCAGGGAGTTTGCCATTGTT
CCCCTGCATGCGGGCCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT
CTATGACGTCTACCTGGATGTCCAAGAGAAAATGGGGCTTGGAGGACG
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTC
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG
CTGAAGTGAGCAGCCCCTCCCCACACCAGTTGAACTGCAG

309/498

FIG. 74B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Leu Leu Gln
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
Glu Val Met Leu Lys

310/498

FIG. 75A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG
CCCTGTGGATGCGCCTCCTGCCCCTGCTGGCGCTGCTGGCCCTCTGGG
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGGCTCAC
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA
GGTGGAGCTGGGCGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG
CAGCCCGCAGGCAGCCCCCACC CGCCCTCCTGCACCGAGAGAGA
TGGAATAAAGCCCTTGAACCAGC

FIG. 75B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

311/498

FIG. 76A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCCT
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC
GGGCCAGGGTTCACCCCAACACACGGCGGTCTTTTGGGGTGGAGCCC
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCCTG
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAACCTCCACAACA
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGGCCTATATTTTCCT
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCCTGTTCCGACTACTGTC
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC
ATGGAGAGCACAACATCAGGATTCCTAGGACCCCTGCTCGTGTTACA
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT
AGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGGAGCACCCACGTG
TCCTGGCCAAAATTTCGCAGTCCCAACCTCCAATCACTCACCAACCTC
TTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT
ATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTC
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT
CAAGGAACCTCTATGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
GGAAACTGCACTTGTAATCCCATCCCATCATCCTGGGCTTTCGCAAGA
TTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA
GTGCCATTTGTTCAGTGGTTCGCAGGGCTTTCCCCCACTGTTTGGCTTT
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT
TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC
ATTGA

312/498

FIG. 76B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
Trp Val Tyr Ile

313/498

FIG. 77A

CGAACCCTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA
CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC
CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGC
CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT
TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG
AAGTATTCATTCCCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG
TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA
CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA
GCCCCGTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG
CGCCTCTGACAGCAACGTCTATGACCTCCTAAAGGACCTAGAGGAAG
GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT
GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA
CAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG
GAAGGACATGGCAAGGTTCGAGACATTCCTGCGCATCGTGCAGTGCCG
CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG
TGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT
GCCCACCAGCCTTGTCTAATAAAATTAAGTTGCATC

FIG. 77B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp
Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

314/498

FIG. 78A

ATGTATTCCAATGTGATAGGAACTGTAACCTCTGGAAAAAGGAAGGT
TTATCTTTTGTCTTGCTGCTCATTGGCTTCTGGGACTGCGTGACCTGT
CACGGGAGCCCTGTGGACATCTGCACAGCCAAGCCGCGGGACATTCC
CATGAATCCCATGTGCATTTACCGCTCCCCGGAGAAGAAGGCAACTG
AGGATGAGGGGCTCAGAACAGAAGATCCCGGAGGCCACCAACCGGCG
TGTCTGGGAACTGTCCAAGGCCAATTCCCGCTTTGCTACCACTTTCTA
TCAGCACCTGGCAGATTCCAAGAATGACAATGATAACATTTTCCTGTG
ACCCCTGAGTATCTCCACGGCTTTTGCTATGACCAAGCTGGGTGCCTG
TAATGACACCCTCCAGCAACTGATGGAGGTATTTAAGTTTGACACCAT
ATCTGAGAAAACATCTGATCAGATCCACTTCTTCTTTGCCAAACTGAA
CTGCCGACTCTATCGAAAAGCCAACAAATCCTCCAAGTTAGTATCAGC
CAATCGCCTTTTTTGGAGACAAATCCCTTACCTTCAATGAGACCTACCA
GGACATCAGTGAGTTGGTATATGGAGCCAAGCTCCAGCCCCTGGACT
TCAAGGAAAATGCAGAGCAATCCAGAGCGGCCATCAACAAATGGGGT
TCCAATAAGACCGAAGGCCGAATCACCGATGTCATTCCCTCGGAAGC
CATCAATGAGCTCACTGTTCTGGTGCTGGTTAACACCATTTACTTCAA
GGGCCTGTGGAAGTCAAAGTTCAGCCCTGAGAACACAAGGAAGGAAC
TGTTCTACAAGGCTGATGGAGAGTCGTGTTTCAAGCATCTATGATGTACC
AGGAAGGCAAGTTCCGTTATCGGCGCGTGGCTGAAGGCACCCAGGTG
CTTGAGTTGCCCTTCAAAGGTGATGACATCACCATGGTCCTCATCTTG
CCCAAGCCTGAGAAGAGCCTGGCCAAGGTGGAGAAGGAACCTCACCCC
AGAGGTGCTGCAGGAGTGGCTGGATGAATTGGAGGAGATGATGCTGG
TGGTCCACATGCCCCGCTTCCGCATTGAGGACGGCTTCAGTTTGAAGG
AGCAGCTGCAAGACATGGGCCTTGTCGATCTGTTTCAAGCCCTGAAAAG
TCCAAACTCCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTC
TCAGATGCATTCCATAAGGCATTTCTTGAGGTAAATGAAGAAGGCAG
TGAAGCAGCTGCAAGTACCGCTGTTGTGATTGCTGGCCGTTTCGCTAAA
CCCCAACAGGGTGACTTTCAAGGCCAACAGGCCTTTCCTGGTTTTTAT
AAGAGAAGTTCCTCTGAACACTATTATCTTCATGGGCAGAGTAGCCA
ACCCTTGTGTTAAGTAA

315/498

FIG. 78B

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val Tyr Leu Leu
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser Pro Val Asp
Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys Ile Tyr Arg Ser
Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr
Asn Arg Arg Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Ile His
Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser
Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu
Thr Tyr Gln Asp Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe
Lys Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Ser Pro Glu
Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser
Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln
Val Leu Glu Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys
Pro Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg
Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val Asp
Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu Gly Arg Asp Asp
Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser
Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys

316/498

FIG. 79A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCAG
AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCCA
ATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCCA
CTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAGA
GTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATGGG
GGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTT
ATTATCACAAATCTTAA

FIG. 79B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

317/498

FIG. 79C

ATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCAT
CAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCA
CCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCG
TGCTGCAGGGGGTCCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACC
GCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCCGCGCGGCG
TGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCAC
TCTGCCGCGCAGCACCCTGACTGCGGGGGTCCCAAGGACCACCCC
TTGACCTGTGATGACCCCGCTTCCAGGACTCCTCTTCCTCAAAGGCC
CCTCCCCCAGCCTTCCAAGCCCATCCCGACTCCCGGGGGCCCTCGGAC
ACCCCGATCCTCC CACAATAA

FIG. 79D

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr
Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala
Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly
Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val
Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg
Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys
Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp
Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser
Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln

318/498

FIG. 80A

ATGCGTCCCCTGCGCCCCCGCGCCGCGCTGCTGGCGCTCCTGGCCTCG
CTCCTGGCCGCGCCCCCGGTGGCCCCGGCCGAGGCCCCGCACCTGGT
GCAGGTGGACGCGGCCCCGCGCGCTGTGGCCCCCTGCGGGCGCTTCTGGA
GGAGCACAGGCTTCTGCCCCCGCTGCCACACAGCCAGGCTGACCAG
TACGTCCTCAGCTGGGACCAGCAGCTCAACCTCGCCTATGTGGGCGCC
GTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCACTGGCTGCTGGA
GCTTGTCAACCACCAGGGGGTCCACTGGACGGGGCCTGAGCTACAAC
TCACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCC
TCCCAGGGTTTGAGCTGATGGGCAGCGCCTCGGGCCACTTCACTGACT
TTGAGGACAAGCAGCAGGTGTTTGAGTGGAAGGACTTGGTCTCCAGC
CTGGCCAGGAGATACATCGGTAGGTACGGACTGGCGCATGTTTCCAA
GTGGAACCTTCGAGACGTGGAATGAGCCAGACCACCACGACTTTGACA
ACGTCTCCATGACCATGCAAGGCTTCCCTGAACTACTACGATGCCTGCT
CGGAGGGTCTGCGCGCCGCCAGCCCCGCCCTGCGGCTGGGAGGCCCC
GGCGACTCCTTCCACACCCACCGCGATCCCCGCTGAGCTGGGGCCTC
CTGCGCCACTGCCACGACGGTACCAACTTCTTCACTGGGGAGGCGGG
CGTGCGGCTGGACTACATCTCCCTCCACAGGAAGGGTGCGCGCAGCT
CCATCTCCATCCTGGAGCAGGAGAAGGTCGTCGCGCAGCAGATCCGG
CAGCTCTTCCCAAGTTCGCGGACACCCCATTTACAACGACGAGGCG
GACCCGCTGGTGGGCTGGTCCCTGCCACAGCCGTGGAGGGCGGACGT
GACCTACGCGGCCATGGTGGTGAAGGTCATCGCGCAGCATCAGAACC
TGCTACTGGCCAACACCACCTCCGCCTTCCCCTACGCGCTCCTGAGCA
ACGACAATGCCTTCTGAGCTACCACCCGCACCCCTTCGCGCAGCGCA
CGCTCACCGCGCGCTTCCAGGTCAACAACACCCGCCCGCCGCACGTG
CAGCTGTTGCGCAAGCCGGTGCTCACGGCCATGGGGCTGCTGGCGCT
GCTGGATGAGGAGCAGCTCTGGGCGCGAAGTGTCGCGAGGCCGGGACCG
TCCTGGACAGCAACCACACGGTGGGCGTCCTGGCCAGCGCCACCGC
CCCCAGGGCCCCGGCCGACGCCTGGCGCGCCGCGGTGCTGATCTACGC
GAGCGACGACACCCGCGCCACCCCAACCGCAGCGTCGCGGTGACCC
TGCGGCTGCGCGGGGTGCCCCCGGCCCGGGCCTGGTCTACGTCACG
CGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGGCGGCG
CCTGGGCCCGGCCGTCTTCCCCACGGCAGAGCAGTTCCGGCGCATGC
GCGCGGCTGAGGACCCGGTGGCCGCGGCGCCCCGCCCTTACCCGCC
GGCGGCCGCTGACCCTGCGCCCCGCGCTGCGGCTGCCGTGCTTTTG
CTGGTGCACGTGTGTGCGCGCCCCGAGAAGCCGCCCGGGCAGGTCAC
GCGGCTCCGCGCCCTGCCCTGACCCAAGGGCAGCTGGTTCTGGTCTG
GTCGGATGAACACGTGGGCTCCAAGTGCCTGTGGACATACGAGATCC
AGTTCTCTCAGGACGGTAAGGCGTACACCCCGGTCAGCAGGAAGCCA
TCGACCTTCAACCTCTTTGTGTTTCAGCCAGACACAGGTGCTGTCTCT
GGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCCCGACCAGGCC
CTTCTCGGACCCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCC
CCCATCCCCGGGCAATCCAT GA

319/498

FIG. 80B

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu
Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val Gln Val Asp Ala Ala
Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu
Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala
Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu
Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His
Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu
Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val
Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly
Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp
Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys
Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp
Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His
Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln
Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala
Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala
Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr
Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro
His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu
Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala
Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro
Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu
Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp
Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg
Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu
Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala
Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln
Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr
Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro
Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr
Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro
Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

320/498

FIG. 81A

ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCGCT
TCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACT
GGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGG
AGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCAGATTCCCTGC
ATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGA
AGGCTGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTG
GATGGCTCCCCAAAGAGATTCAGAAGGCAGACTTCAGGCAGACCCTC
AGCGCTTTCCTCATGGGATTCGCCAGCTAGCTAATTATGTTACACAGCA
AAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGC
GCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCAGACC
TTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGT
GACAGTTTGGAAAATTTGGCAGATGGTTATAAGCACATGTCCTTG GCC
CTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCTCTT
TATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGACAGTAC
TGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGT
ATAAAGAGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTT
GATGTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGAT
TGGCAACTTTGGCCTCAGCTGGAATCAGCAAGTAACTCAGATGGCCCT
CTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACA
CATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGC
CATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGG
GAGACAACCTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGG
GCTGTAGCTATGATAAACCGGCAGGAGATTGGTGGACCTCGCTCTTAT
ACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCTGCC
TGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTTCTAT
GAATGGACTTCAAGGTTAAGAAGTCACATAAATCCACAGGCACTGT
TTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAAAGACTTACT
TTAA

321/498

FIG. 81B

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe
Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala
Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met Cys Asn Leu Asp
Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys Leu Phe Met Glu Met Ala Glu
Leu Met Val Ser Glu Gly Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp
Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln
Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys
Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly Ser Phe
Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys
Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn Leu Ala Asp Gly Tyr Lys His
Met Ser Leu Ala Leu Asn Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro
Leu Tyr Met Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu
Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro Gly Gly Trp
Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu Ser Trp Asn Gln Gln
Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp
Leu Arg His Ile Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala
Ile Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn
Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser Leu Gly Lys
Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu Leu Pro Val Lys Arg Lys
Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr
Val Leu Leu Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu

322/498

FIG. 82A

ATGGCGCCCGTCGCCGTCTGGGCGCGCTGGCCGTCGGACTGGAGCT
CTGGGCTGCGGCGCACGCCTTGCCCGCCCAGGTGGCATTACACCCTA
CGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG
GACAGCACATAACCCAGCTCTGGAAGTGGGTTCGAGTGTGCTTGAG
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAAACTCAAGCCTGCAC
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG
TGCCGCCCCGGGCTTCGGCGTGGCCAGACCAGGAACTGAAACATCAGA
CGTGGTGTGCAAGCCCTGTGCCCGGGGACGTTCTCCAACACGACTTC
ATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACGTGGTGGCCAT
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCAGCCAGTGTCC
ACACGATCCCAACACACGCAGCCAACCTCCAGAACCCAGCACTGCTCC
AAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTCATCATGAC
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC
CTCACTTGCCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCCACTCGGAACCAGC
CACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC
CAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCCAGG
TCAATGTCACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT
CACAGTGCTCCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC
AGCCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCCCTTCTCCAAGGA
GGAATGTGCCTTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGG
GGAGCACCGAAGAGAAGCCCCCTGCCCTTGGAGTGCTGATGCTGGG
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTGCTAGCCAAGG
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGCCCTGGTCCTT
CCAGGC

323/498

FIG. 82B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
Asp Ala Gly Met Lys Pro Ser

324/498

FIG. 83A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 83B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
Gly Thr Leu Val Thr Val Ser Ser

325/498

FIG. 84A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ser

FIG. 84B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

326/498

FIG. 85A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA
GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGC
ATCCACTGGTATCAGCAAAGAACAATGGTTCTCCAAGGCTTCTCATA
AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC
AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT
GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC
ACGTTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA
GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT
CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAACTGGG
TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA
TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
AGGTTCAACATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA
ATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCCAGG
AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC
ACAGTCTCC

FIG. 85B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val
Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln
Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro
Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly
Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr
Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg
Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

327/498

FIG. 86A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTCCA
GGTTCCACTGGTGACGTCAGGCGAGGGCCCCGGAGCCTGCGGGGCAG
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC
TGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACGCCGCGGC
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG
CCGCAGGAGTCGGTGGGCGCGGGGGGCCGGCGAGGCGGCGGTGCGACA
AAACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGA
CCGTGAGTCTTCTTCCCCCAAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA
CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGG
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACG
CCTCCCGTGTTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC
ACCGTGGAACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
CCCTGTCTCCCGGGAAATGA

328/498

FIG. 86B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

329/498

FIG. 87

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

FIG. 88

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr
Leu Val Thr Val Ser Ala

FIG. 89

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

FIG. 90

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
Thr Leu Val Thr Val Ser Ser

330/498

FIG. 91

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 Ser Phe Asn Arg Gly Glu Cys

FIG. 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
 Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
 Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

331/498

FIG. 93A

ATGGATTTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA
GTCATAATGTCCAGAGGGCAAATTGTTCTCTCCCAGTCTCCAGCAATC
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGCCAG
CTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGATCCTC
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC
TGTTTCGCTTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT
GGACTAGTAACCCACCCACGTTCTGGAGGGGGGACCAAGCTGGAAATC
AAA

FIG. 93B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

332/498

FIG. 94A

ATGGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG
CCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATTT
ACCAGTTACAATATGCACTGGGTAAAACAGACACCTGGTCGGGGCCT
GGAATGGATTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAA
TCAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 94B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ala

333/498

FIG. 95A

GACGTCGCGGGCCGCTCTAGGCCTCCAAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAACTGGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCCACAGAATTAATTTCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT
TATGGGACTTTCCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGATAGC
GGTTTGACTCACGGGGATTTCCTCAAGTCTCCACCCCATTTGACGTCAATG
GGAGTTTGTTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCTGTA
ACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCACAGATCTCTCACCATGAGGGTCCCCGCTCAGCTCCT
GGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGATGGTACCAA
GGTGGAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCT
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAG
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAG
TGTTGAATTCAGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCT
GTGACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCT
TGACCCTGGAAGGTGCCACTCCCCTGTCCTTTTCTTAATAAAATGAGG
AAATTGCATCGCATTGTCTGAGTAGGTGTCTATTCTATTTGGGGGGTG
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG
GCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGAC
AGCTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGC
CCGCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCCTACTT
GGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT
TTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGA
TTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTTTTGGCAC

334/498

FIG. 95B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCCTCACATTCAAGTATCAGCACTGAACACAGACCC
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA
TGCCACCGTGCCAGCACCTGAATCCTGGGGGGACCGTCAGTCTTC
CTCTTCCCCCCTAAACCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCTGCAACAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAGGAACCAGGTCAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGTG
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTTGCCCTCCCCCGTGCCTTCCTTGA
CCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGGG
TGGGGCAGGACAGCAAGGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA
ATGAGAAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGAT
TGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

335/498

FIG. 95C

GCTGCGATTTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAACTGCAT
CGTCGCCGTGTCCCAAATATGGGGATTGGCAAGAACGGAGACCTAC
CCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC
ACAACCTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAG
GAAAACCTGGTTCTCCATTCTGAGAACATCGACCTTTAAAGGACA
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACCACCACGAGGA
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT
CTTTGTGACAAGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCC
AGAAATTGATTTGGGGAAATATAAACTTCTCCCAGAATACCCAGGCG
TCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAA
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGC
TCCCCTCCTAAAGTCATGCATTTTTATAAGACCATGGGACTTTTGCTG
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGT
TTGCCCCCTCCCCCGTGCTTCCCTTGACCCTGGAAGGTGCCACTCCCAC
TGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCAATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT
ATGGAACCAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT
ATTTGCATAATGAGAAAAAAGGAAAATTAATTTTAACACCAATTCA
GTAGTTGATTGAGCAAATGCGTTGCCAAAAGGATGCTTTAGAGACA
GTGTTCTCTGCACAGATAAGGACAAACATTATTCAGAGGGAGTACCC
AGAGCTGAGACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGA
AATATGCTTGTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGG
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGG
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAA
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC
GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT
GTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGA
CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTAT
CGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTGCTCGACGTTG
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG
CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATC
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCG
GATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATC
AGGGGCTCGCGCCAGCCGAACGTTCGCCAGGCTCAAGGCGCGCATG
CCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG

336/498

FIG. 95D

AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGT
GCTTTACGGTATCGCCGCTTCCCGATTTCGCAGCGCATCGCCTTCTATC
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGAC
CGACCAAGCGACGCCCAACCTGCCATCACGAGATTTTCGATTCCACCG
CCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCG
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC
ACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATA
GCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTT
GTGGTTTGTCCAAACTCATCAATCTATCTTATCATGTCTGGATCGCGG
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC
TGTGTGAAATTGTTATCCGCTCACAAATCCACACAACATACGAGCCGG
AGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCAC
ATTAATTGCGTTGCGCTCACTGCCCCGCTTTCAGTCGGGAAACCTGTC
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTC
GGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC
TGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAATC
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC
CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC
CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG
GCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
GTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC
CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA
CAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATT
ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC
GGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTAAAGGGATTTTGG
TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTA
AATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC
TATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC
GAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA
GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTC
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGC

337/498

FIG. 95E

CAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTACAGGCATCGTGG
TGTCACGCTCGTCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCCAAC
GATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTT
AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTG
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC
ATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACCTGATCTTCA
GCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGG
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAA
TACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTA
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

338/498

FIG. 96A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAACTGGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCCACAGAATTAATTCCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT
TATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATACC
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCCATTGACGTCAATG
GGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCACAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT
CAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT
TGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA
GGTCACAATGACTTGCAAGGGCCAGCTCAAGTGTAAGTTACATCCACT
GGTTCCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCA
CATCCAACCTGGCTTCTGGAGTCCCTGTTCGCTTCAGTGGCAGTGGGT
CTGGGACTTCTTACTCTCTCACAAATCAGCAGAGTGGAGGCTGAAGATG
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCG
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCC
TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT
CAACAGGGGAGAGTGTTGAATTCAGATCCGTTAACGGTTACCAACTA
CCTAGACTGGATTTCGTGACAACATGCGGCCGTGATATCTACGTATGAT
CAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTC
CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCC

339/498

FIG. 96B

TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA
GCTGGGGCTCGACAGCTATGCCAAGTACGCCCCCTATTGACGTCAATG
ACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT
GGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTG
ACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTT
TGTTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAAC
CCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC
TATATAAGCAGAGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGA
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT
CGCTGTTGCTACGCGTGTCTGTCCCAGGTACAACCTGCAGCAGCCTGG
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAACAGA
CACCTGGTTCGGGGCCTGGAATGGATTGGAGCTATTTATCCCGGAAAT
GGTGATACTTCCTACAATCAGAAGTTCAAAGGCAAGGCCACATTGAC
TGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGA
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCACC
GTCTCTGCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC
TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG
CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACAC
ATGCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCC AAAACCAAGGACACCCTCATGATCTCCCGGACCCC
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT
GCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACACCT
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
AGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTTCGT

340/498

FIG. 96C

GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC
TTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTG
ACCCTGGAAGGTGCCACTCCCAGTGTCTTTCTAATAAAATGAGGAA
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGG
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC
ATGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAG
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCAT
AATGAGAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGA
TTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTGCGATTTTCG
CGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC
CCCGCTGCCATCATGGTTTCGACCATTGAACTGCATCGTCGCCGTGTCC
CAAAATATGGGGATTGGCAAGAACGGAGACCTACCCTGGCCTCCGCT
CAGGAACGAGTTCAAGTACTTCCAAAGAATGACCACAACCTCTTCAG
TGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGTTC
TCCATTCTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTT
CTCAGTAGAGAACTCAAAGAACCACCACGAGGAGCTCATTTTCTTGC
CAAAAGTTTGGATGATGCCTTAAGACTTATTGAACAACCGGAATTGG
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCTGTTTACC
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG
ATCATGCAGGAATTTGAAAGTGACACGTTTTTCCCAGAAATTGATTTG
GGGAAATATAAACTTCTCCCAGAATACCCAGGCGTCCTCTCTGA
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCCCTCCTAA
AGCTATGCATTTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA
GCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCC
CCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAGTGTCTTTCTTA
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGC
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTTATTTGCATAATG
AGAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGATTGA
GCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCTGCA
CAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAGACT
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTC
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG

341/498

FIG. 96D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTG
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC
AGCGCAGGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA
CGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG
TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCA
ATGCGGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCAC
CAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGG
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC
CAGCCGAACGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAG
GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG
GAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTG
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTAT
CGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGAC
GCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTCTATGA
AAGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTT
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAA
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTG
TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
GCGCTCACTGCCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCA
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGC
GCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTTCGTTCCGGCT
GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA
CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC
ATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC
CCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC
CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAA
GCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTT
ATCCGGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

342/498

FIG. 96E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGC
TGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAA
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC
TCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATC
AAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAAATGAAGTTTTAA
ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC
ACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCG
AGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTA
ATTGTTGCCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAGTTTGC
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGT
TTGGTATGGCTTCATTCAGCTCCGTTCCCAACGATCAAGGCGAGTTA
CATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTC
CGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTA
TGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCT
TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
TGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACC
GCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCT
TCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCC
ATGTAACCCACTCGTGACCCAACTGATCTTCAGCATCTTTTACTTTCA
CCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAA
AAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCT
TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG
ATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGC
GCACATTTCCCCGAAAAGTGCCACCT

343/498

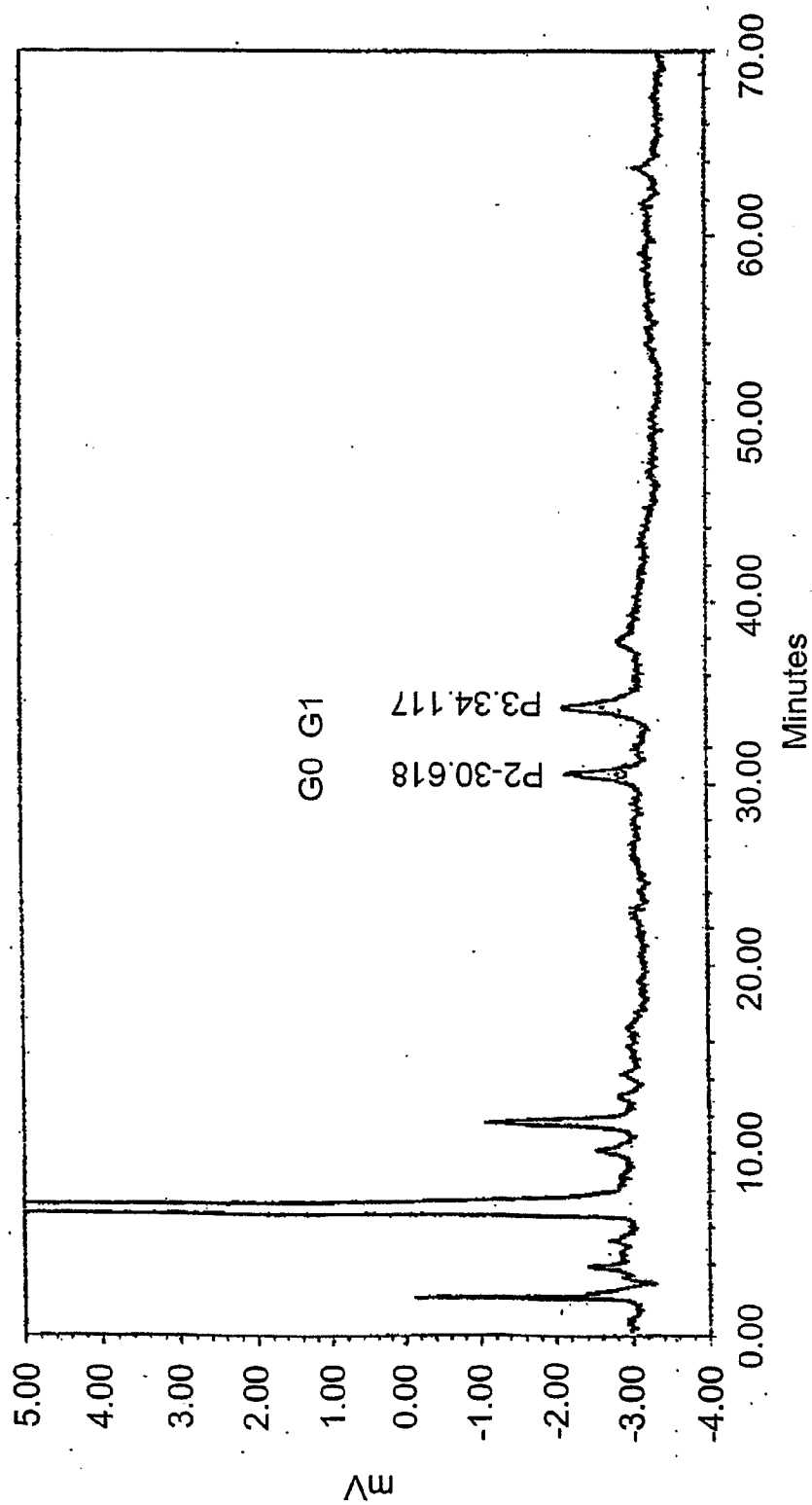


FIG. 97A

344/498

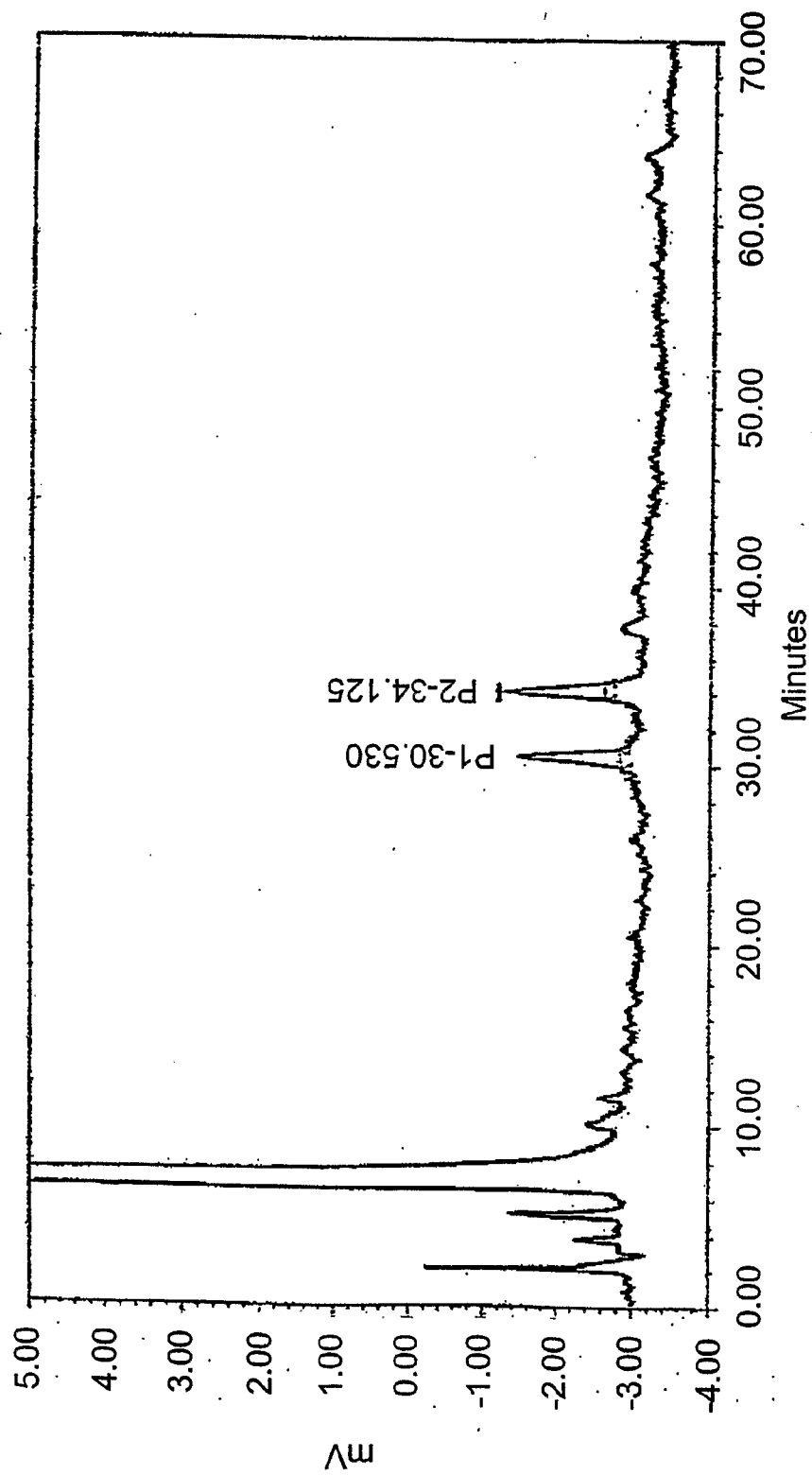


FIG. 97B

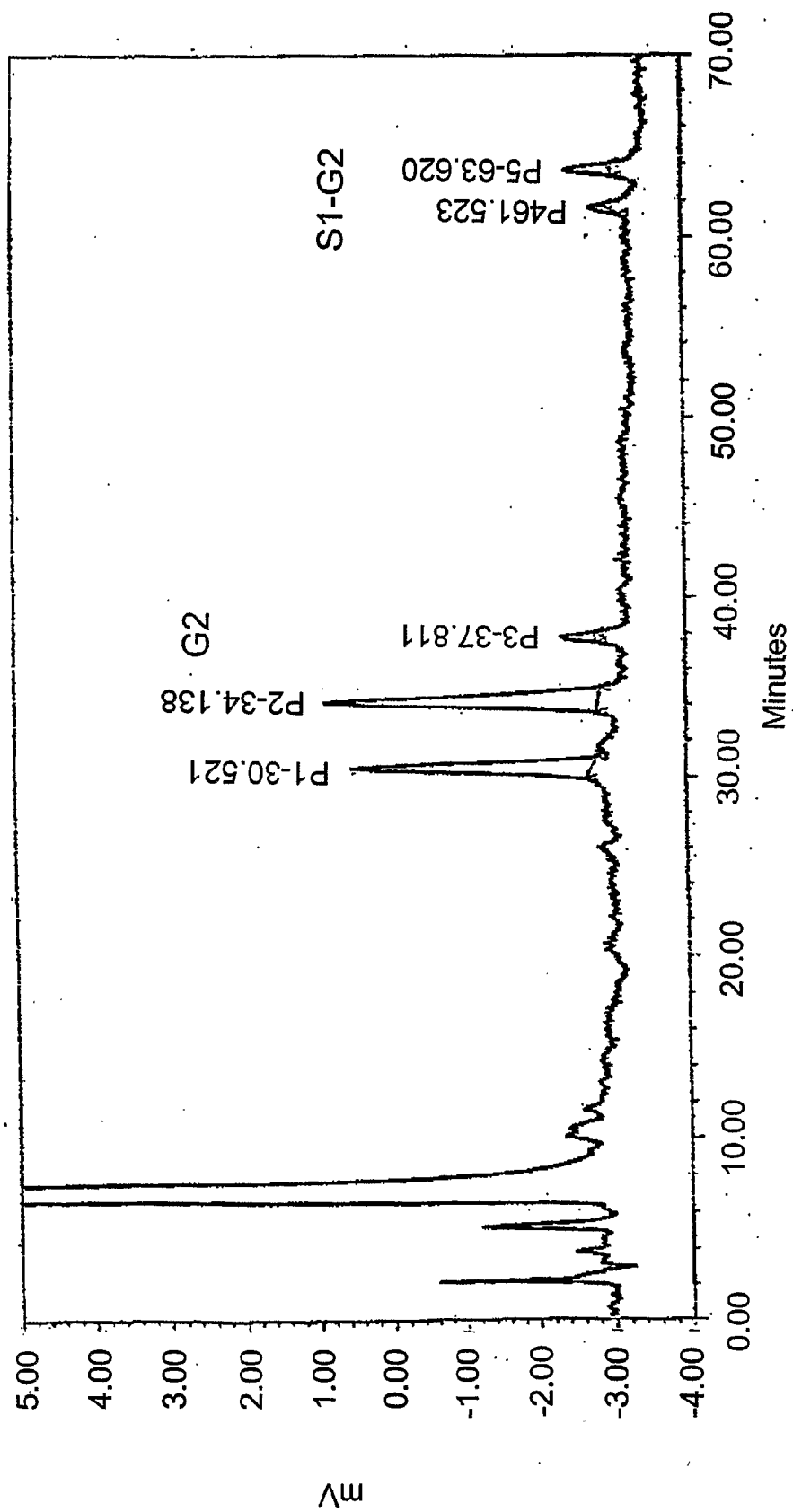


FIG. 97C

346/498

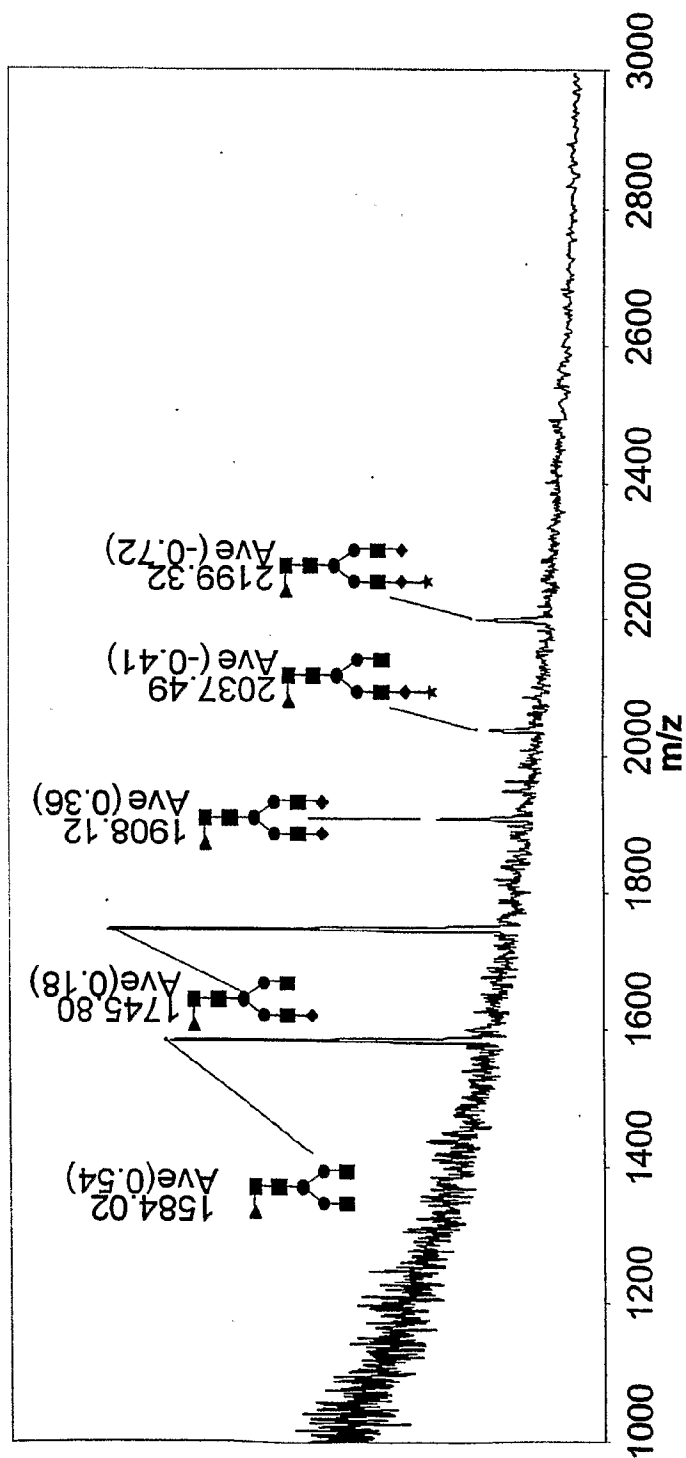


FIG. 98A

347/498

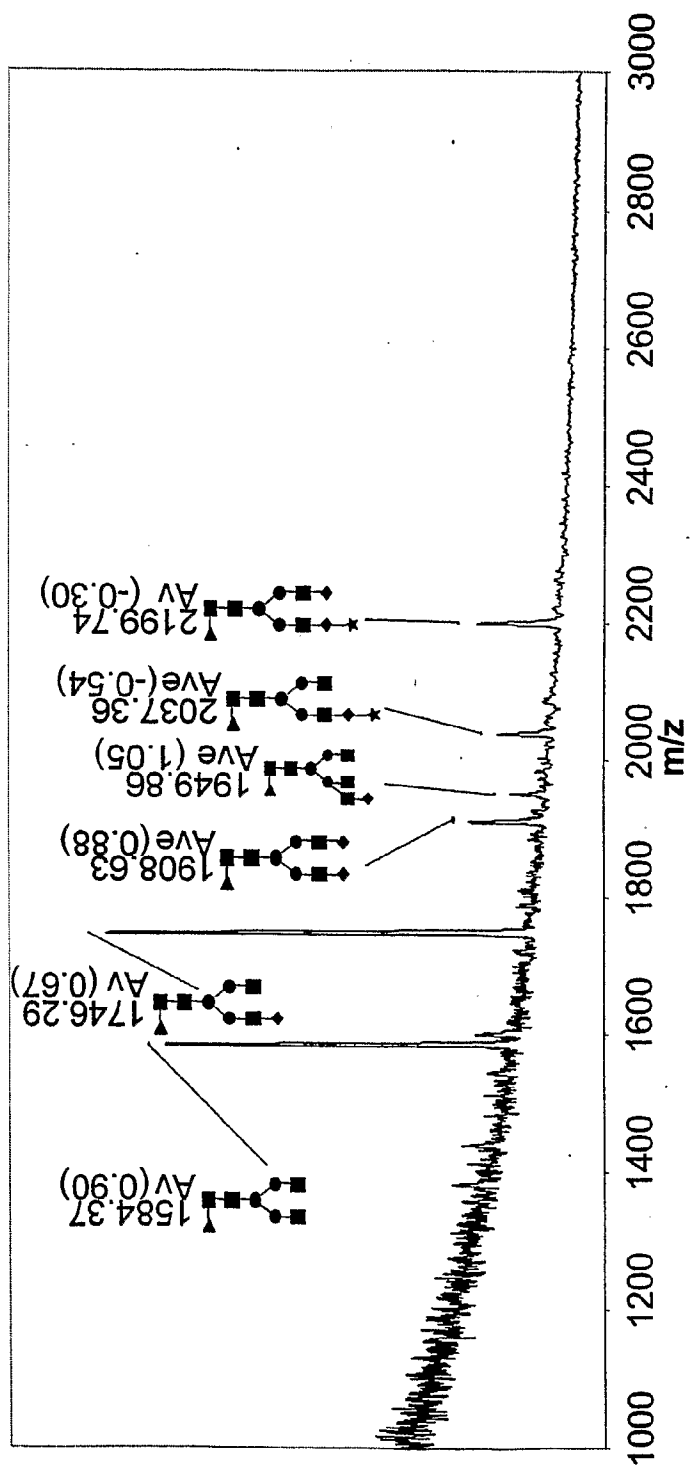


FIG. 98B

348/498

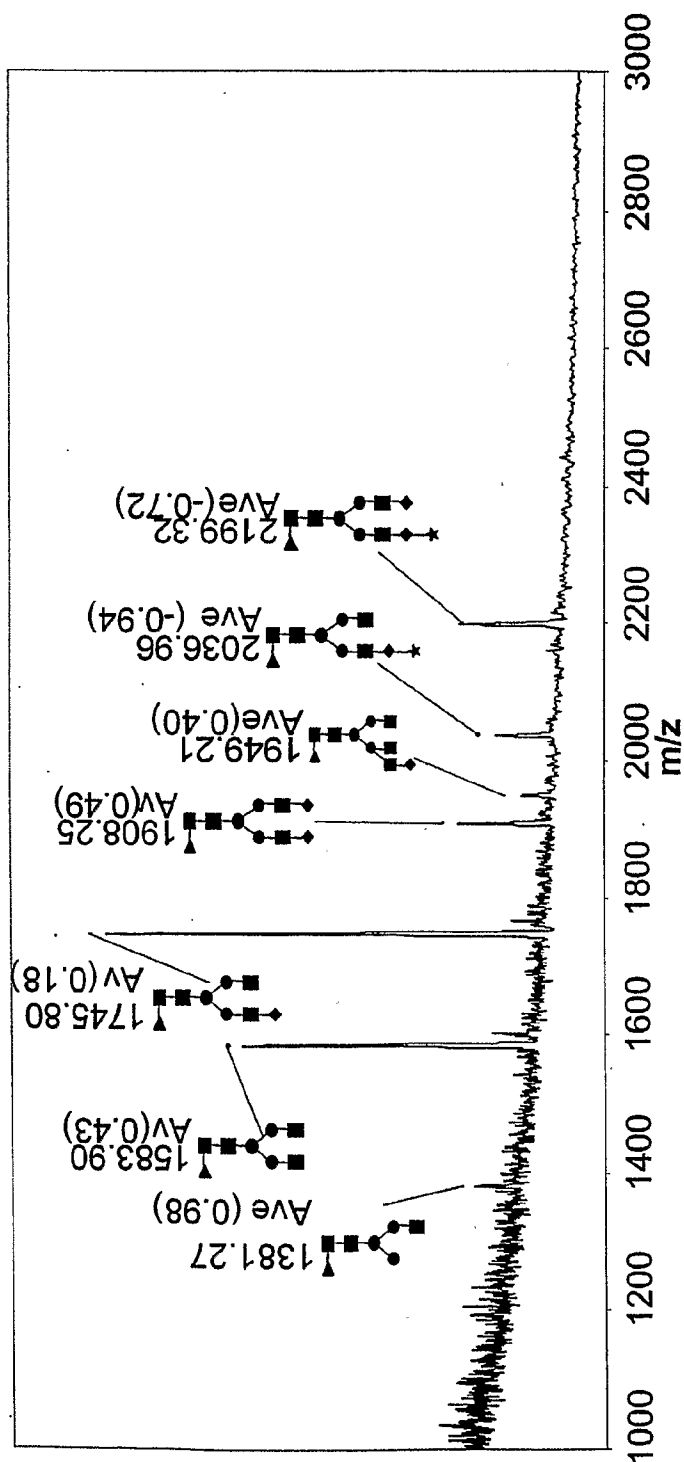


FIG. 98C

349/498

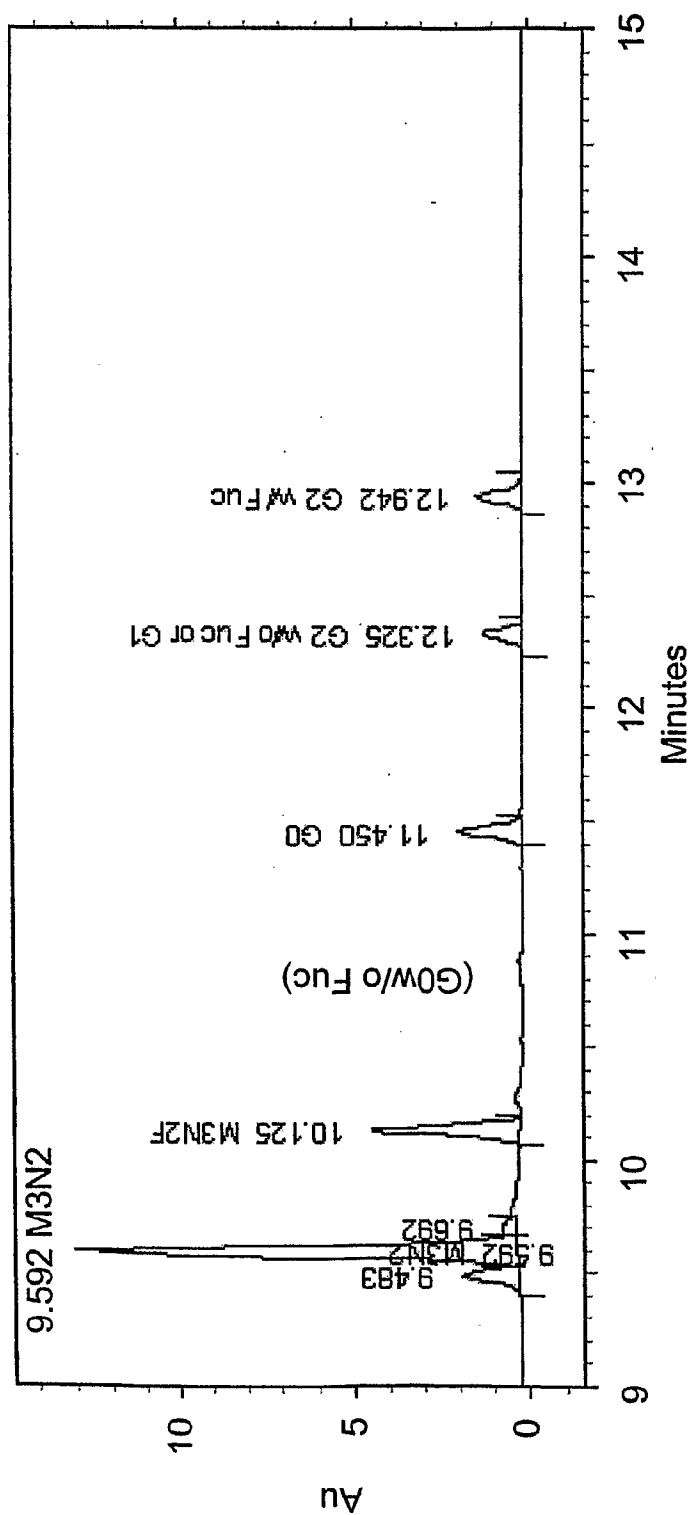


FIG. 99A

350/498

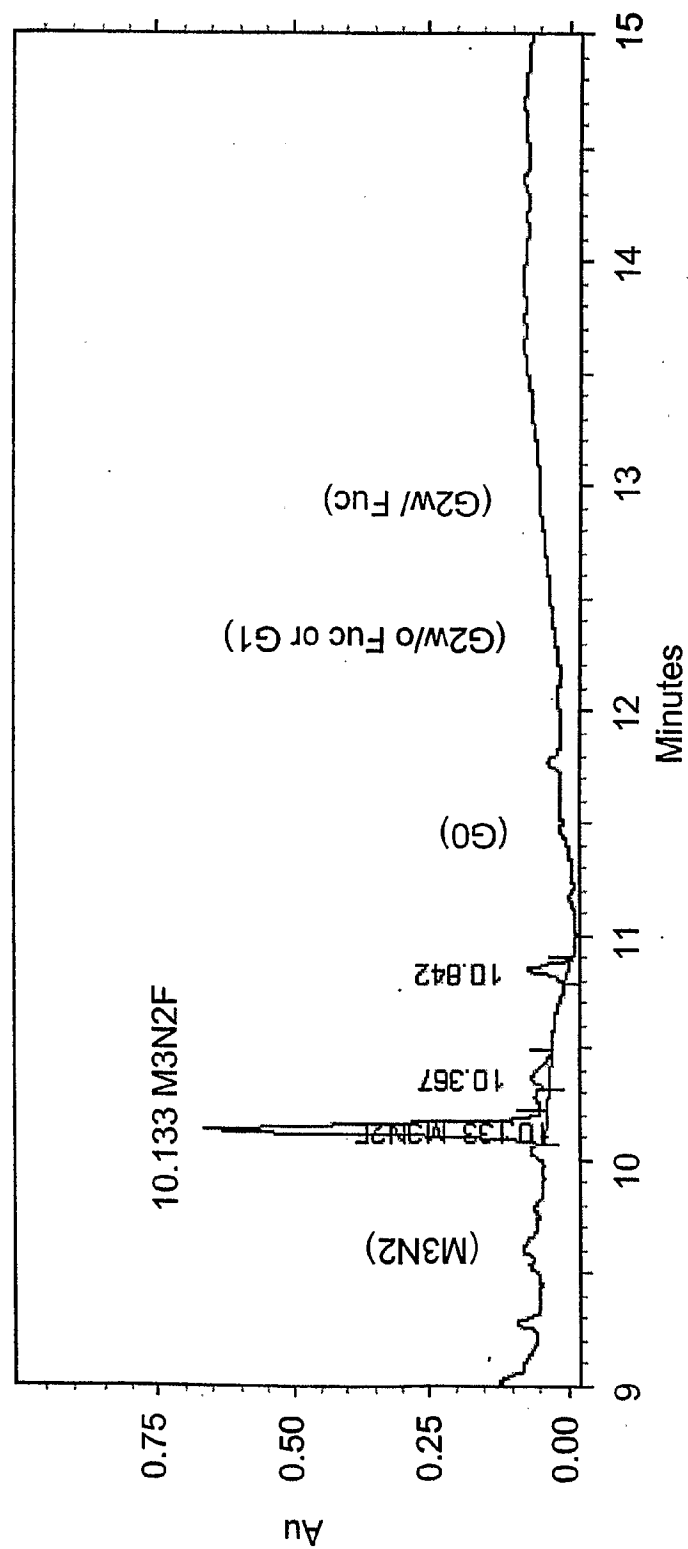


FIG. 99B

351/498

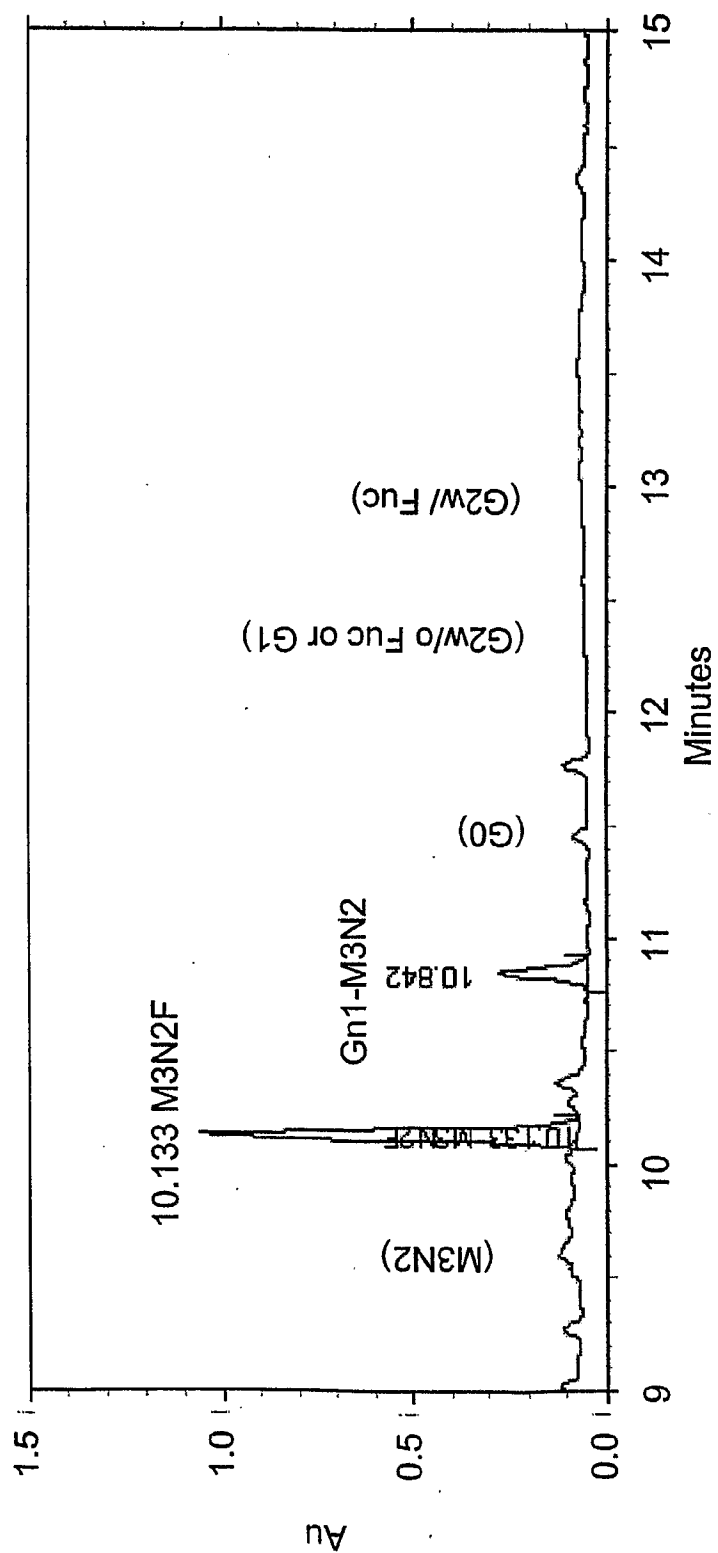


FIG. 99C

352/498

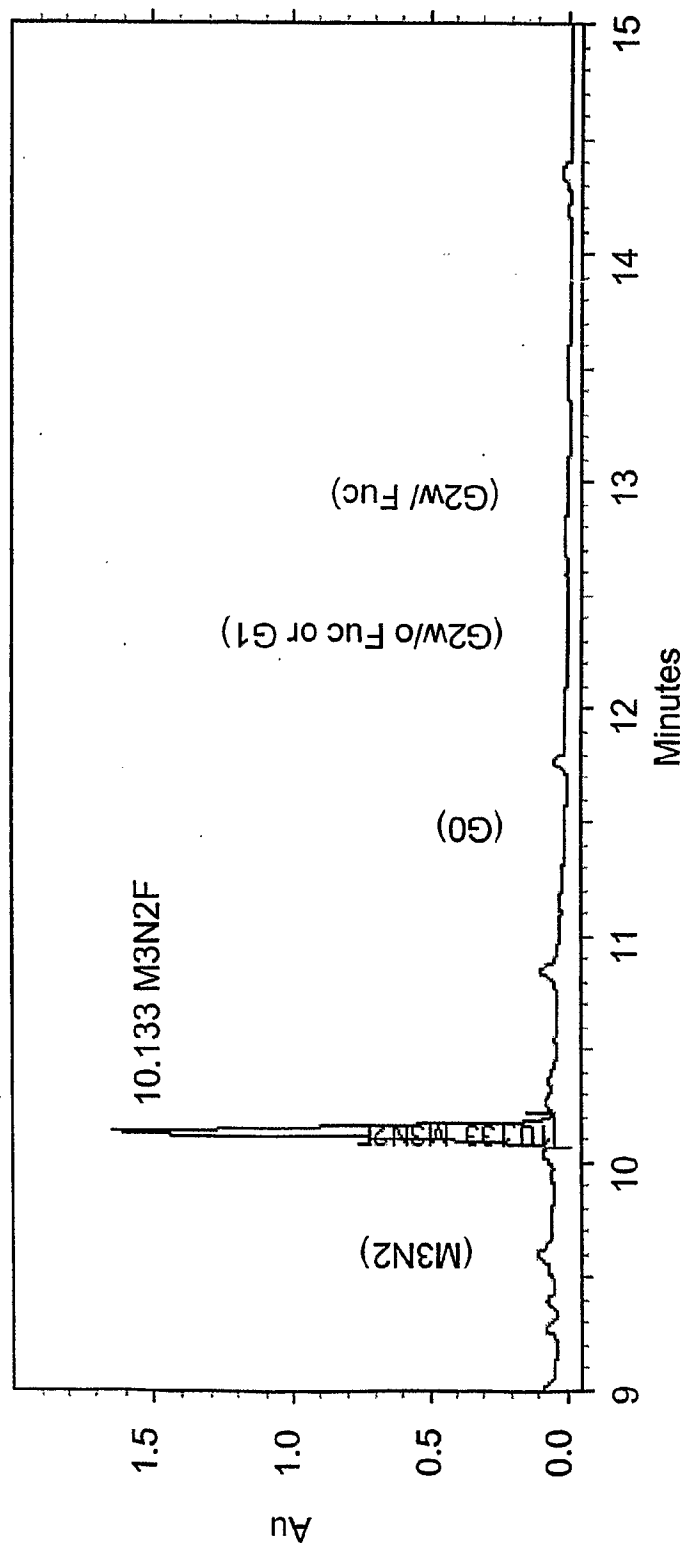


FIG. 99D

353/498

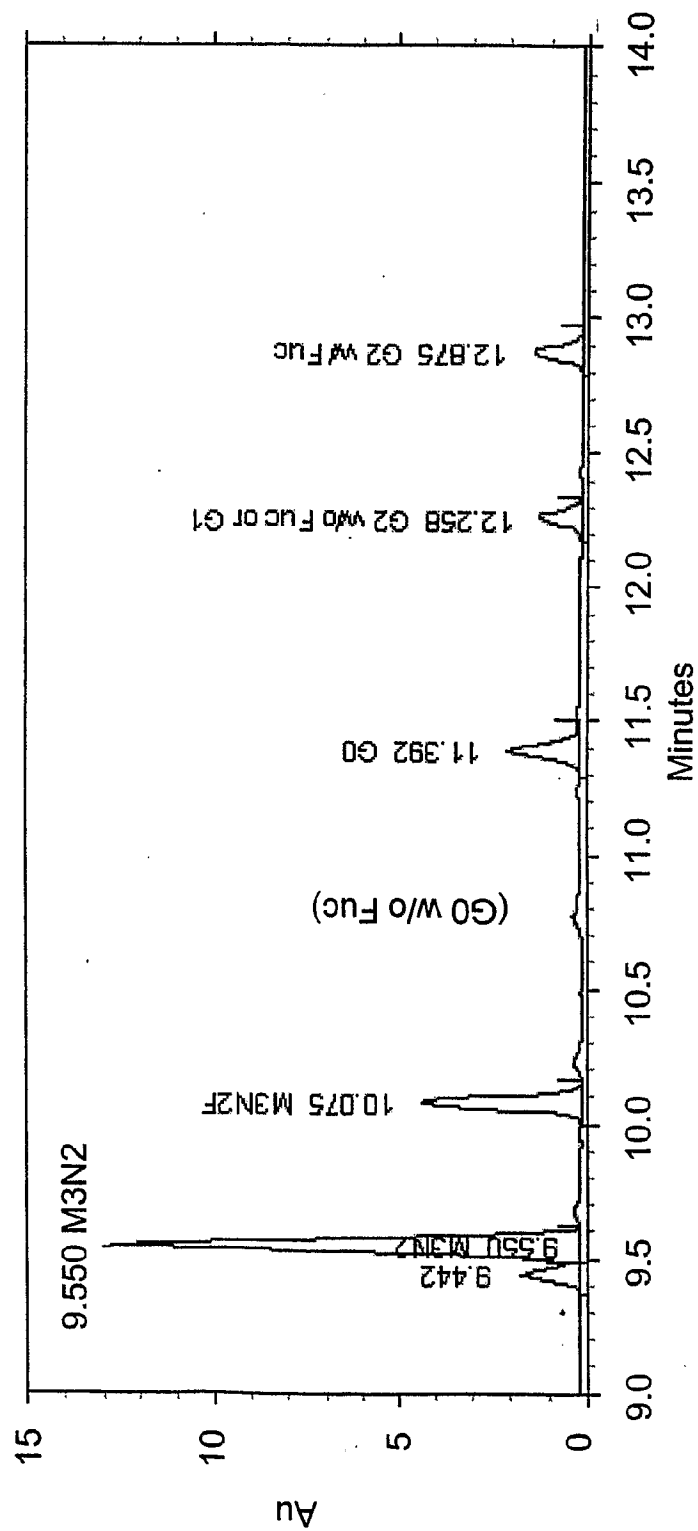


FIG. 100A

354/498

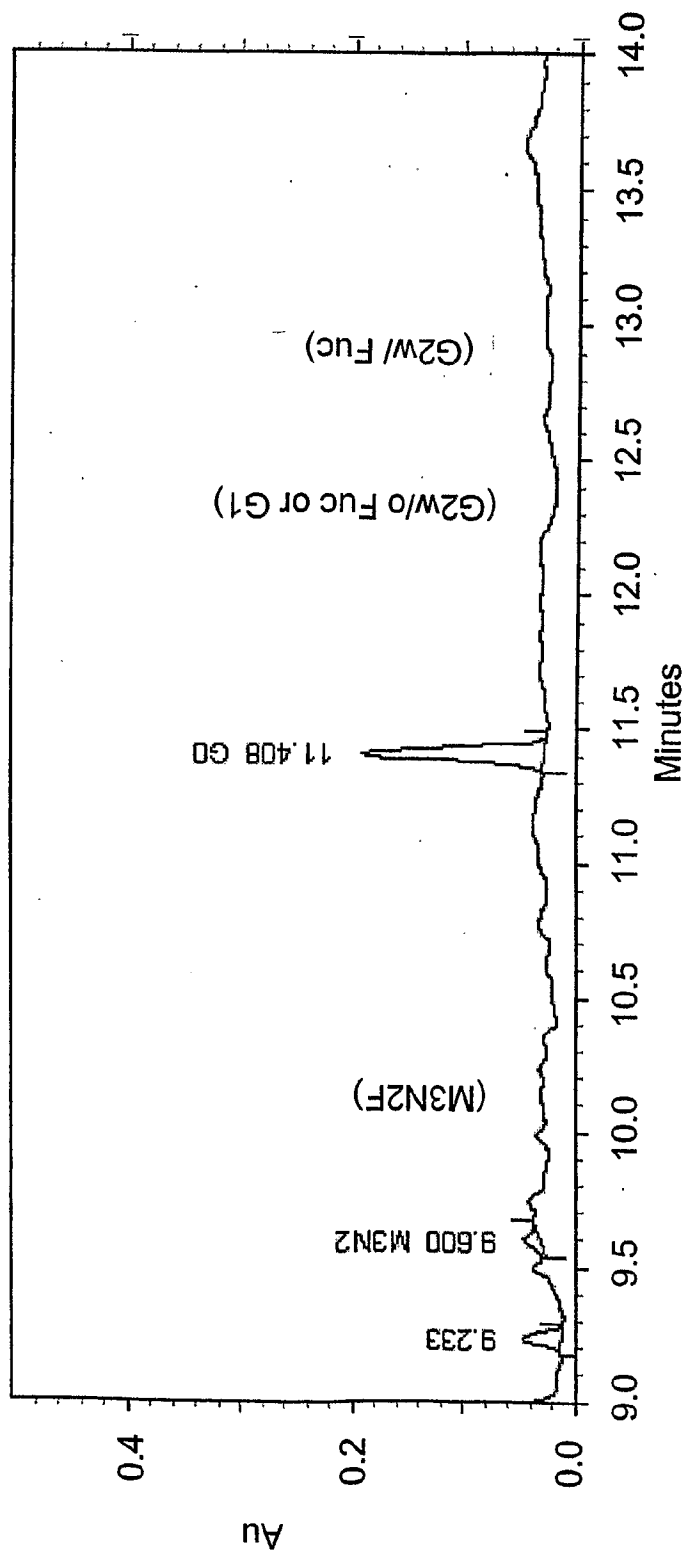


FIG. 100B

355/498

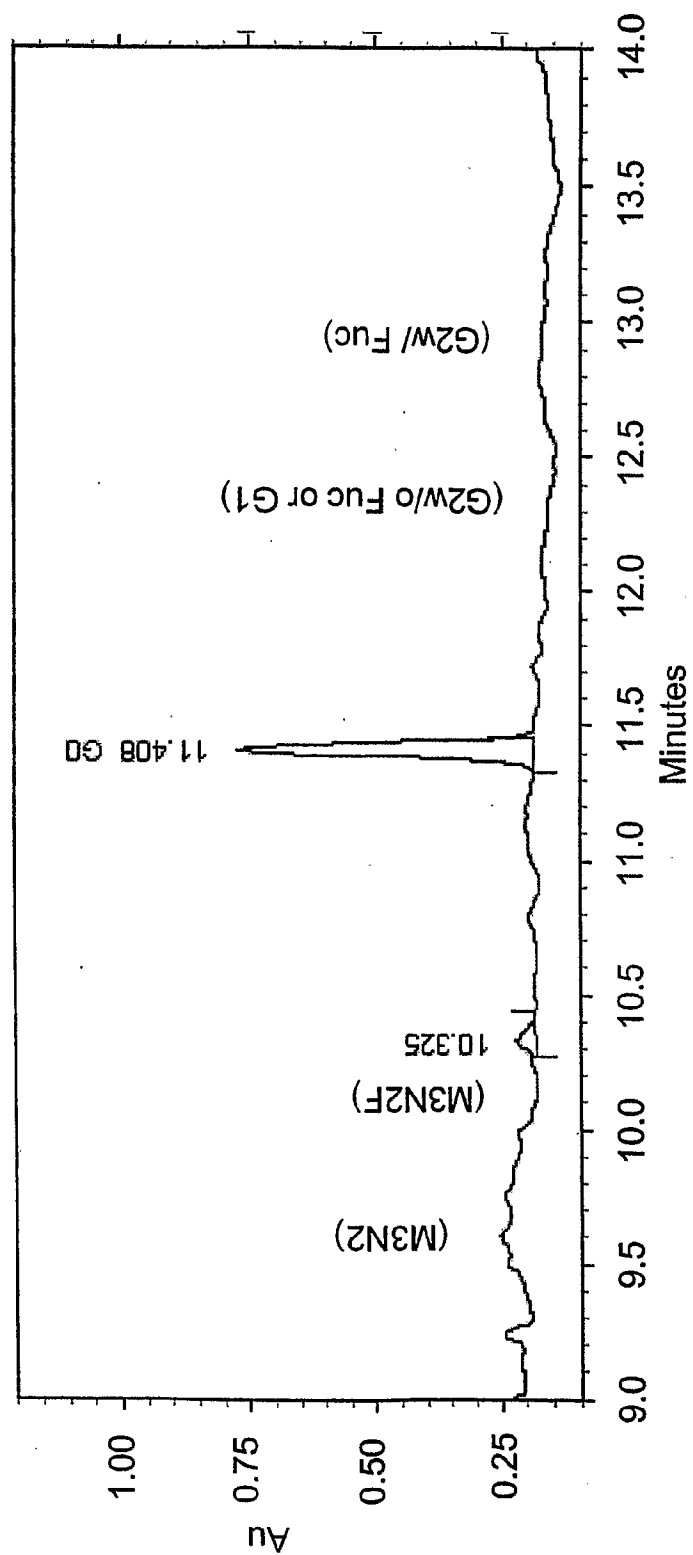


FIG. 100C

356/498

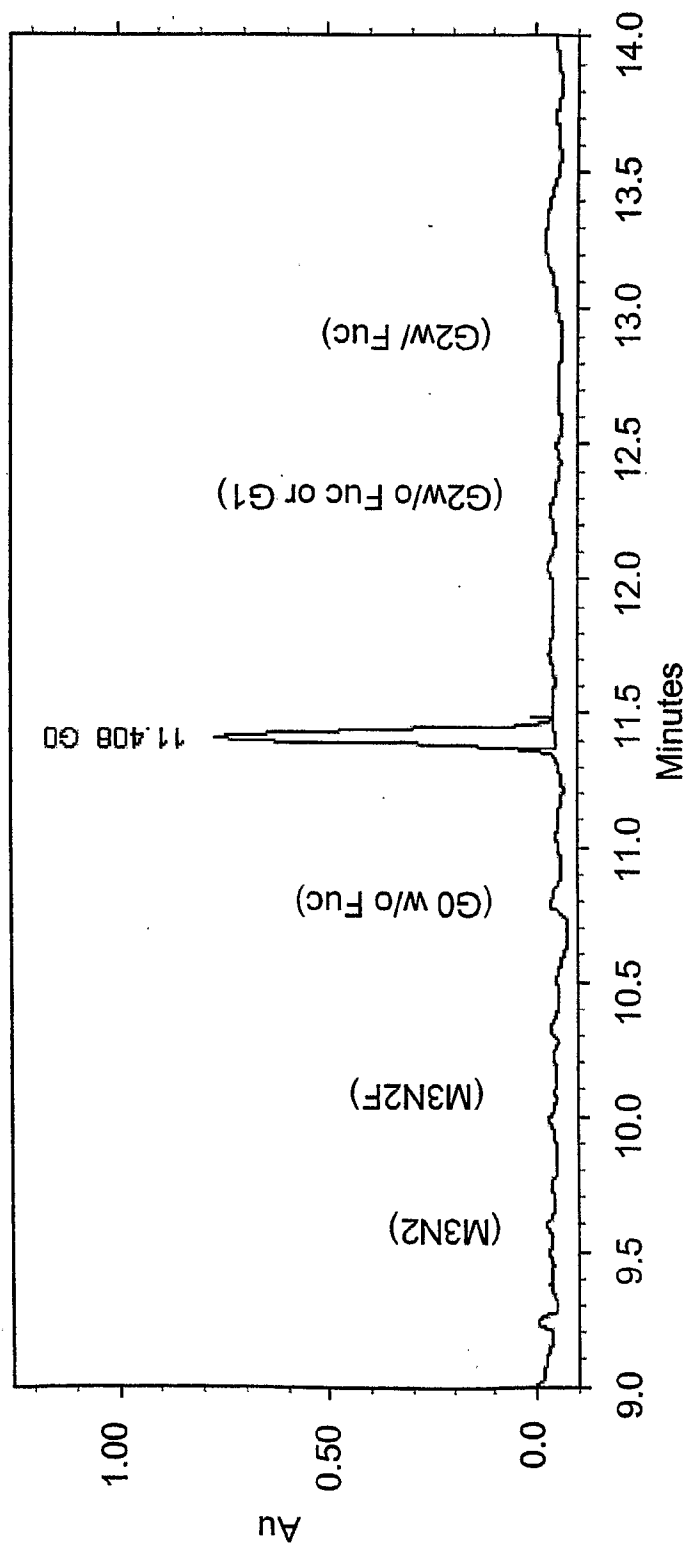


FIG. 100D

357/498

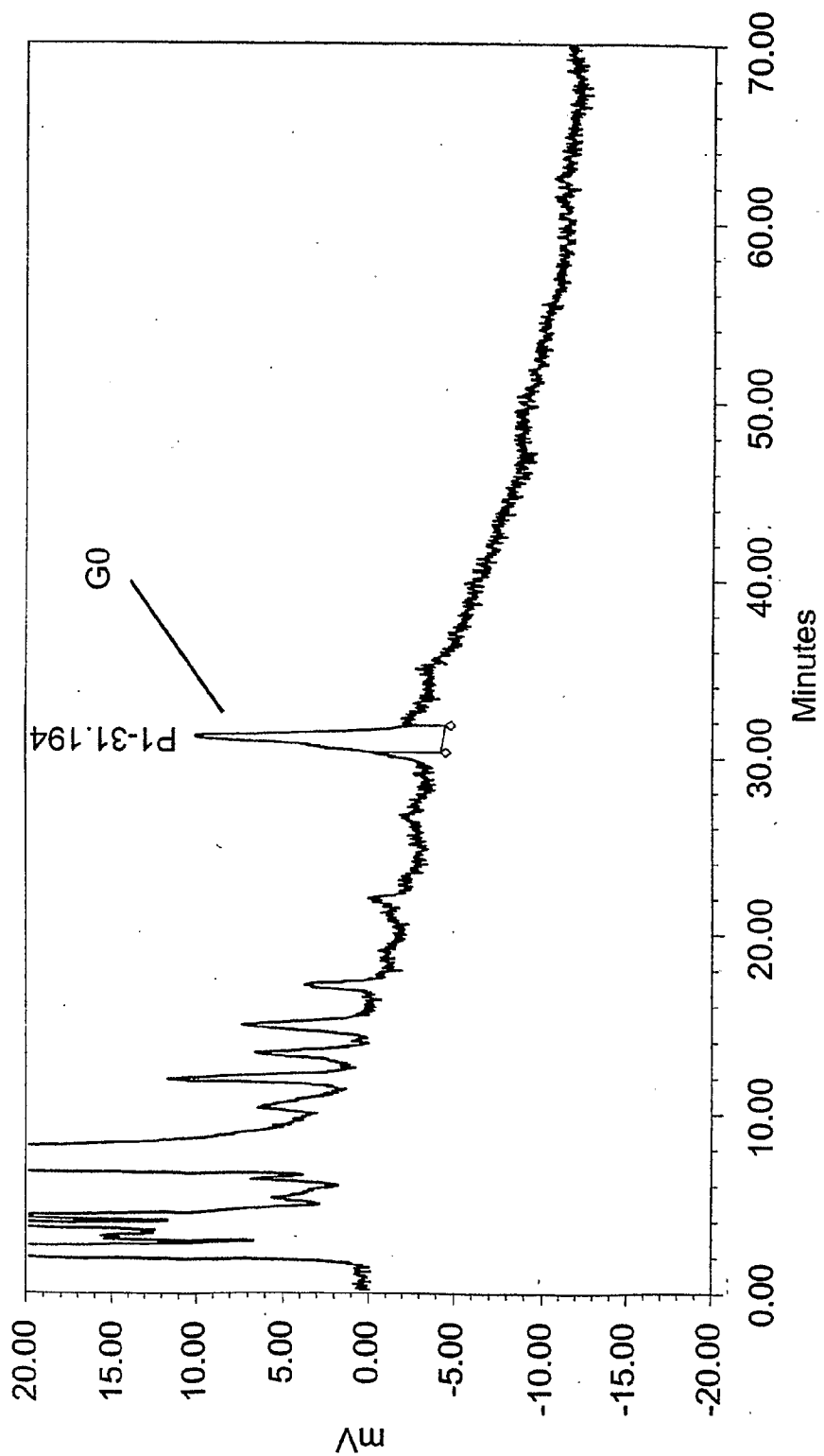


FIG. 101A

358/498

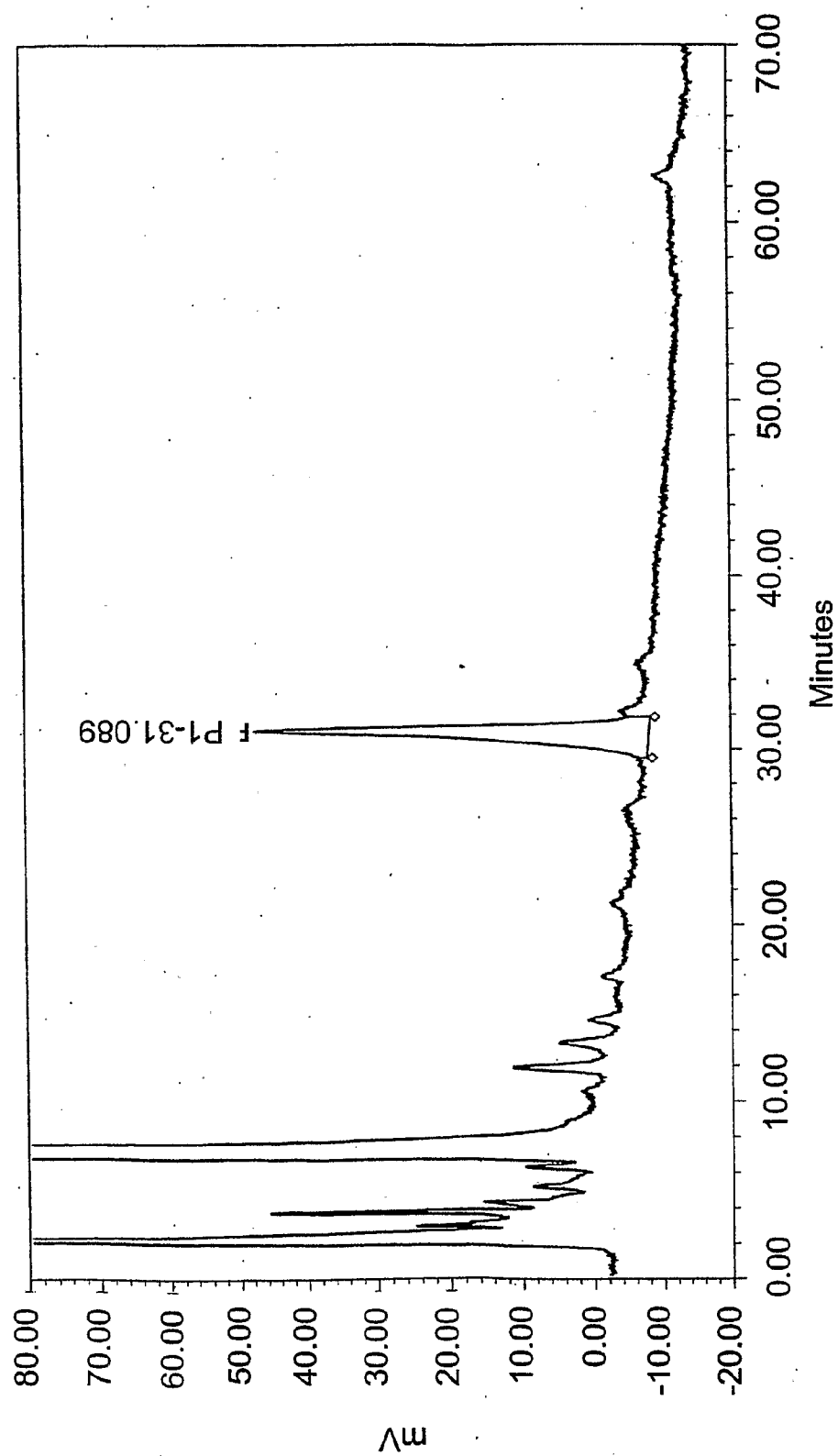


FIG. 101B

359/498

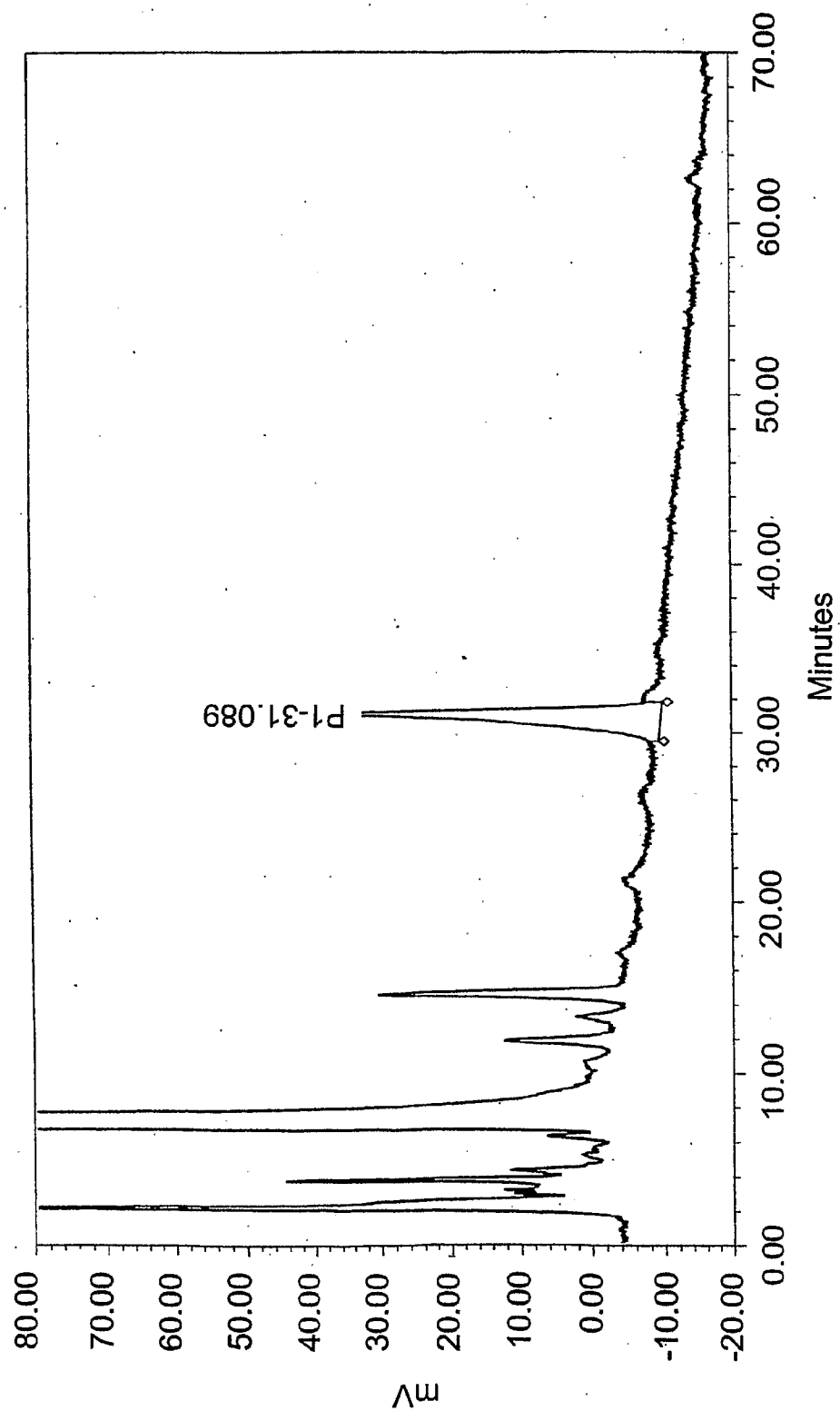


FIG. 101C

360/498

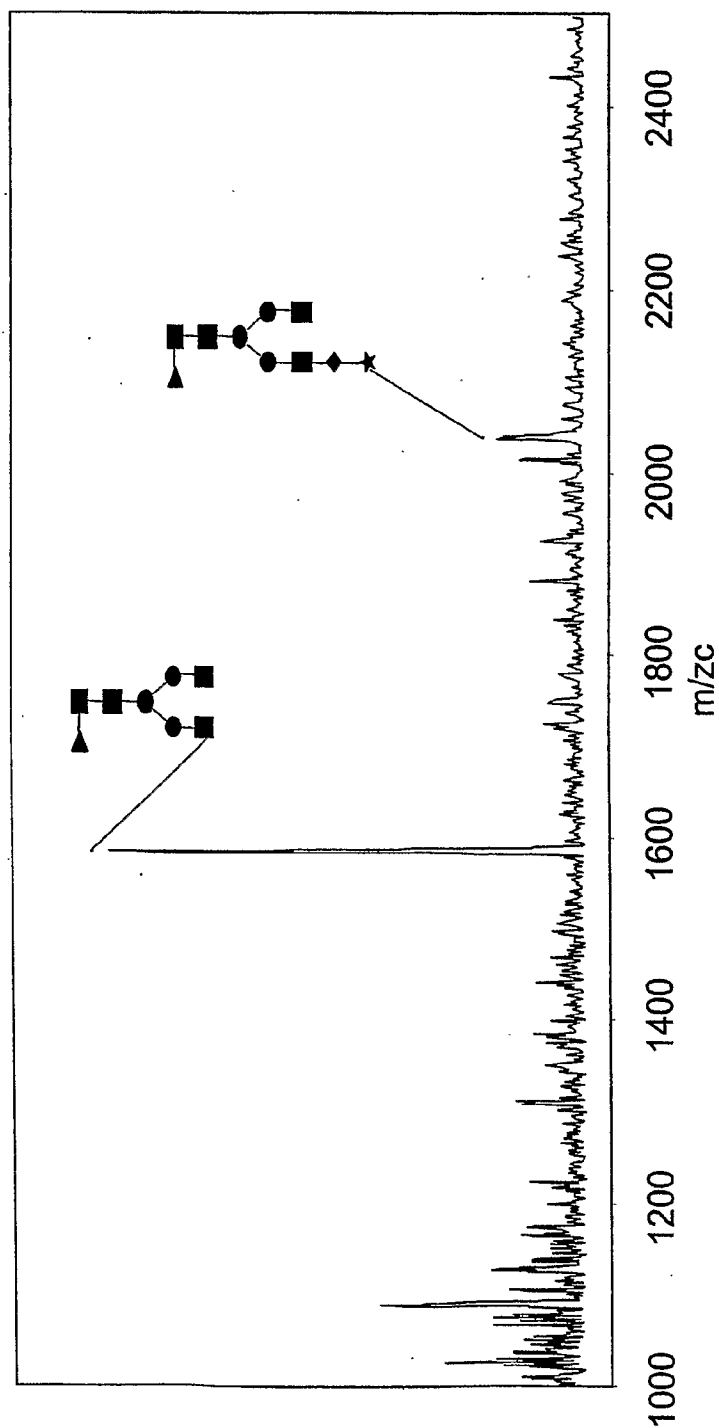


FIG. 102A

361/498

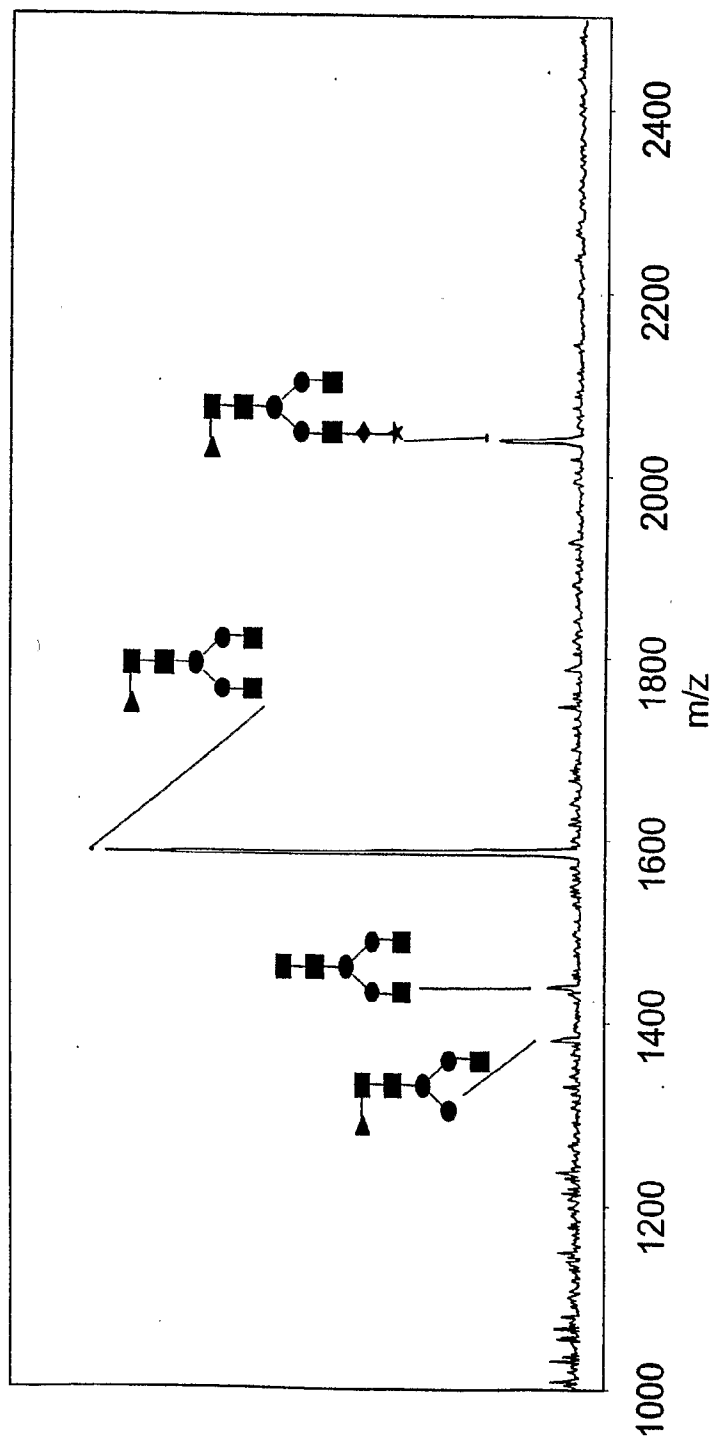


FIG. 102B

362/498

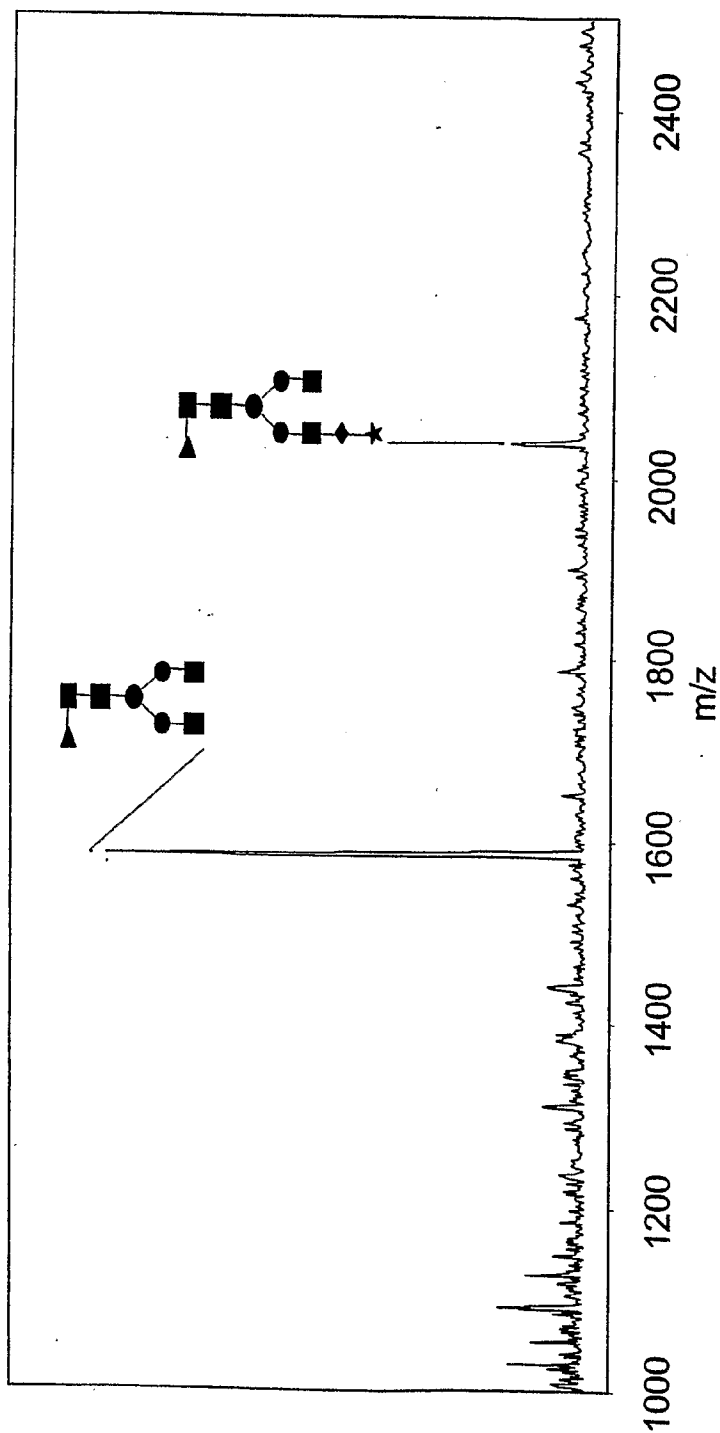


FIG. 102C

363/498

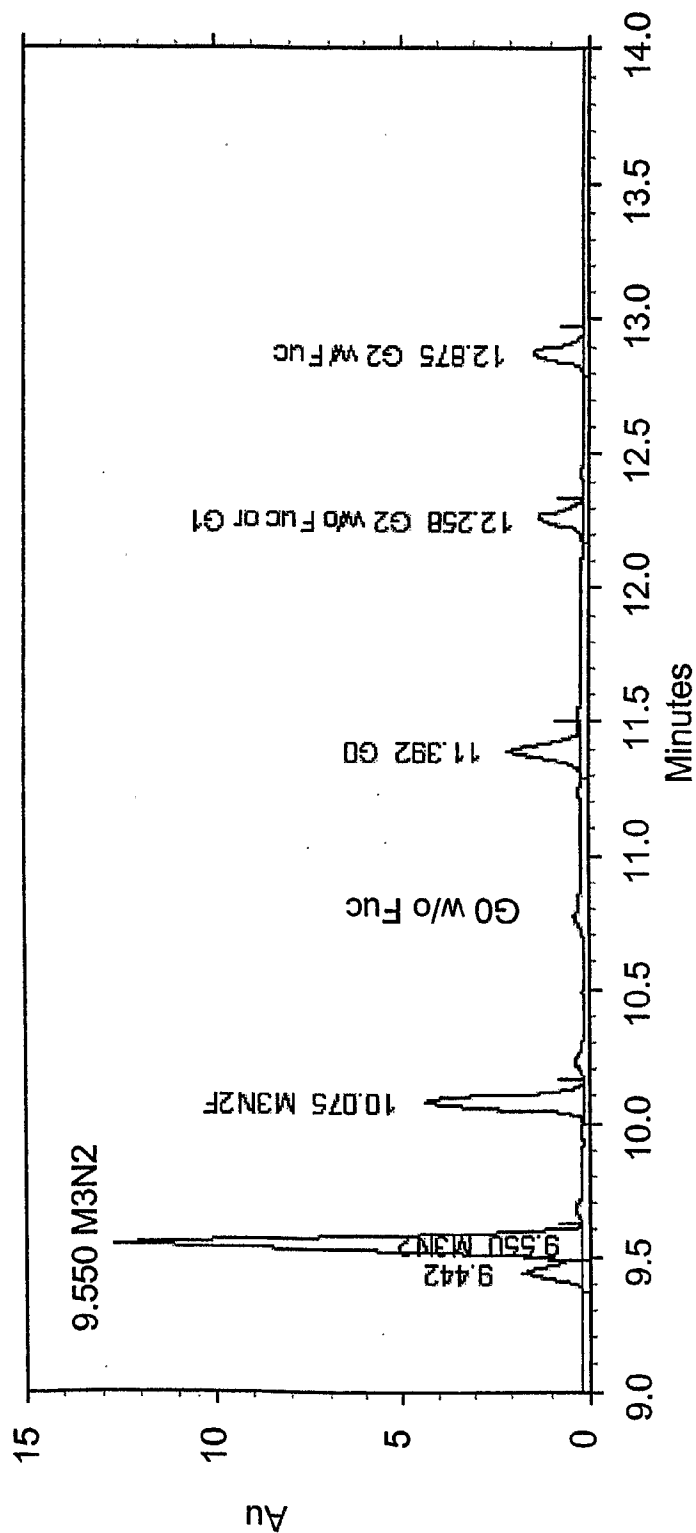


FIG. 103A

364/498

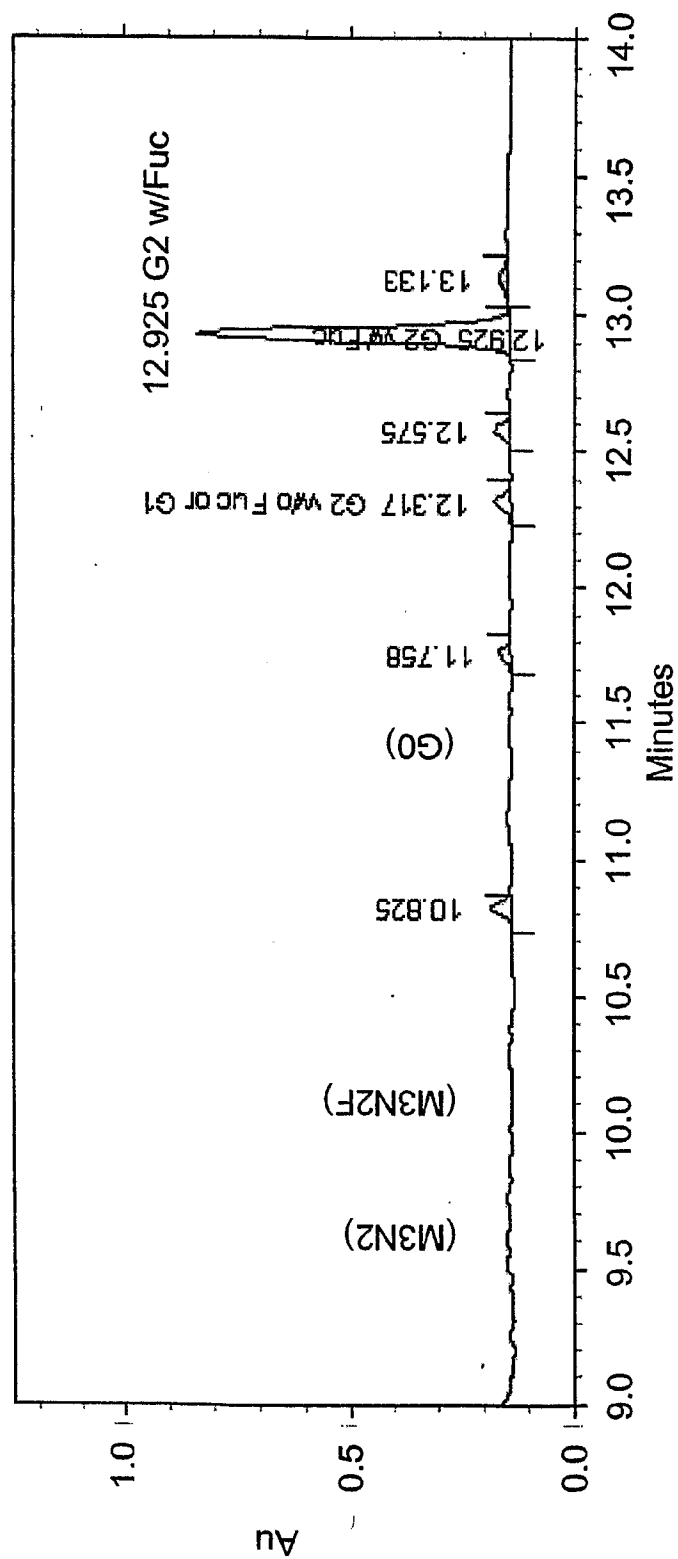


FIG. 103B

365/498

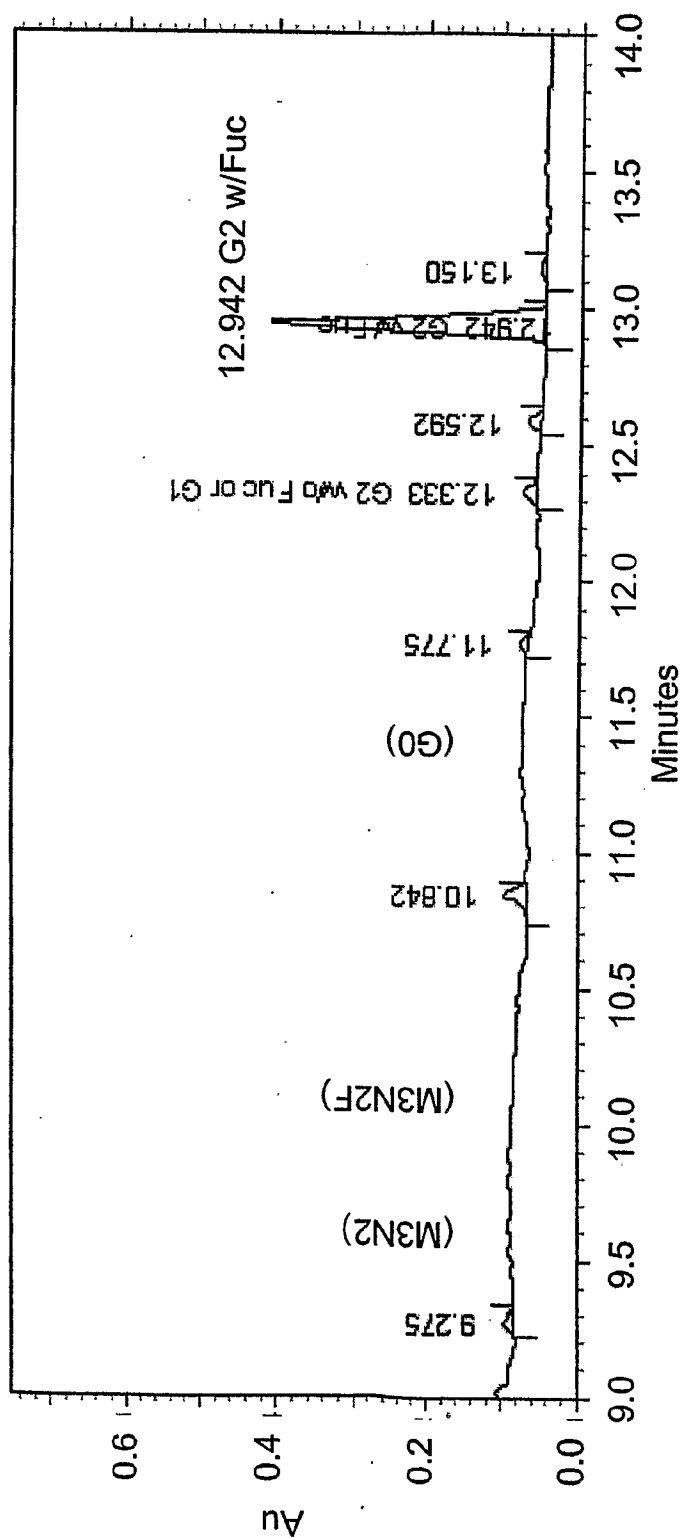


FIG. 103C

366/498

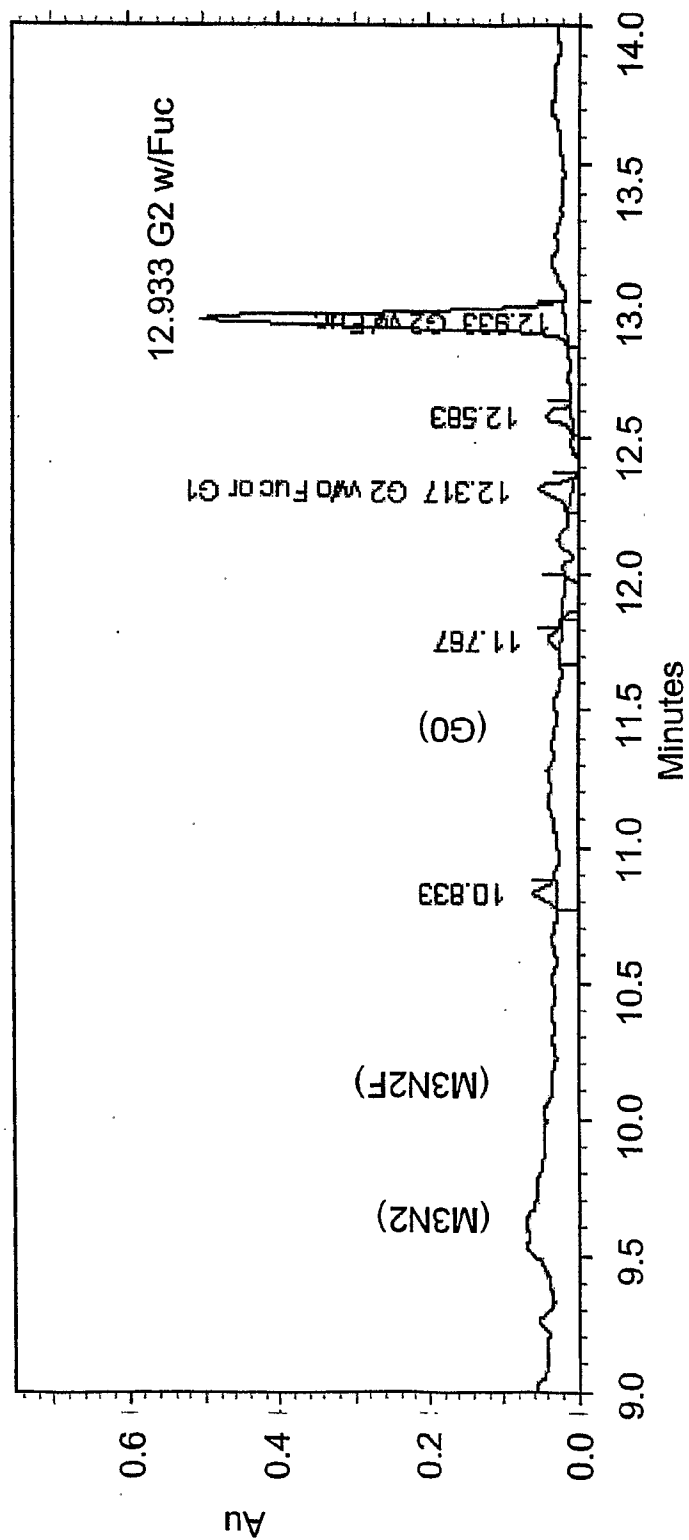


FIG. 103D

367/498

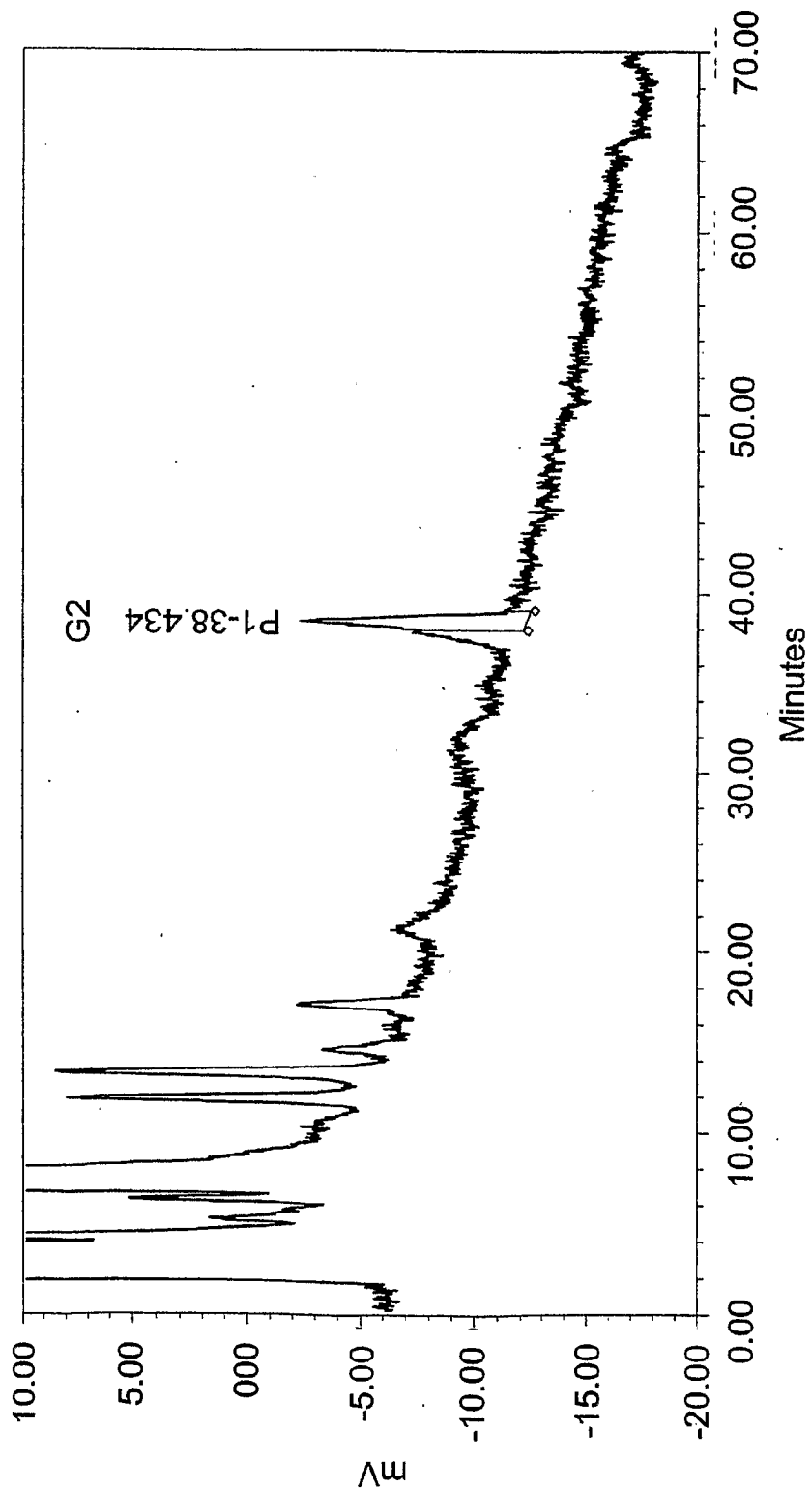


FIG. 104A

368/498

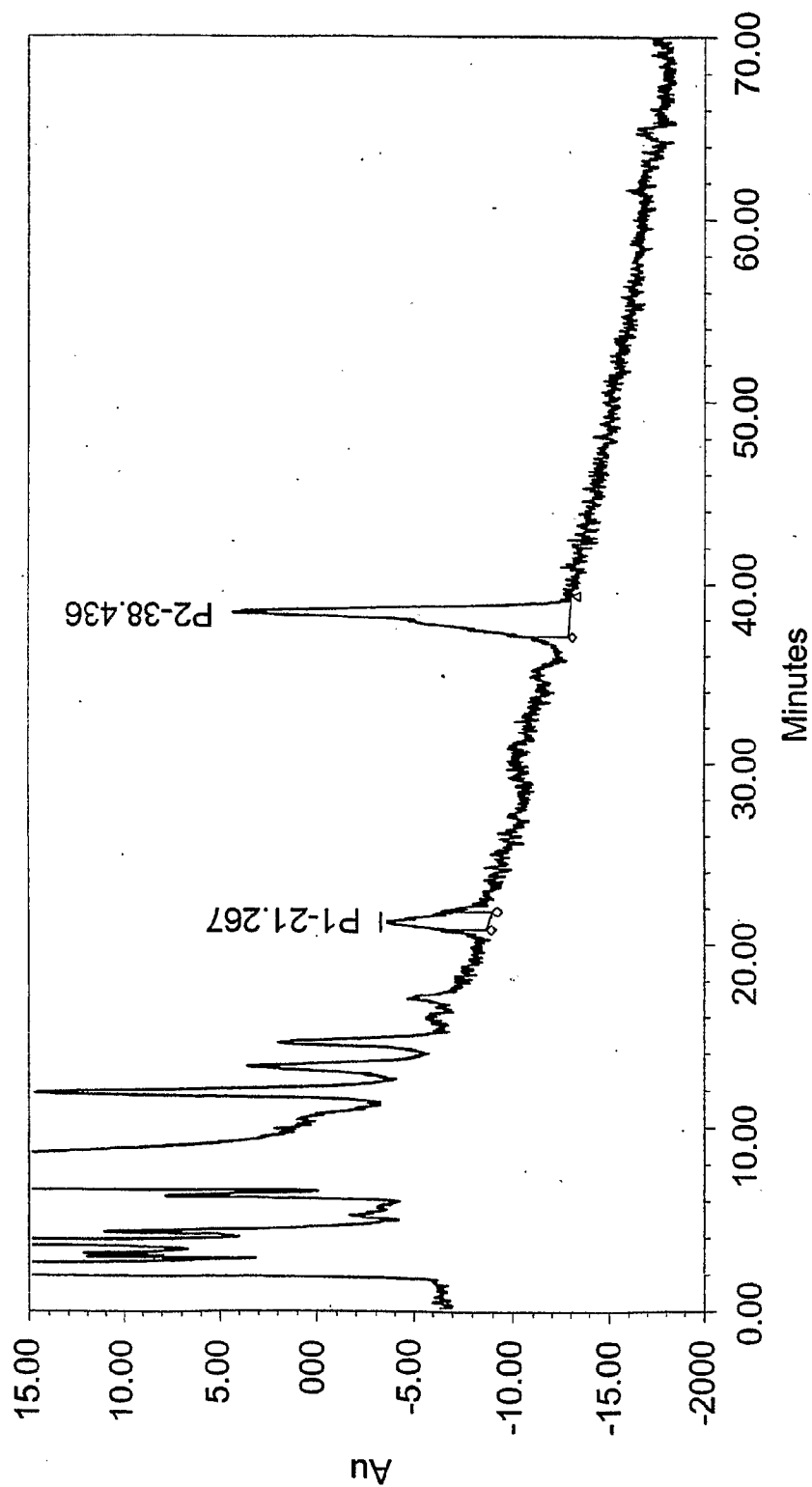


FIG. 104B

369/498

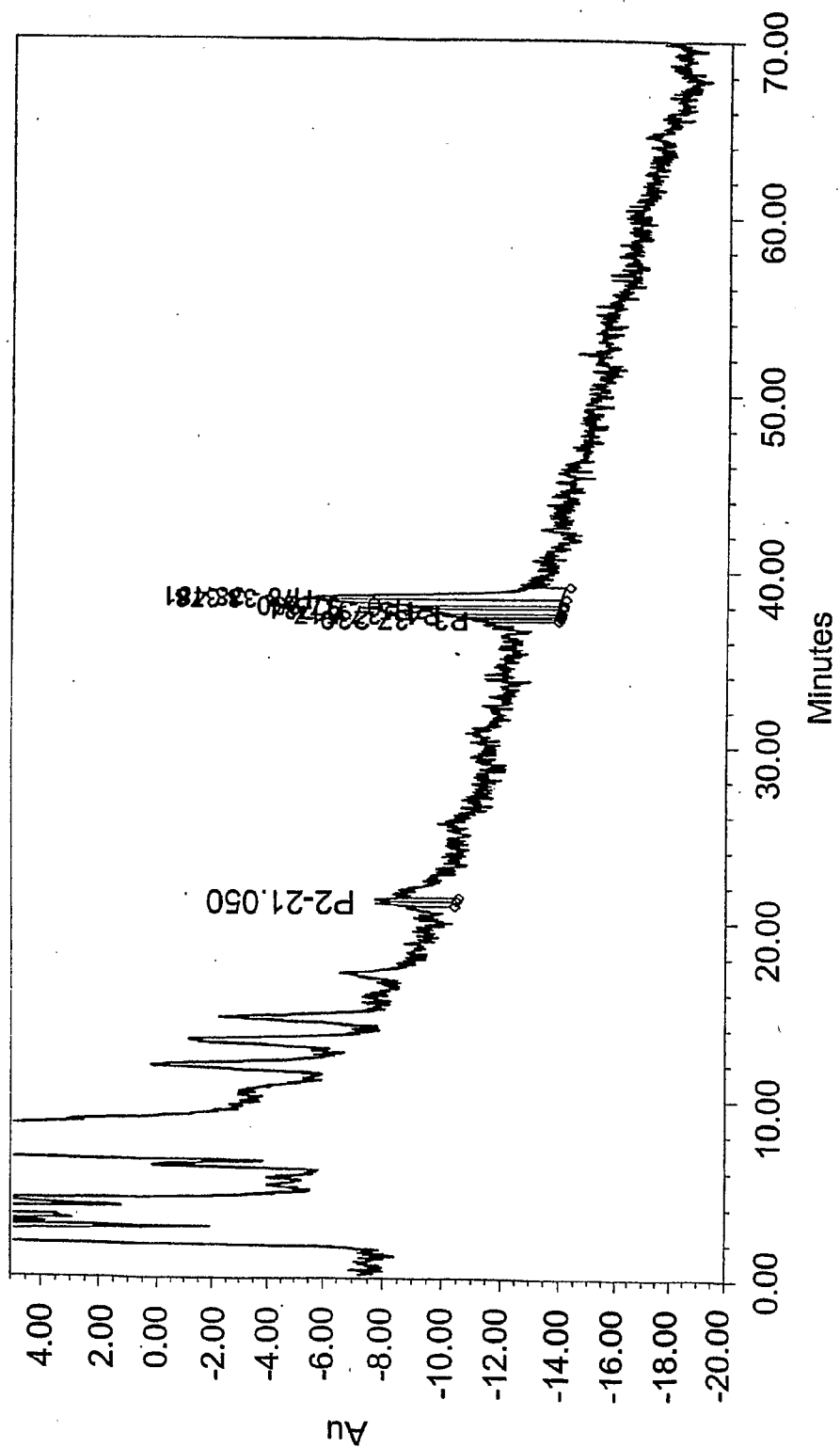


FIG. 104C

370/498

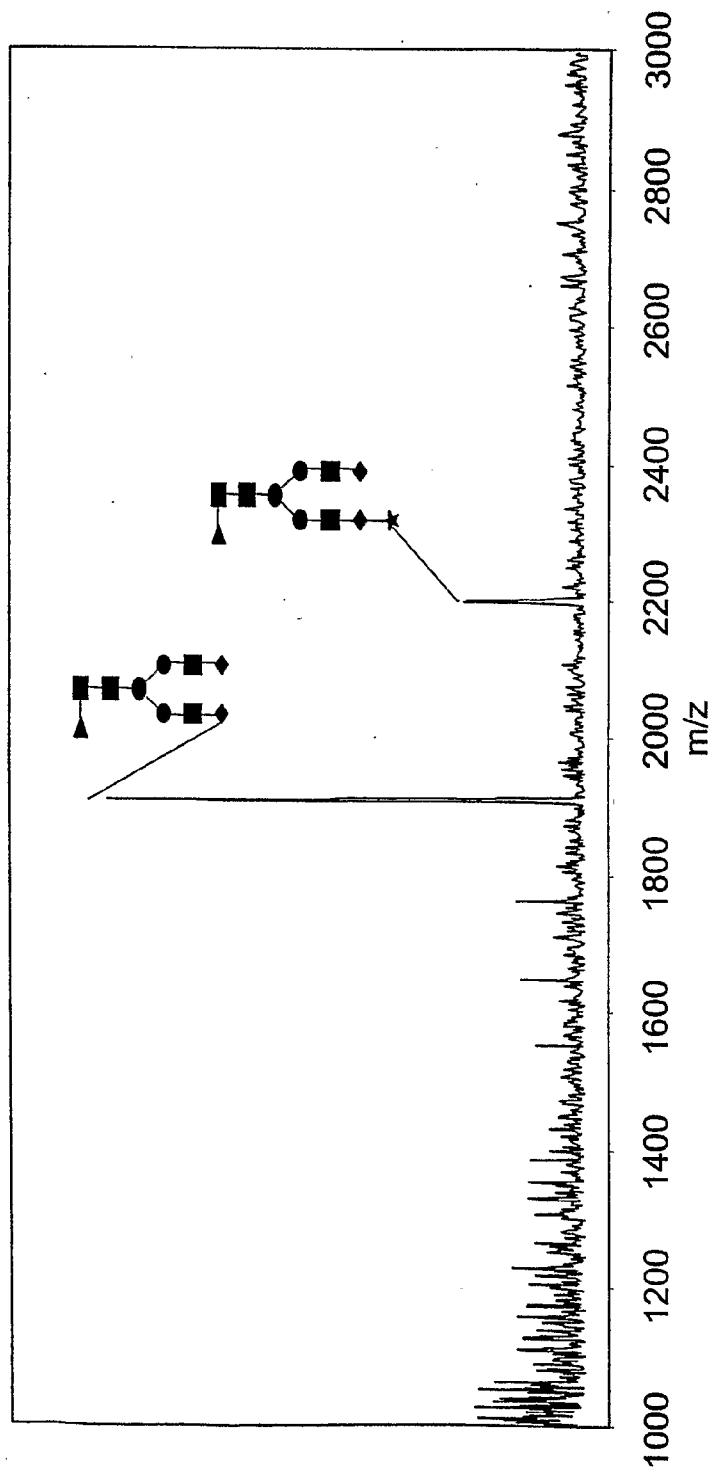


FIG. 105A

371/498

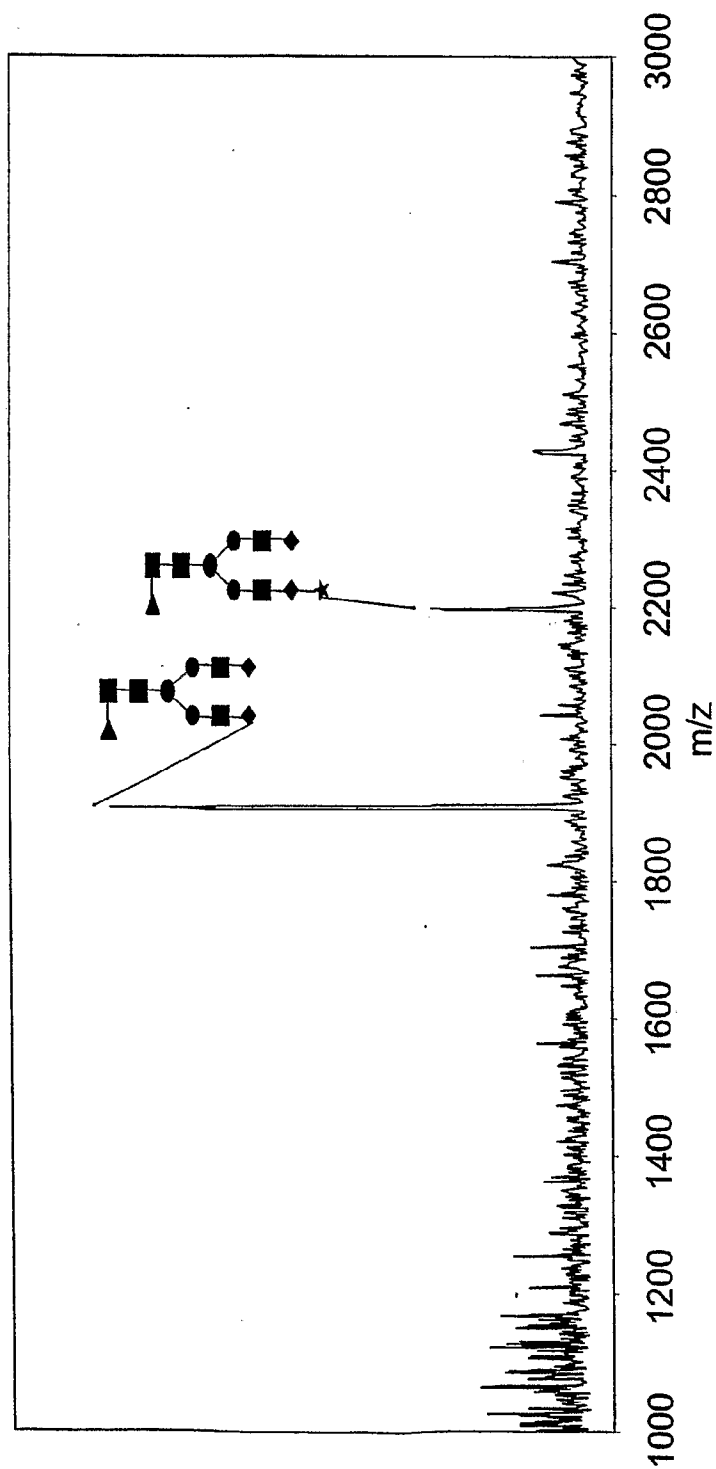


FIG. 105B

372/498

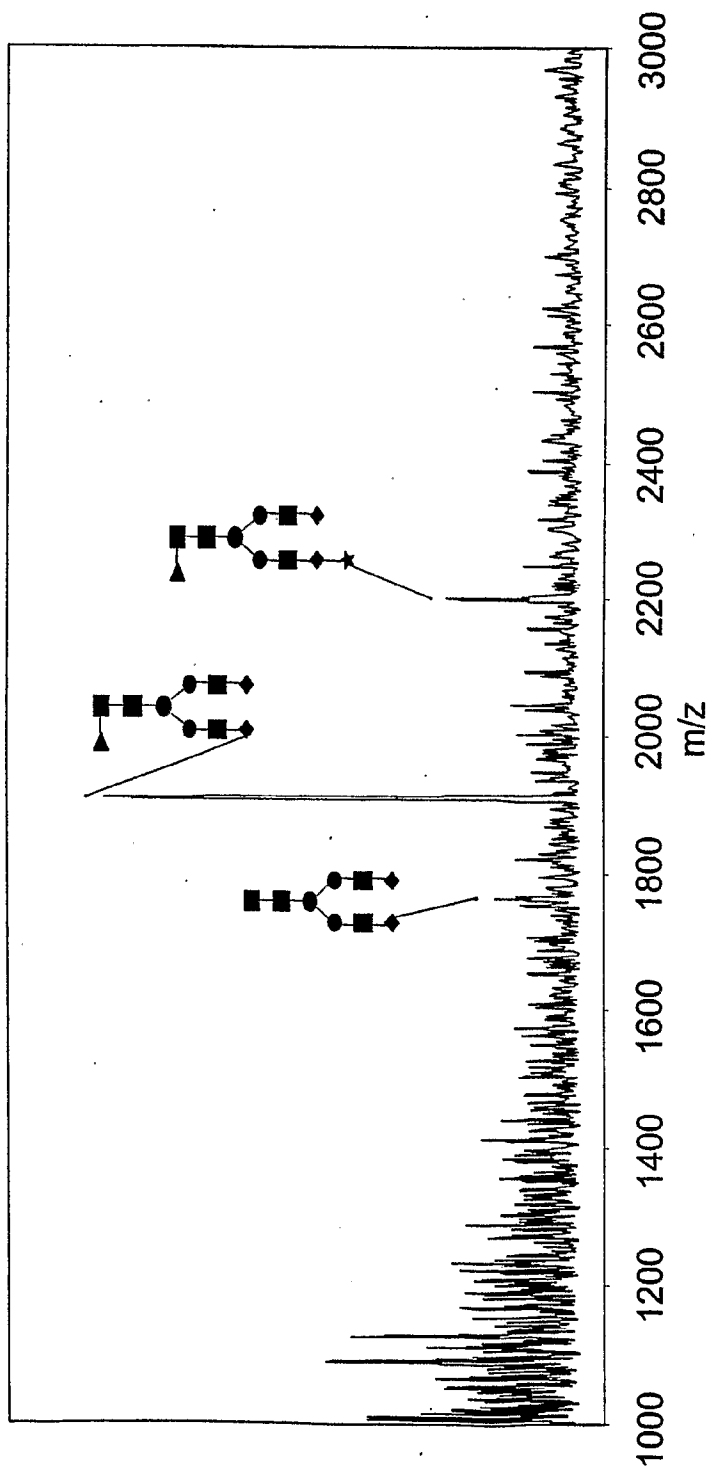


FIG. 105C

373/498

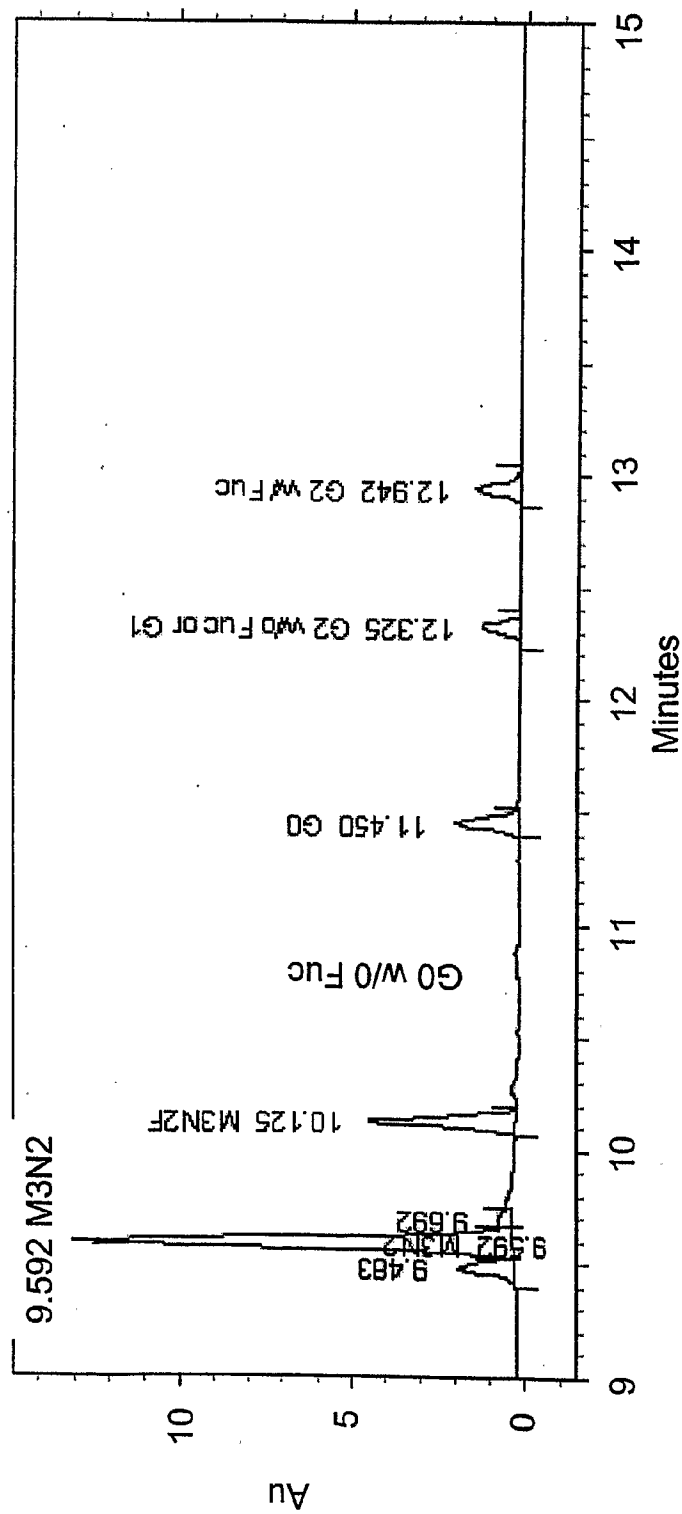


FIG. 106A

374/498

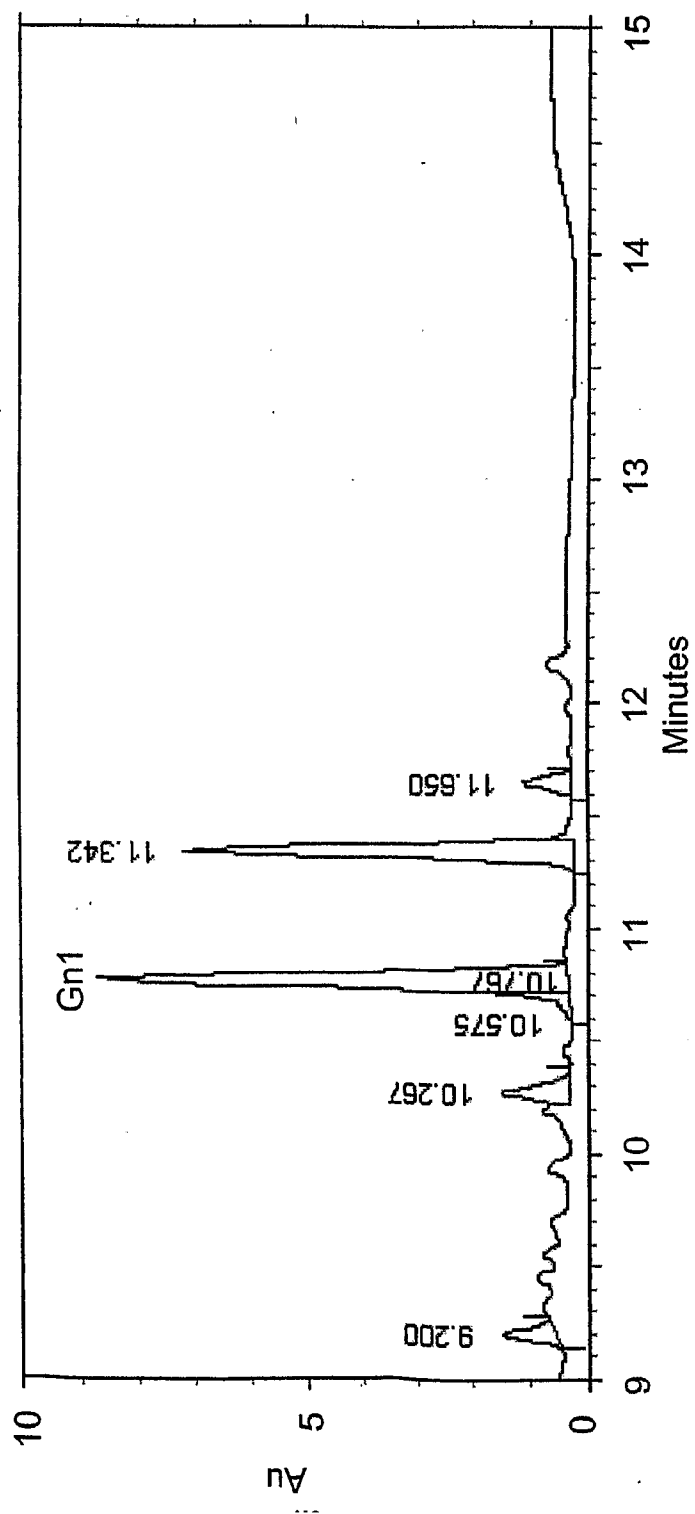


FIG. 106B

375/498

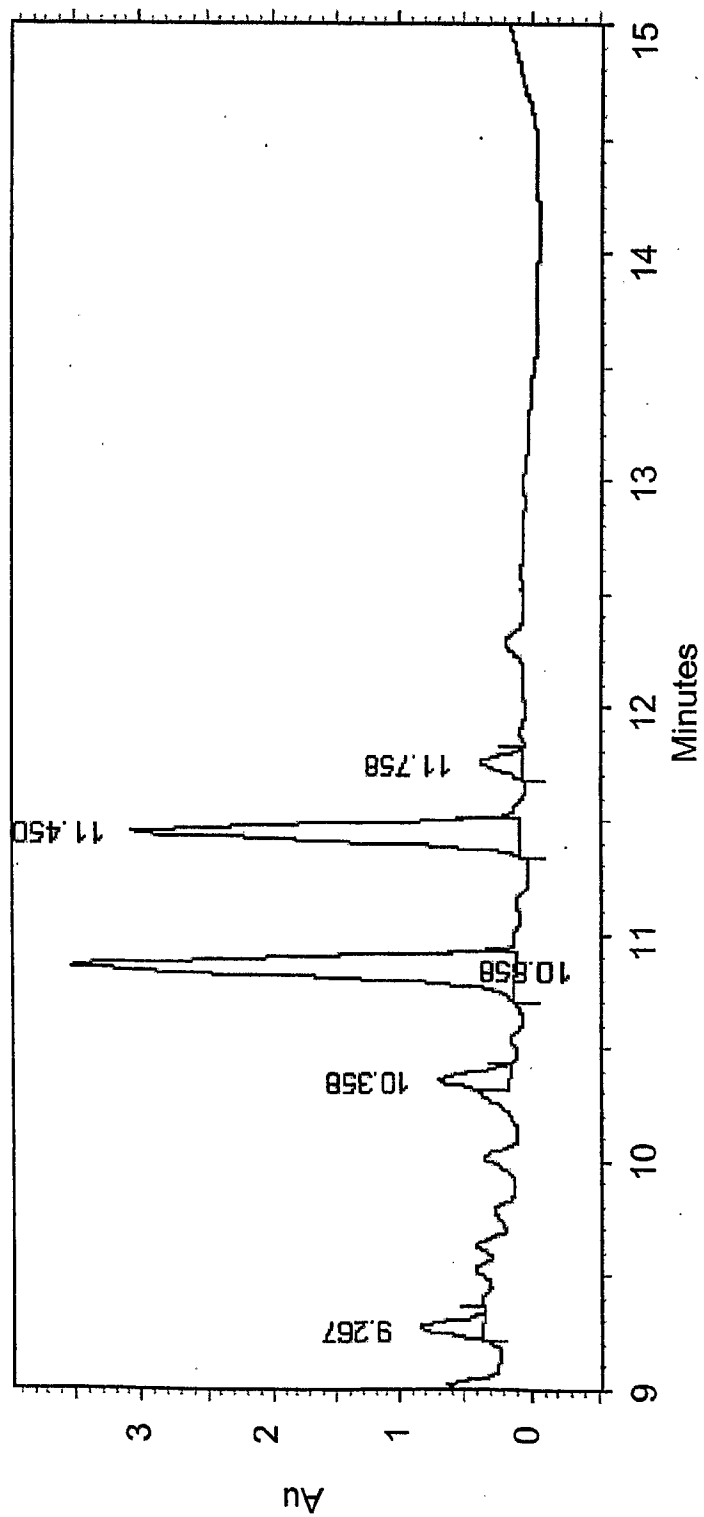


FIG. 106C

376/498

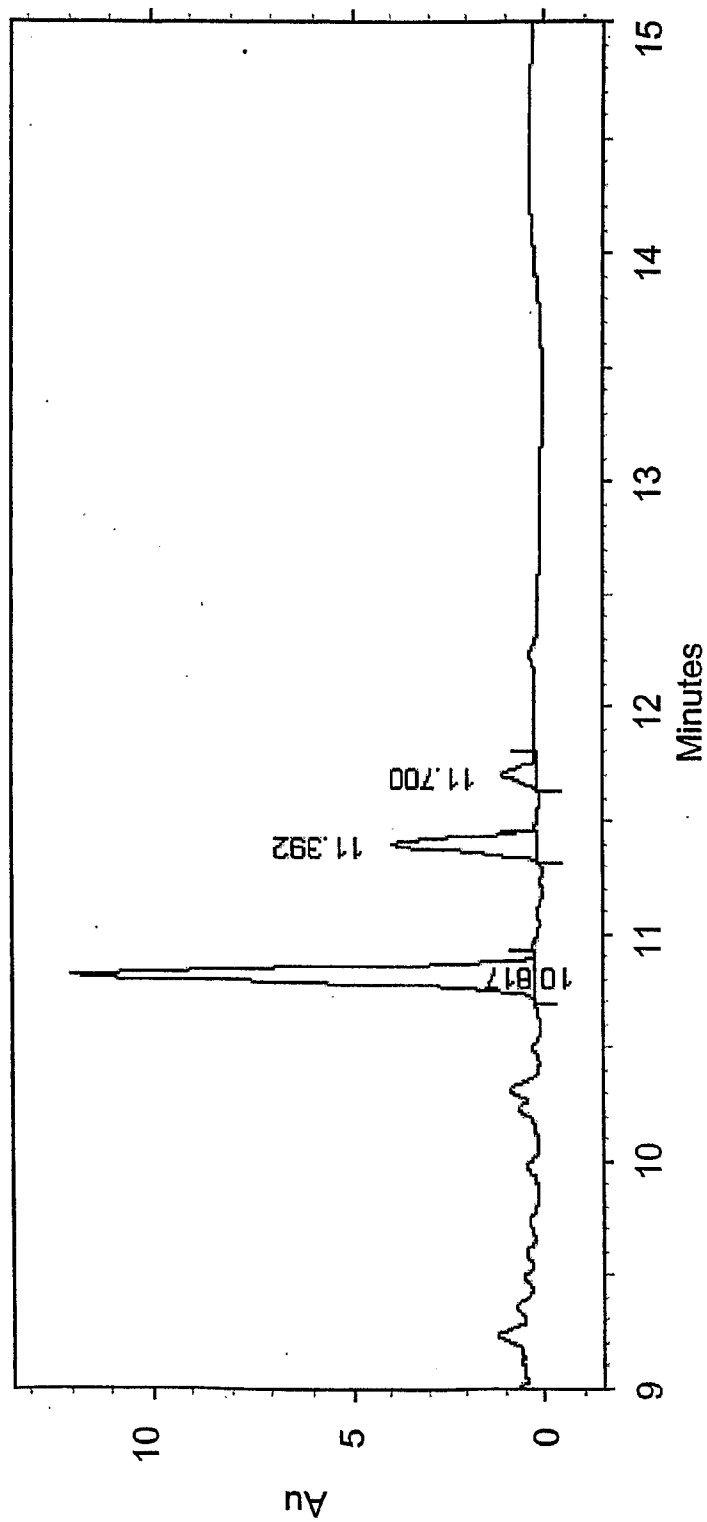


FIG. 106D

377/498

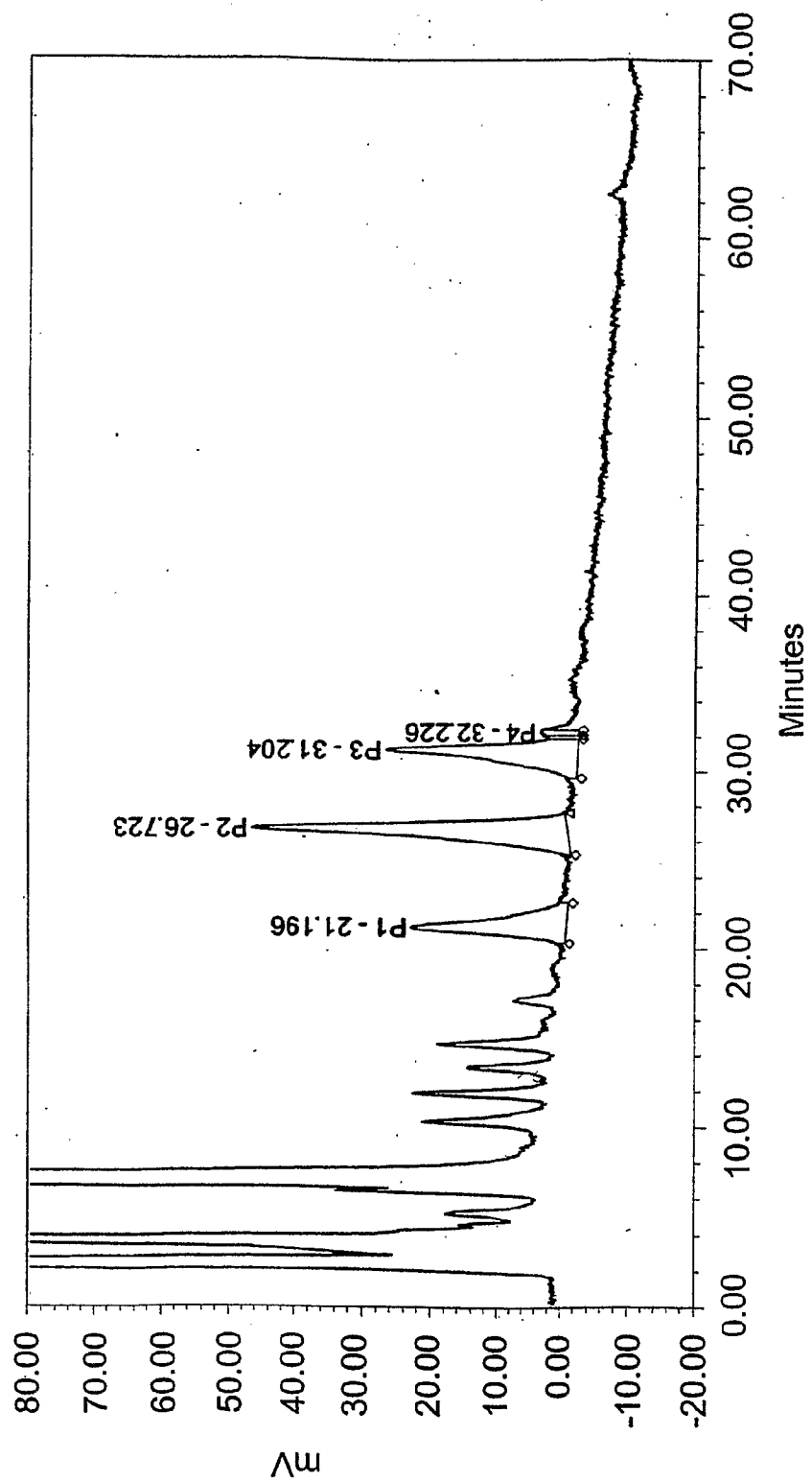


FIG. 107A

378/498

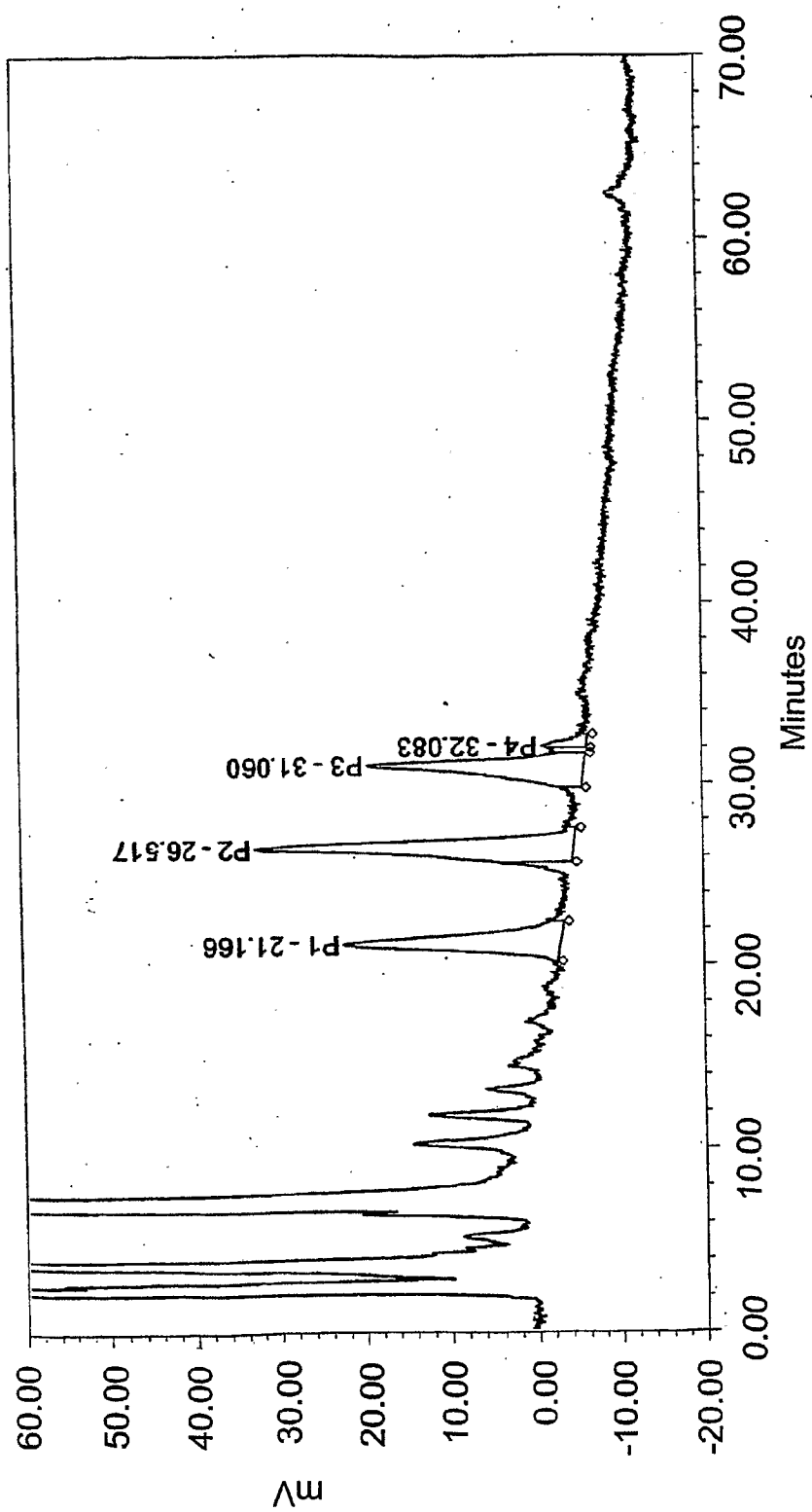


FIG. 107B

379/498

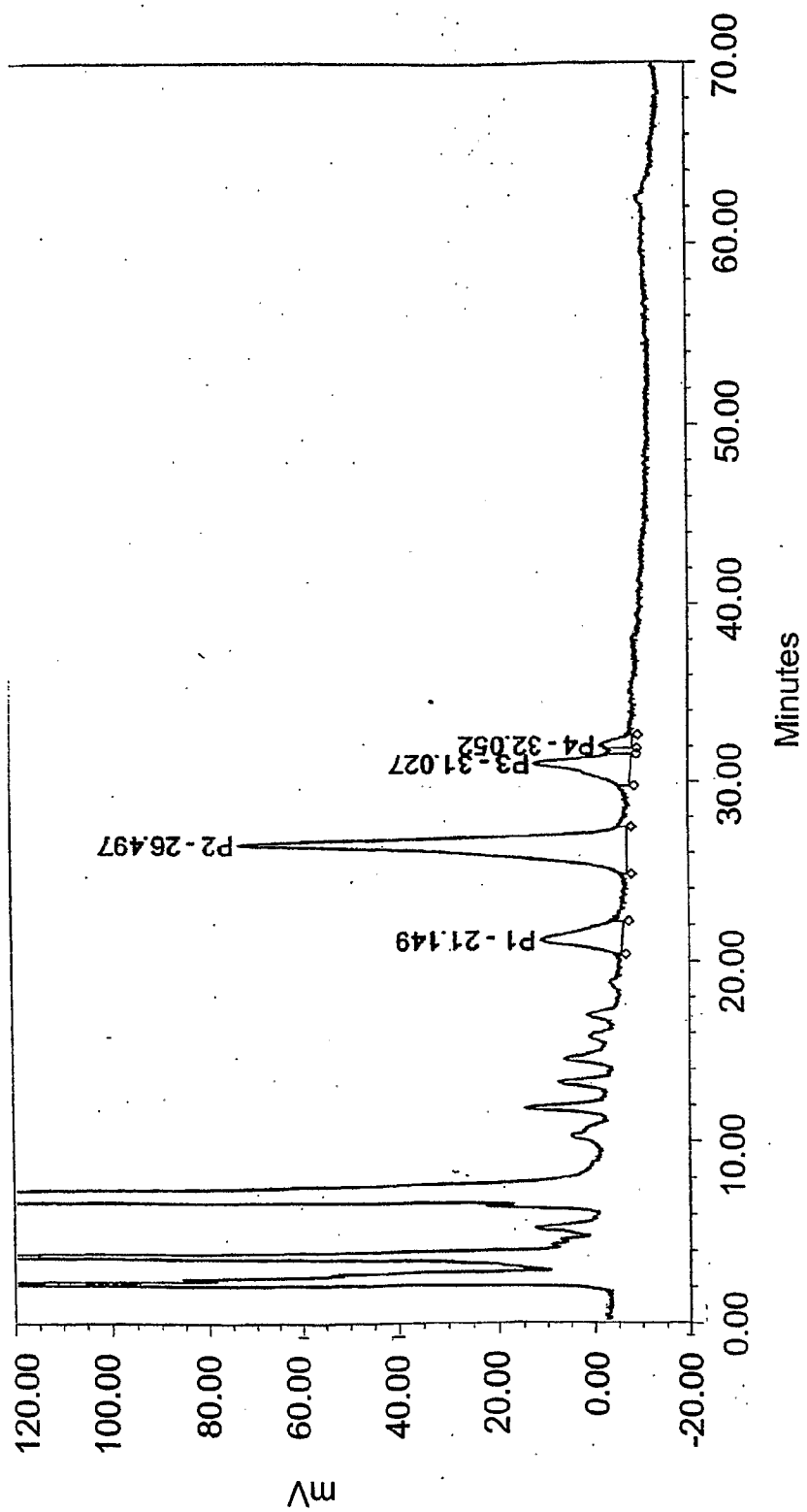


FIG. 107C

380/498

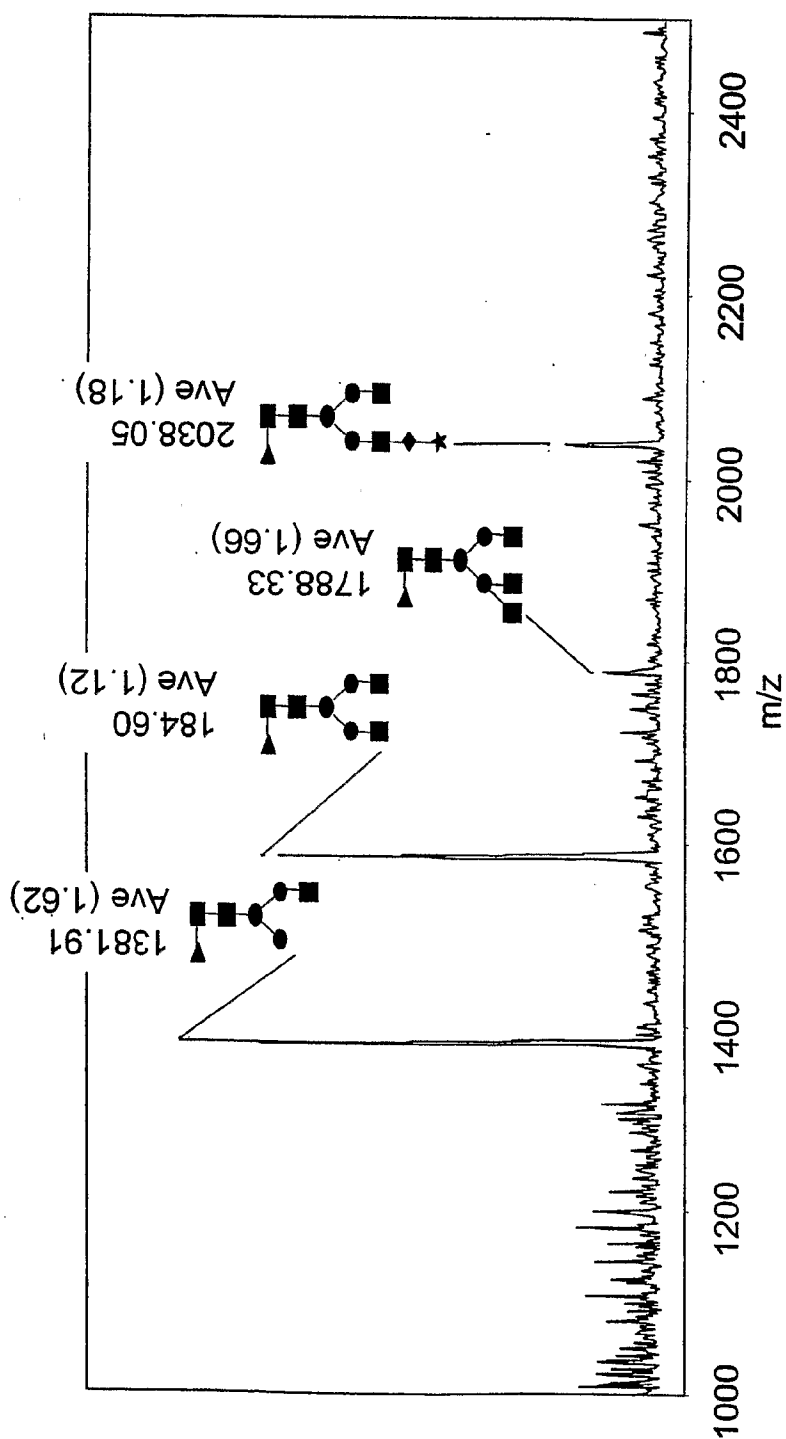


FIG. 108A

381/498

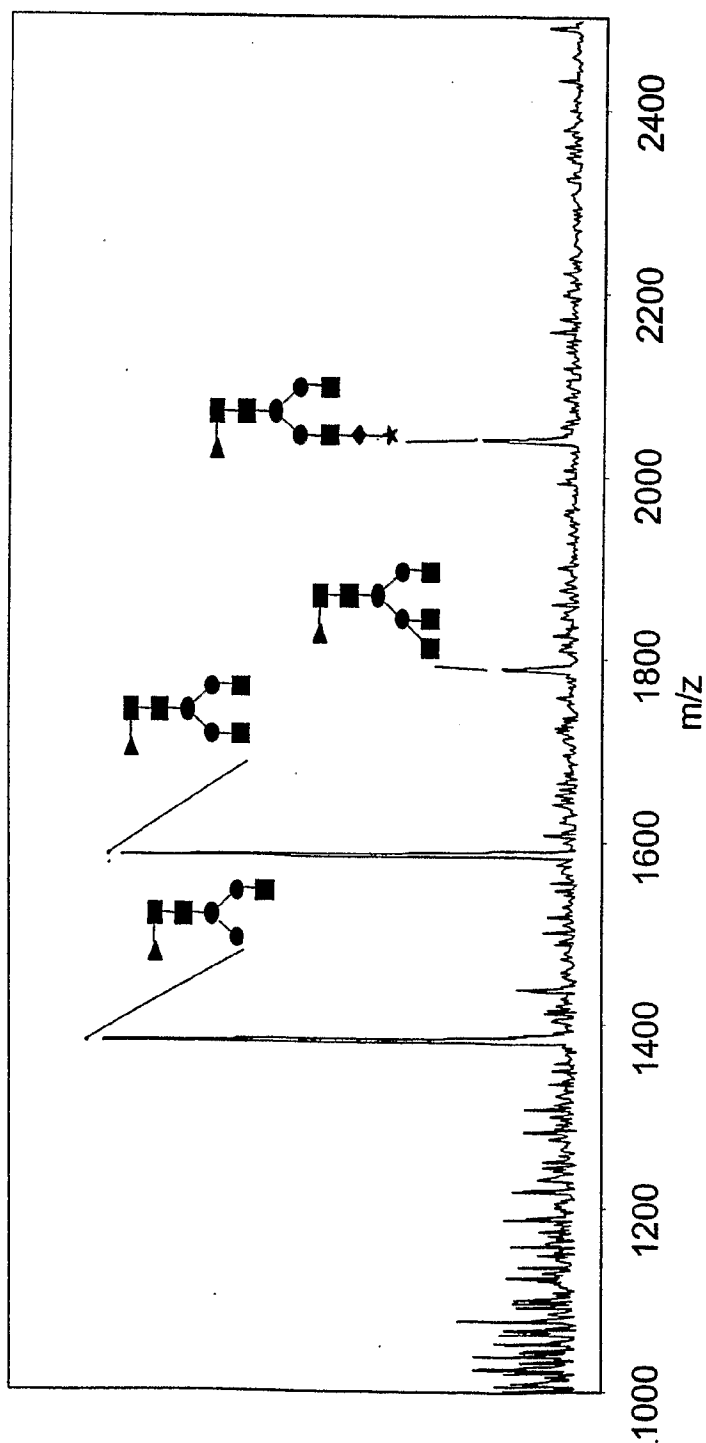


FIG. 108B

382/498

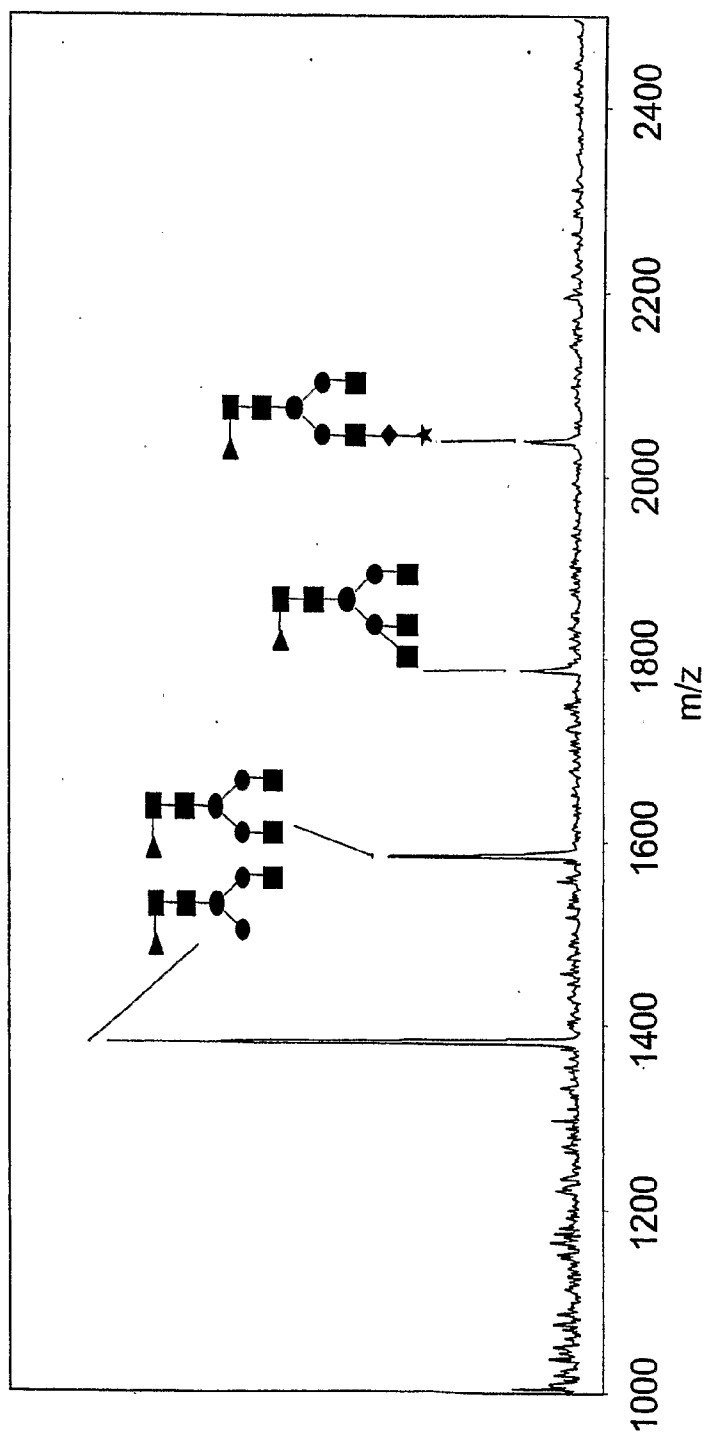


FIG. 108C

383/498

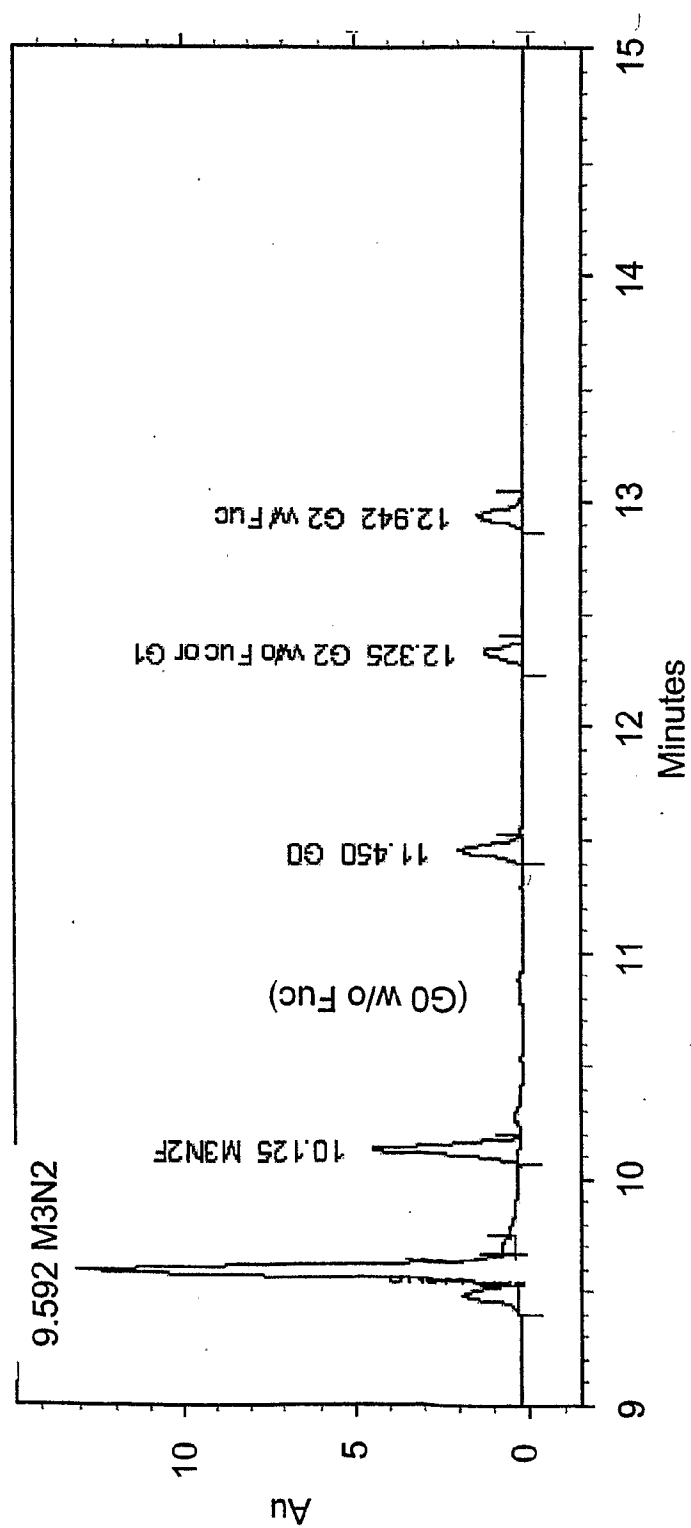


FIG. 109A

384/498

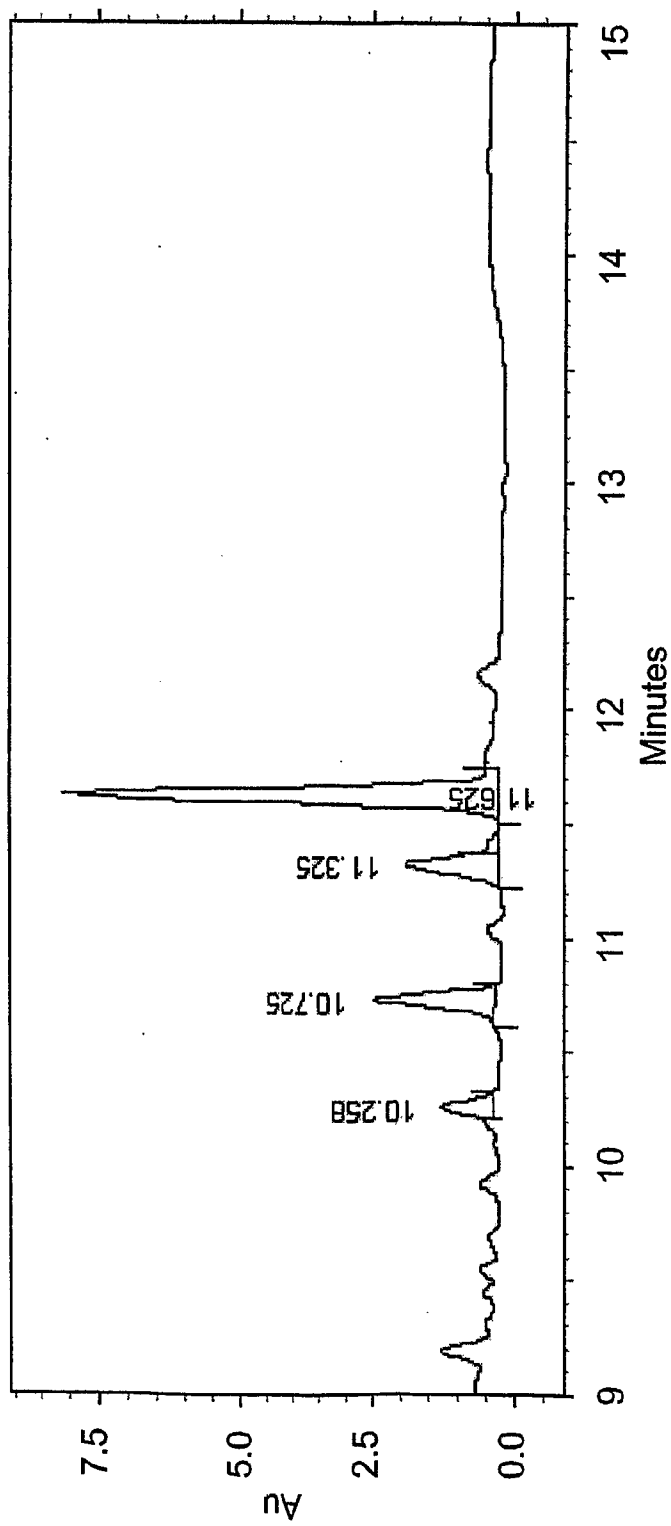


FIG. 109B

385/498

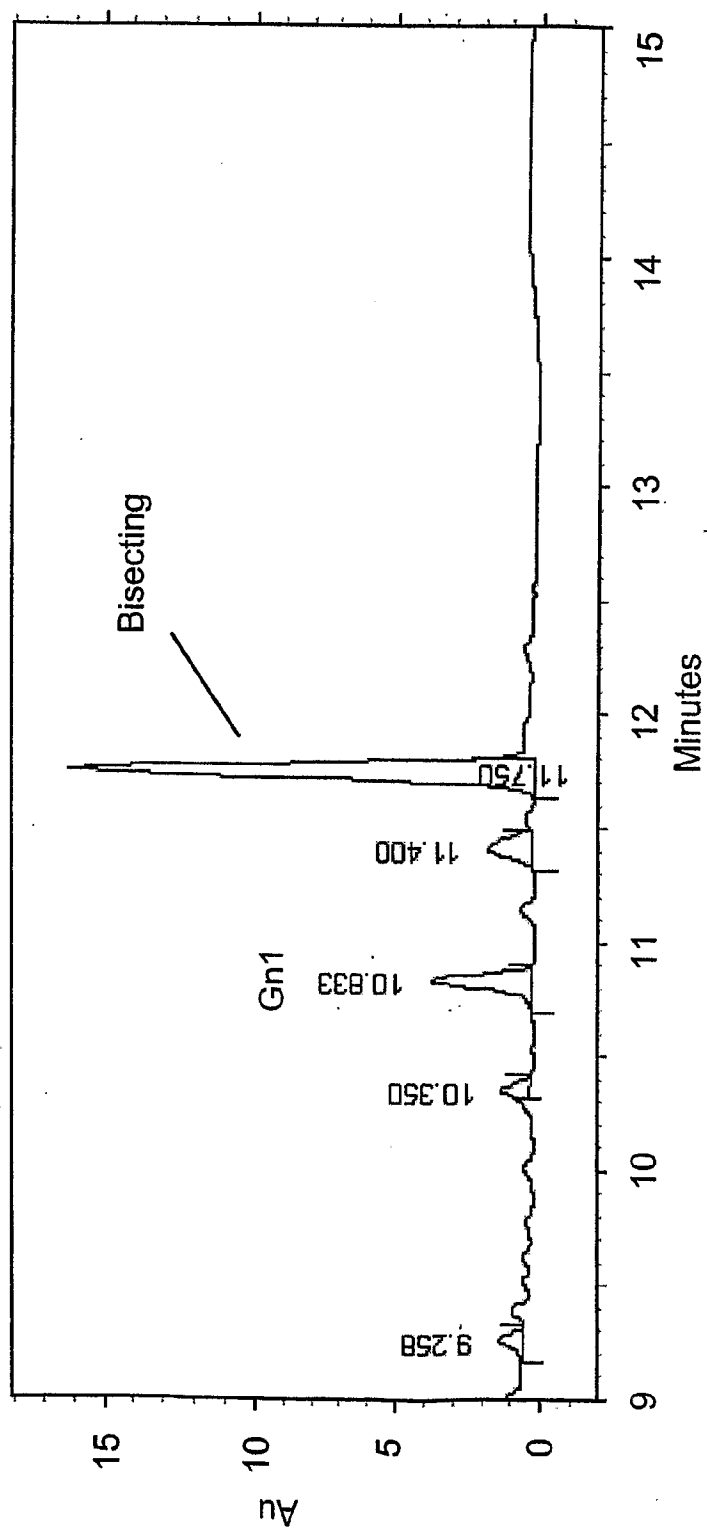


FIG. 109C

386/498

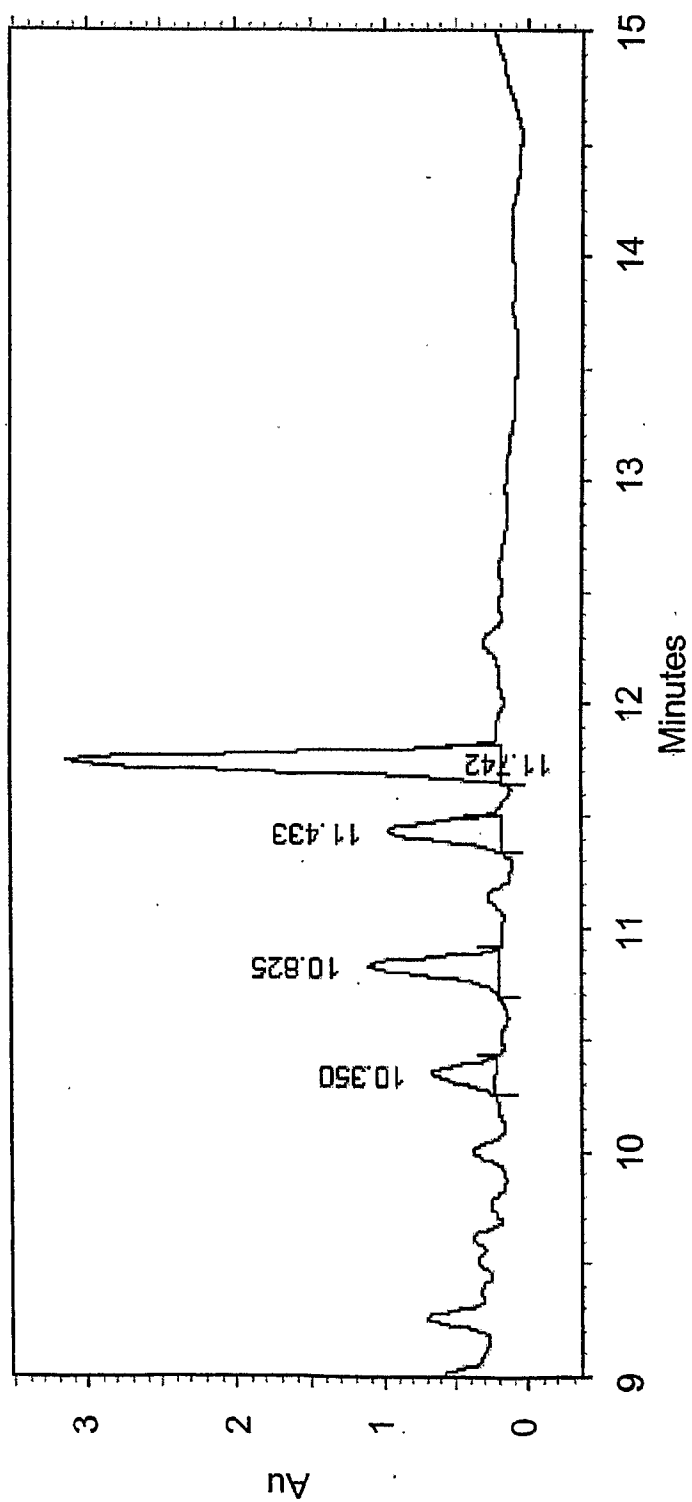


FIG. 109D

387/498

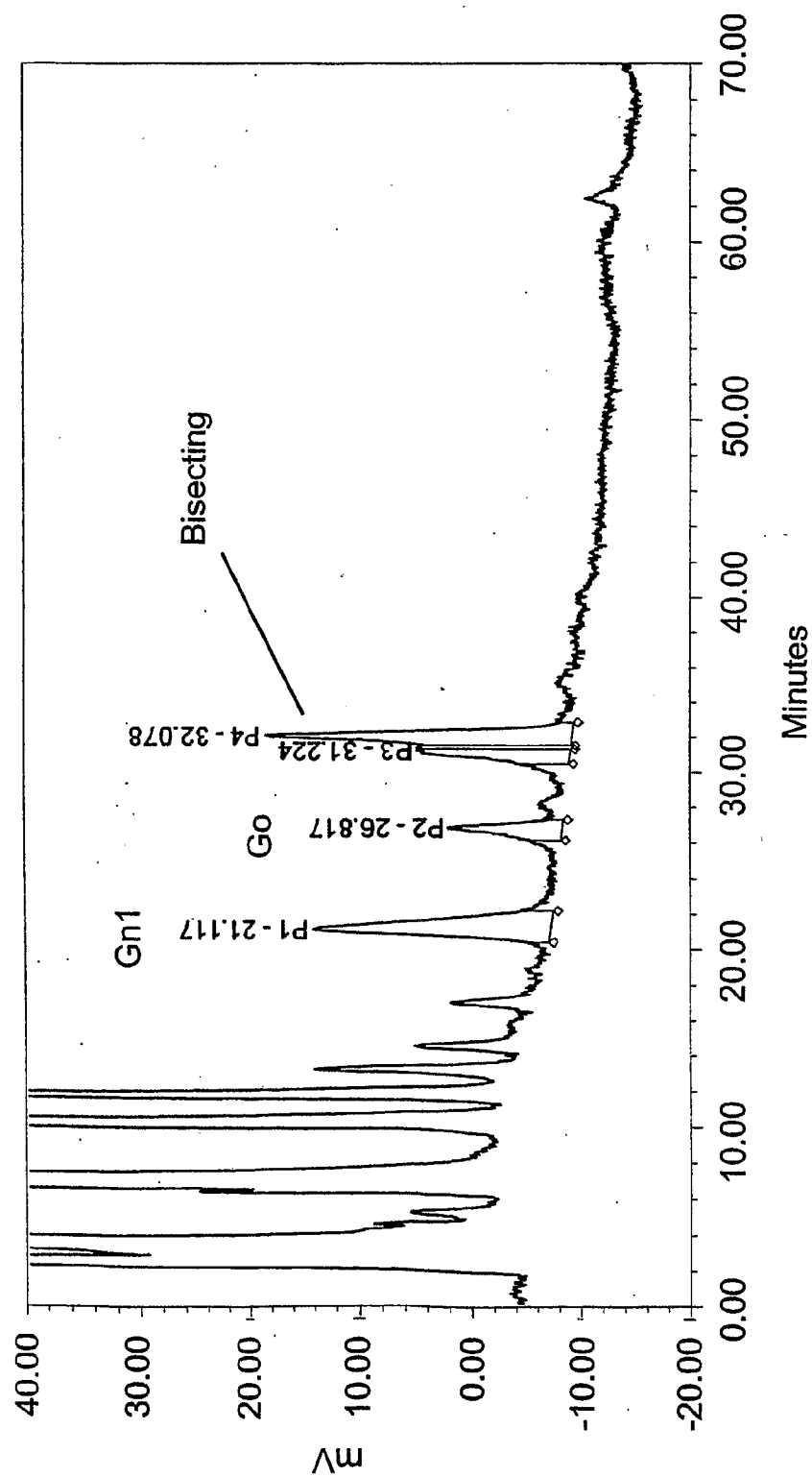


FIG. 110A

388/498

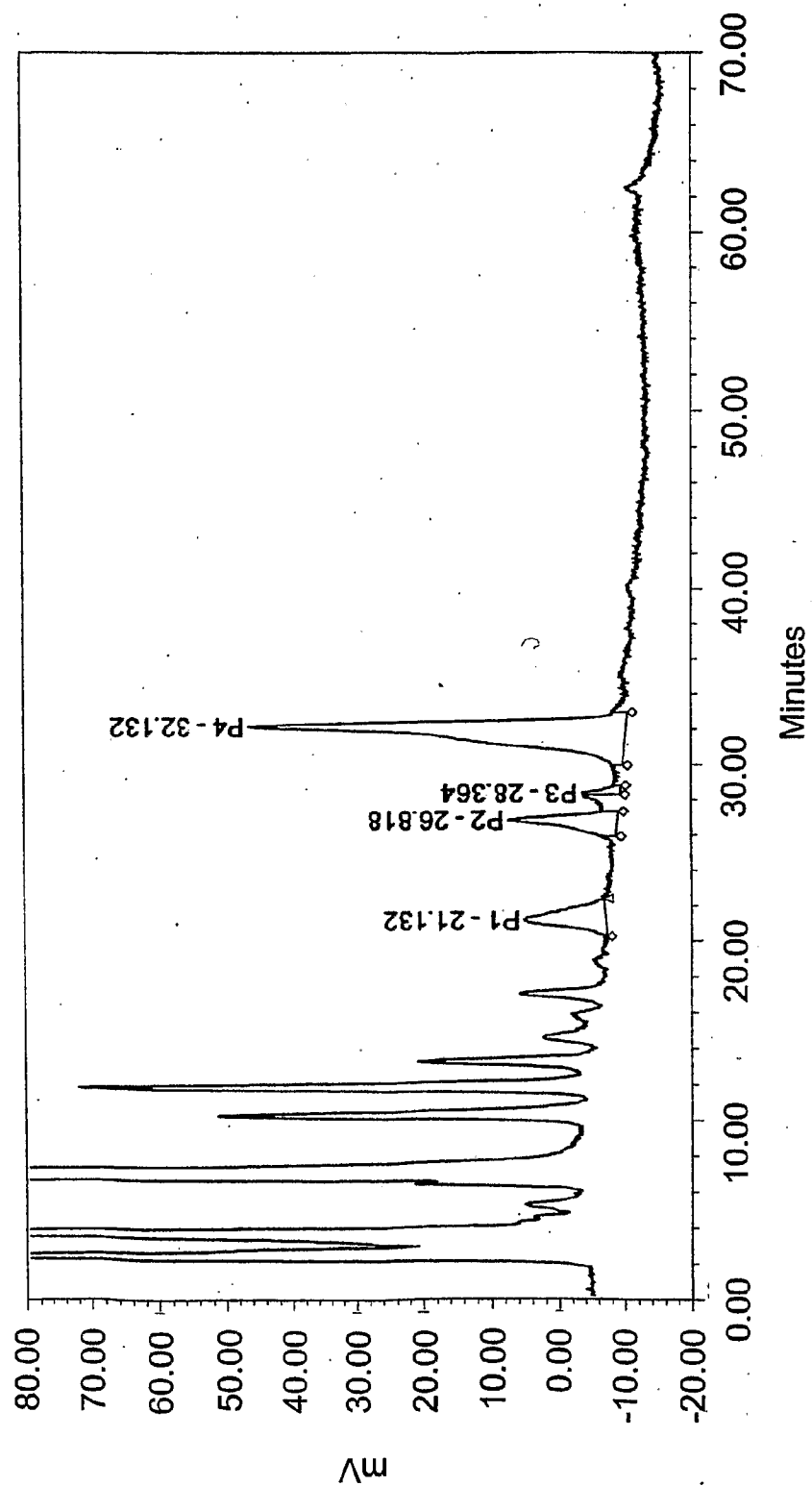


FIG. 110B

389/498

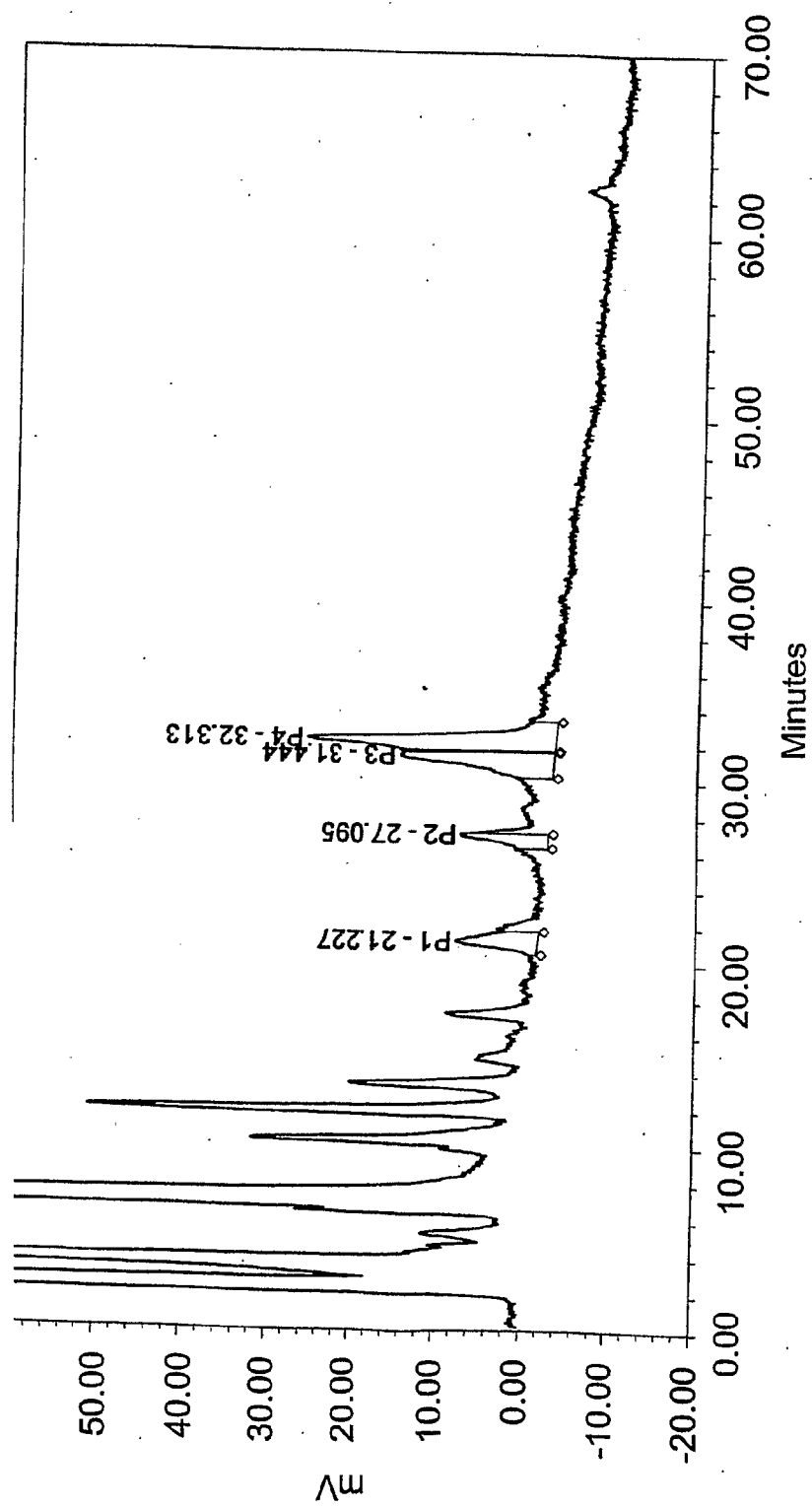


FIG. 110C

390/498

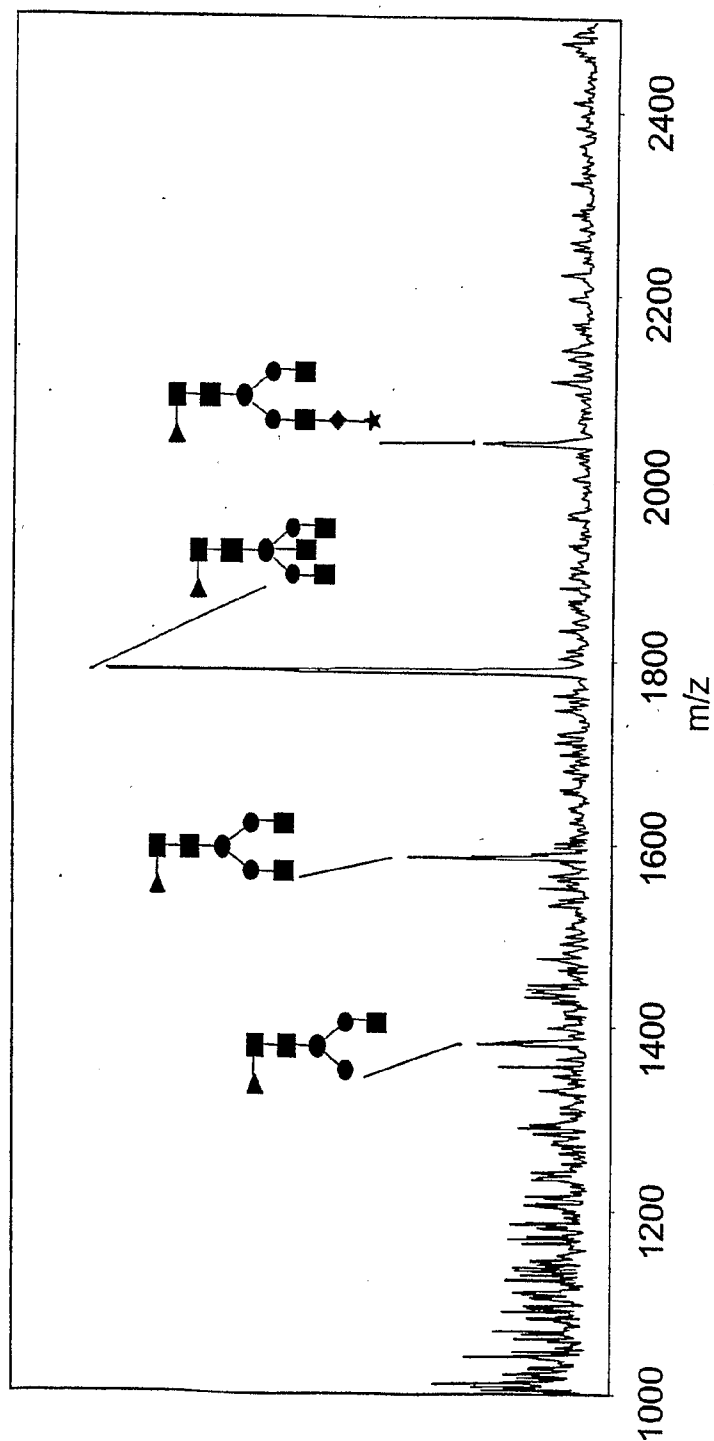


FIG. 111A

391/498

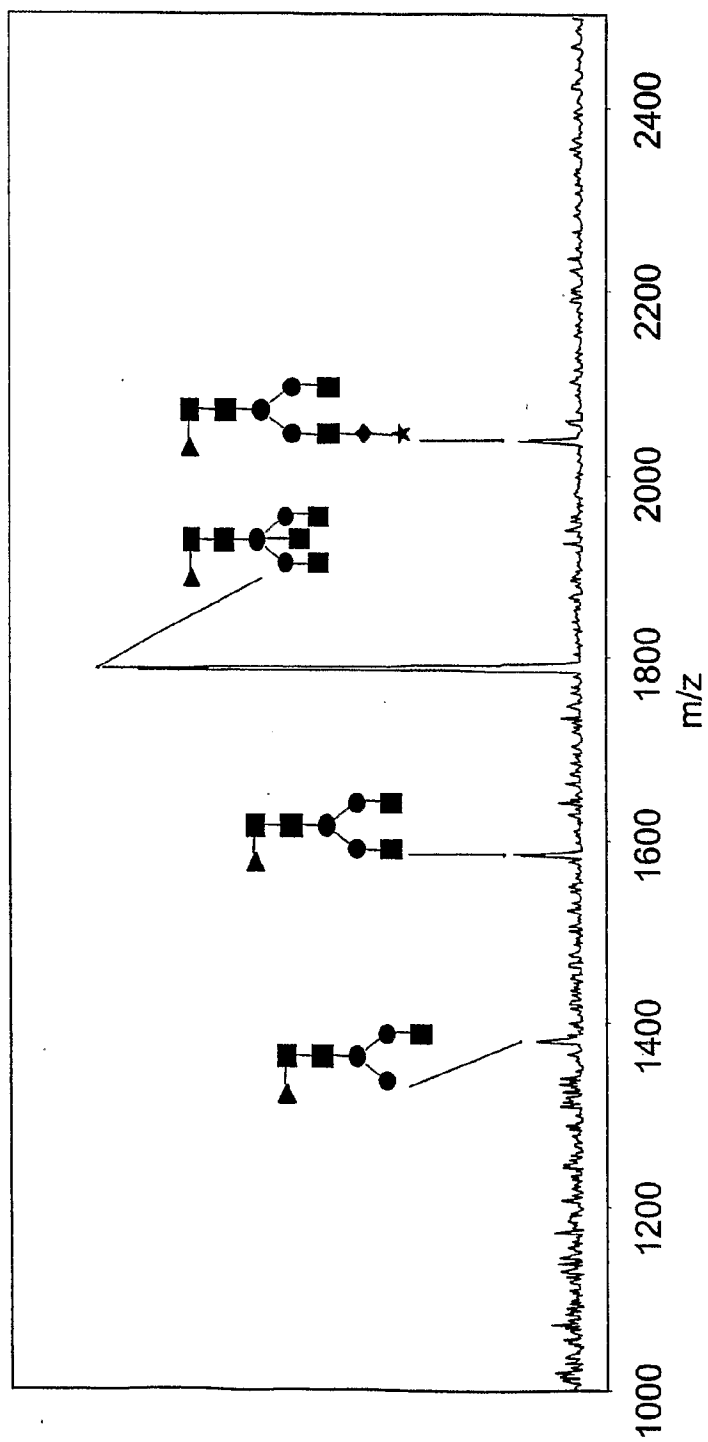


FIG. 111B

392/498

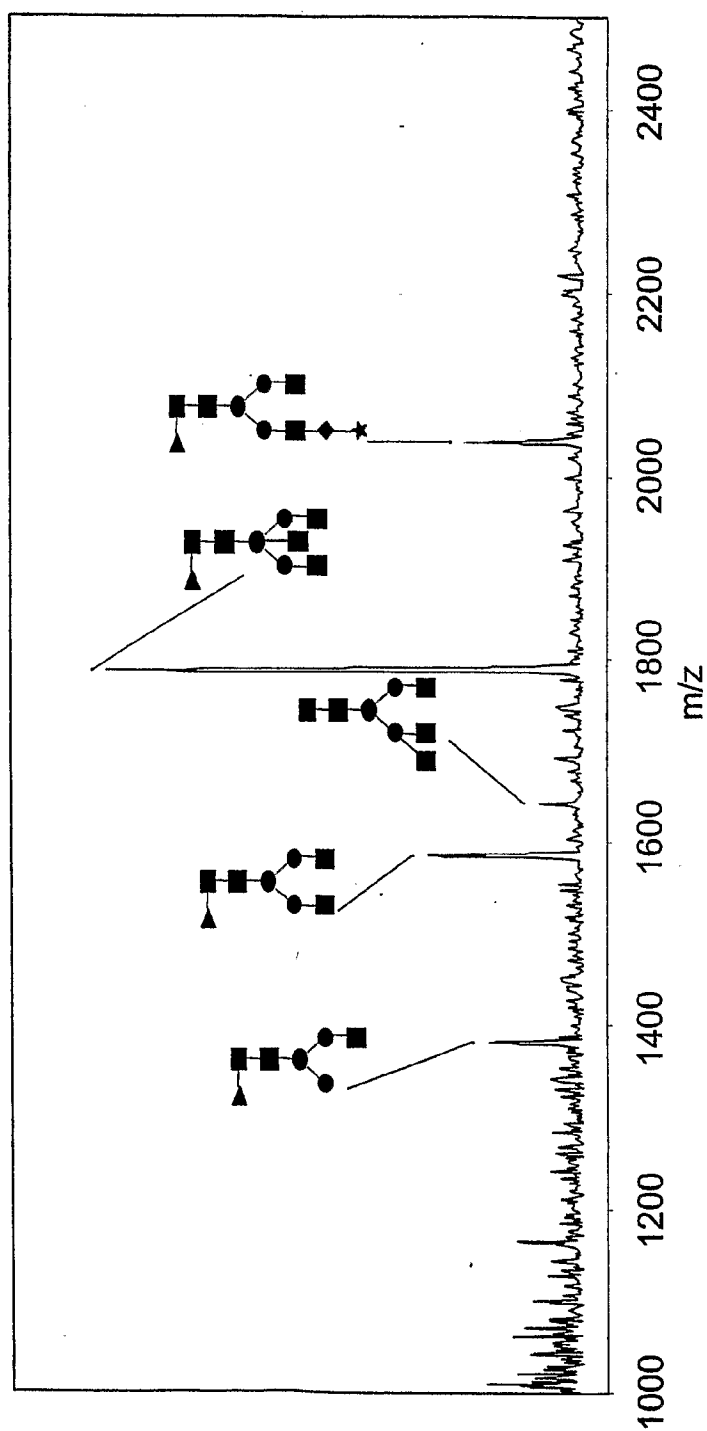


FIG. 111C

393/498

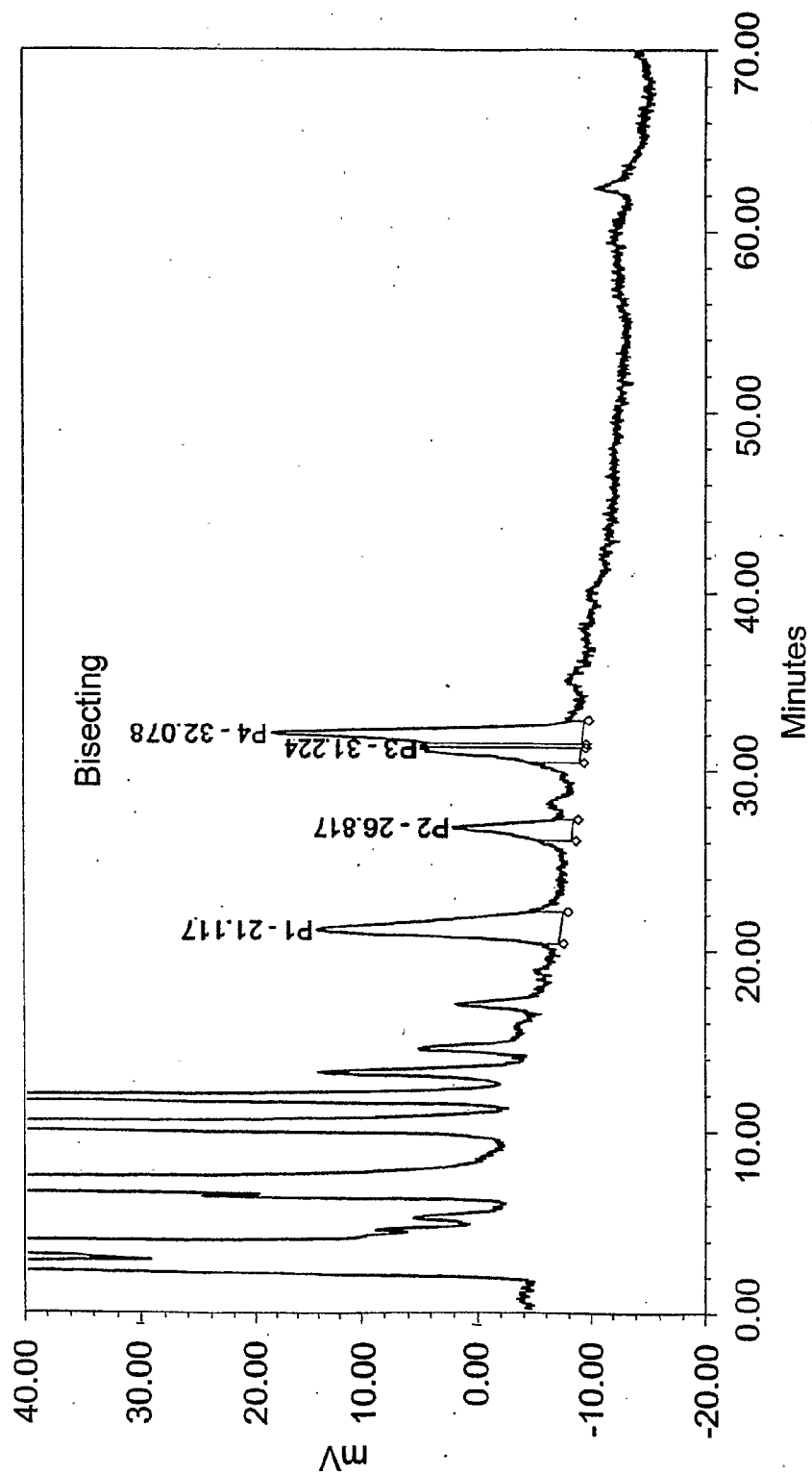


FIG. 112A

394/498

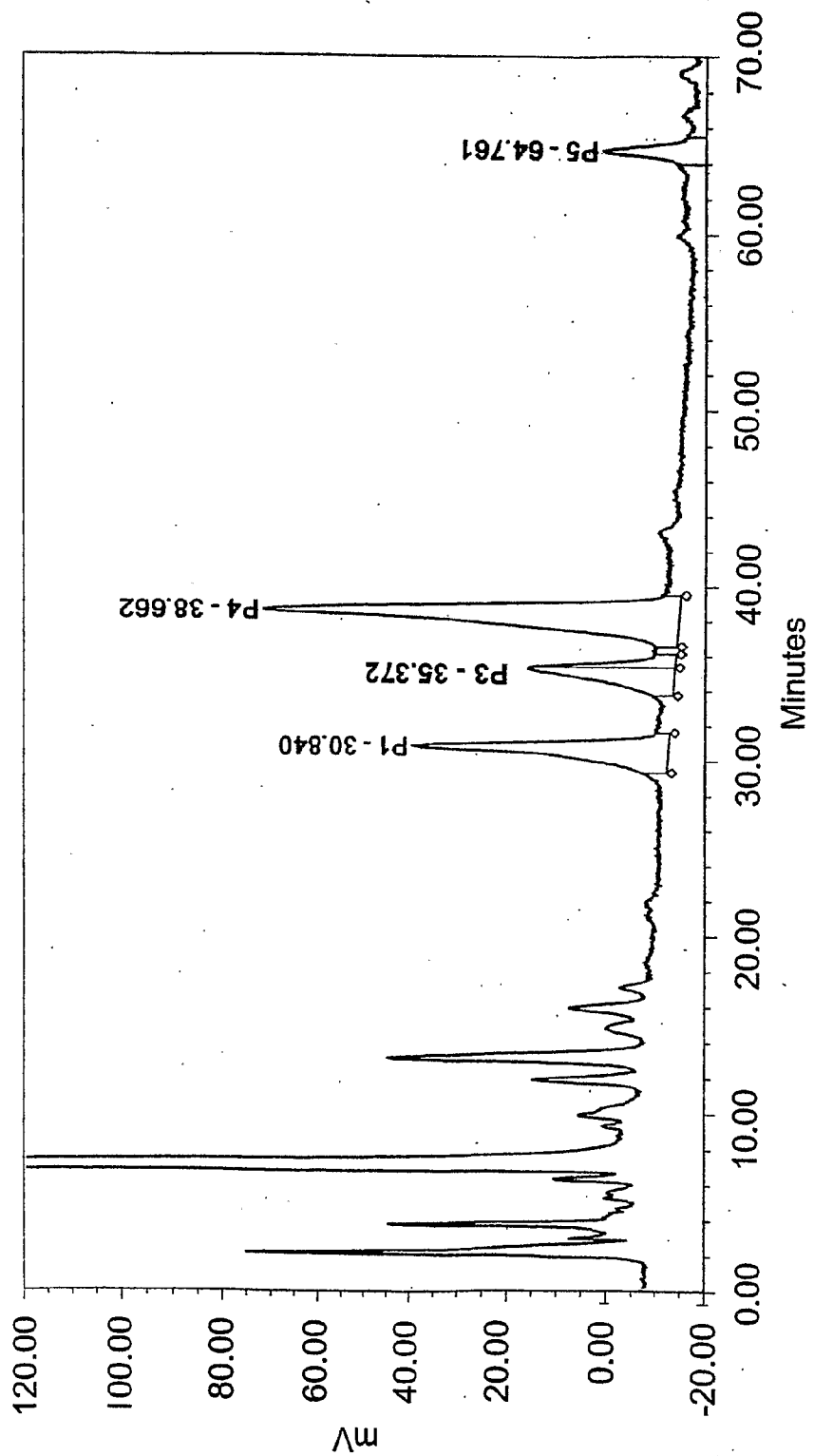


FIG. 112B

395/498

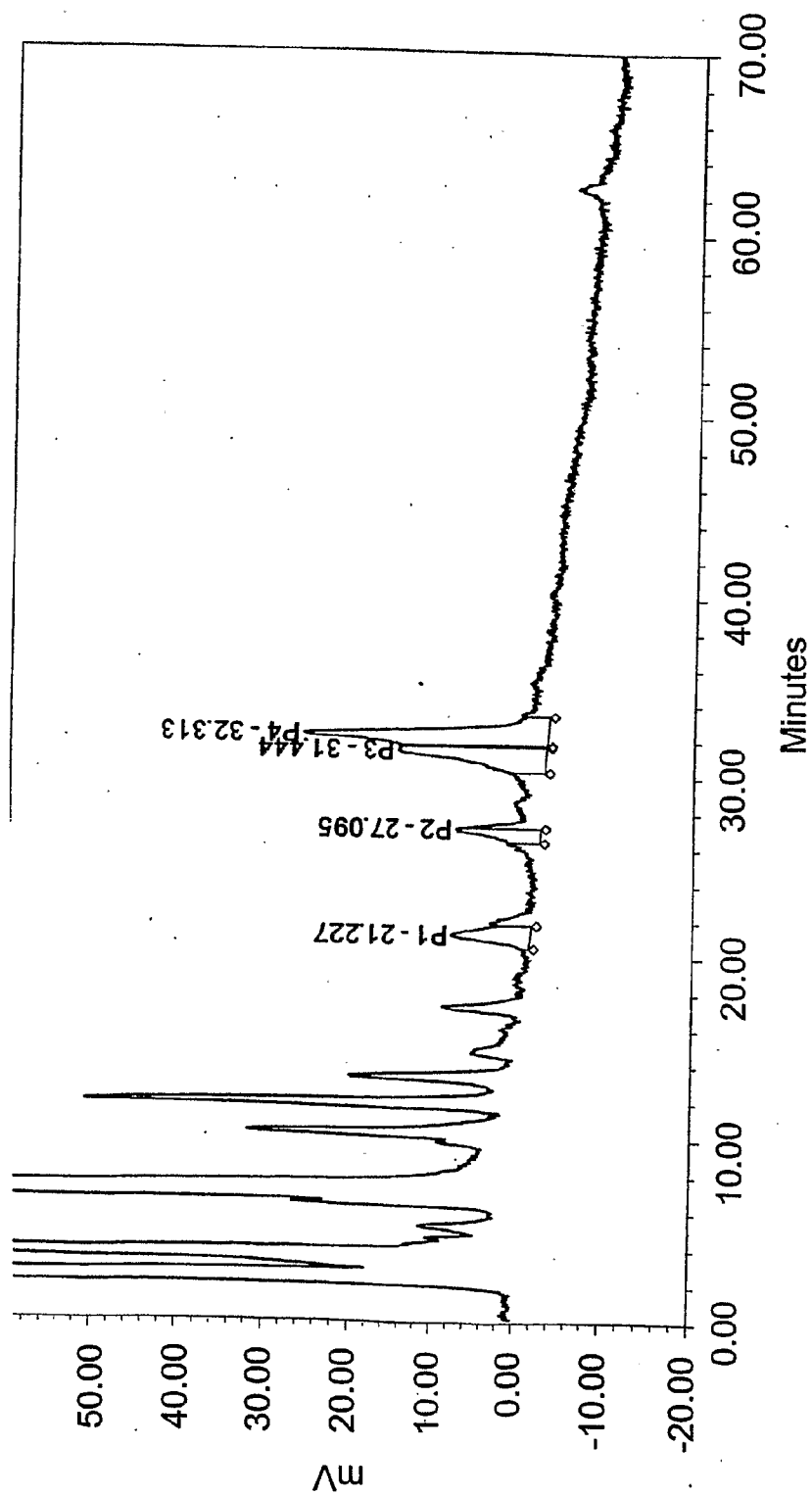


FIG. 112C

396/498

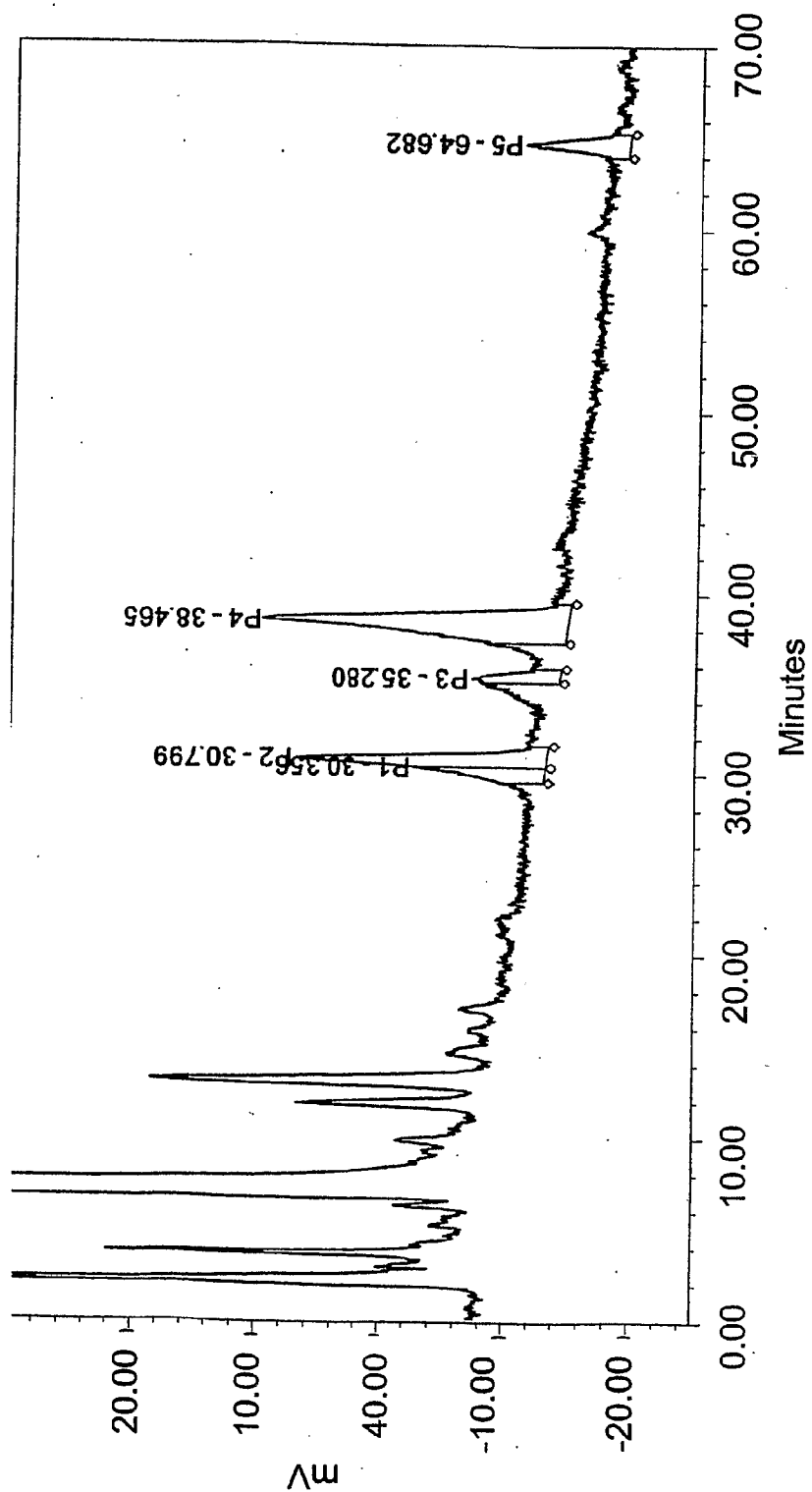


FIG. 112D

397/498

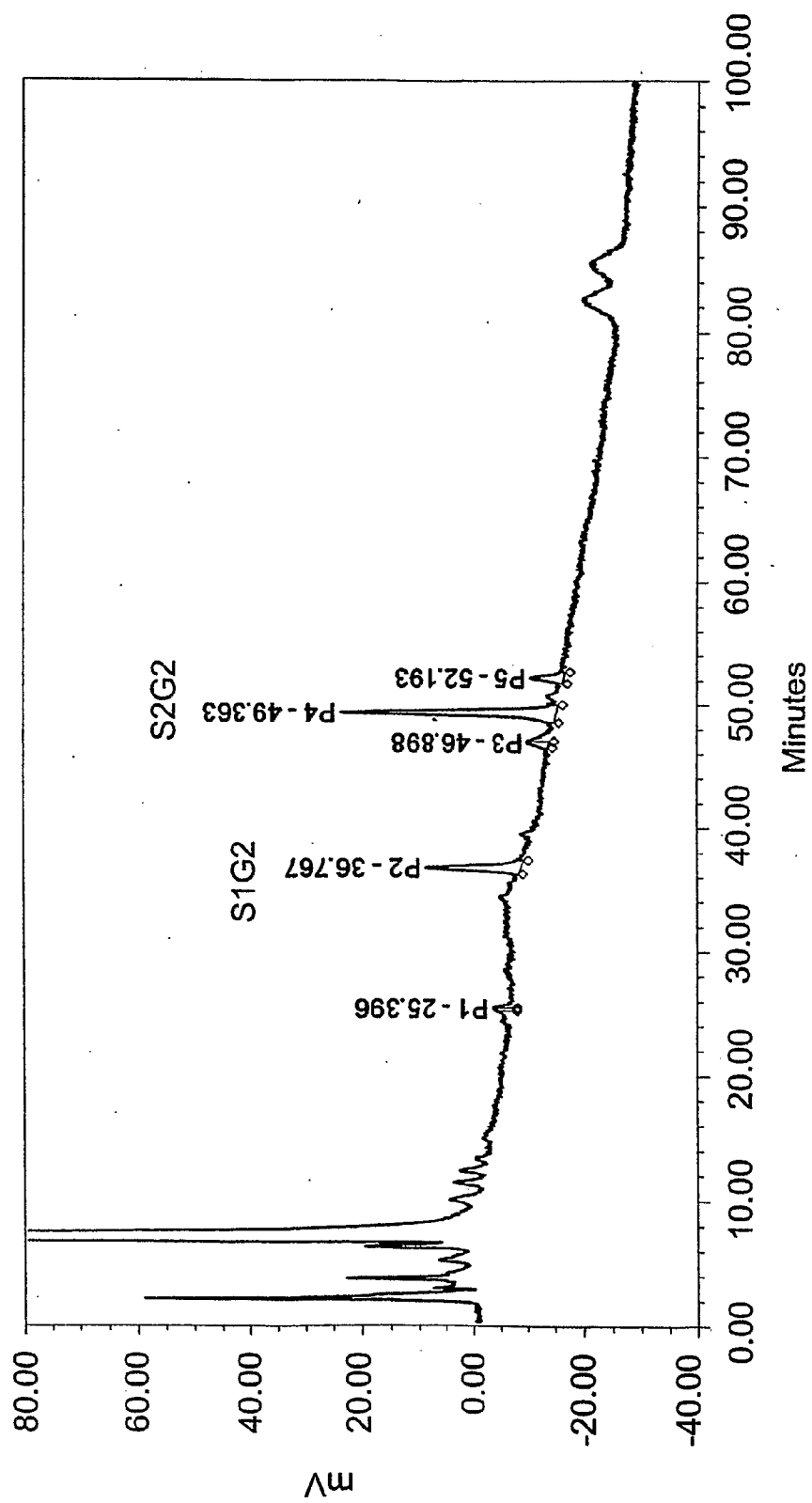


FIG. 113A

398/498

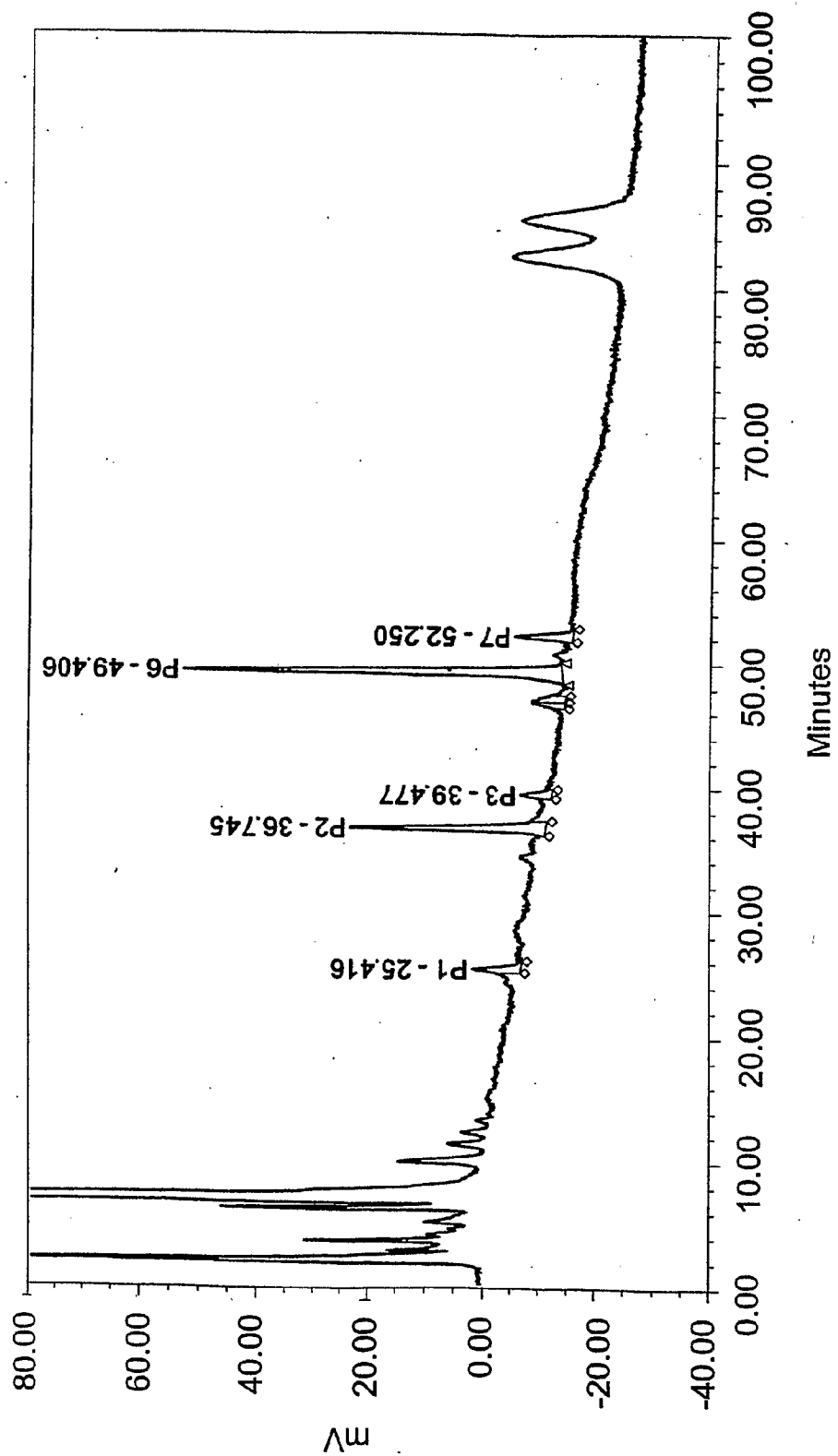
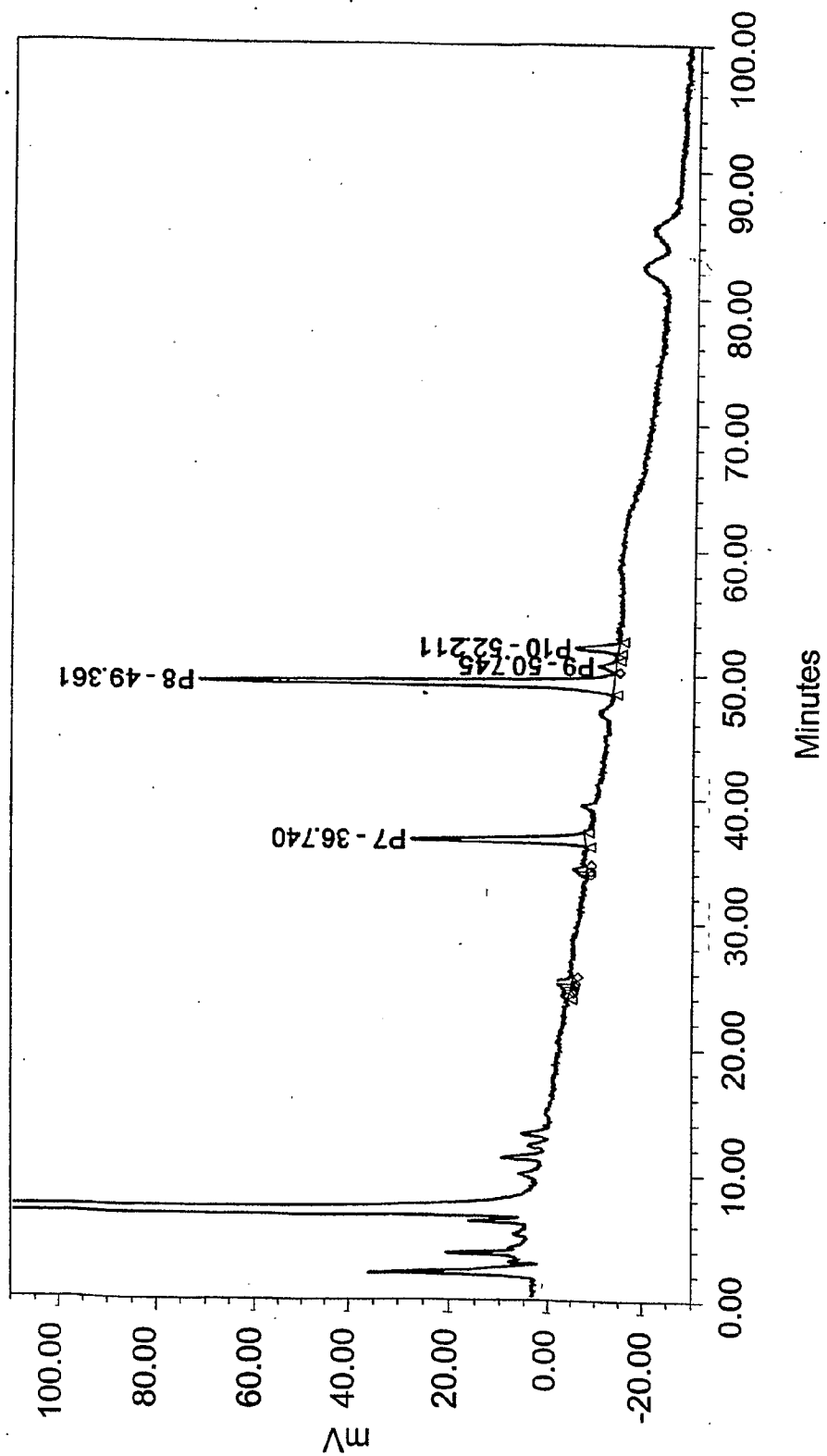


FIG. 113B

399/498



Minutes

FIG. 113C

400/498

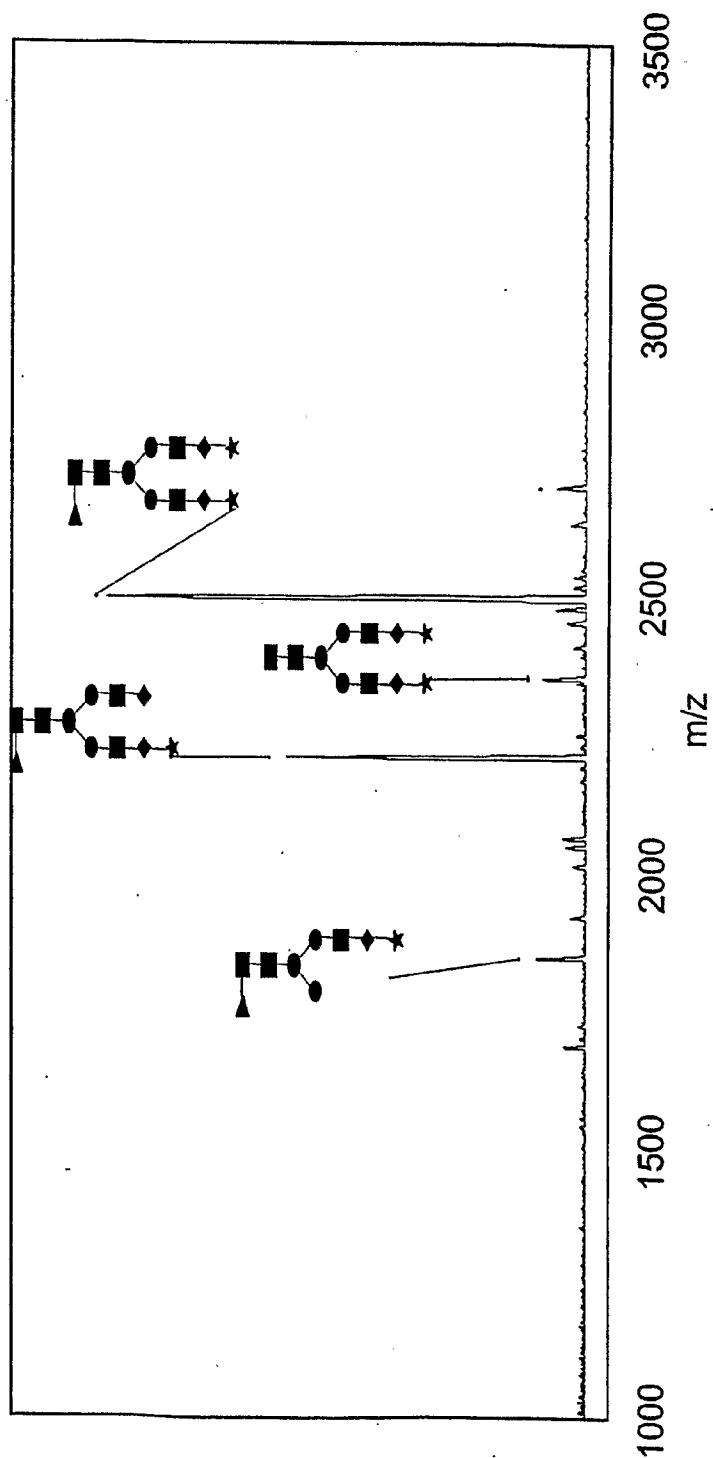


FIG. 114A

401/498

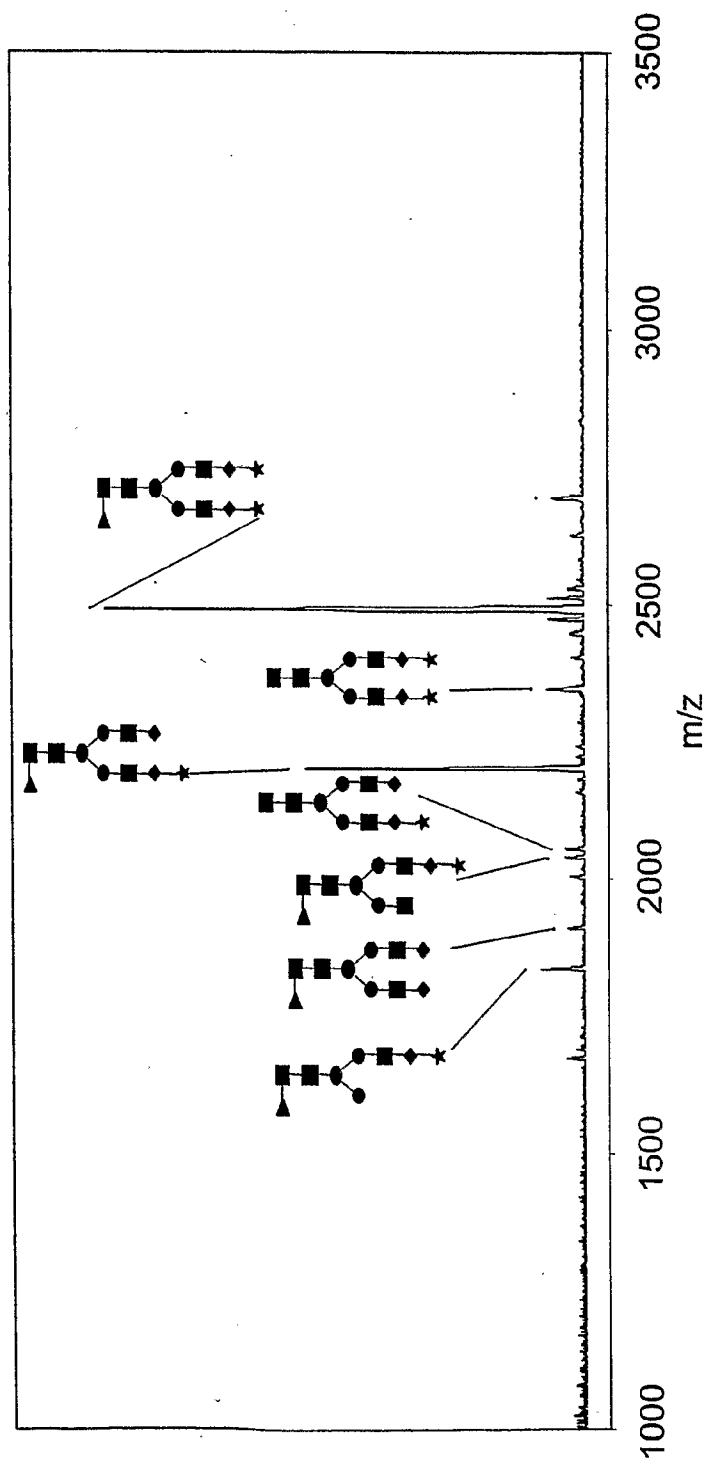


FIG. 114B

402/498

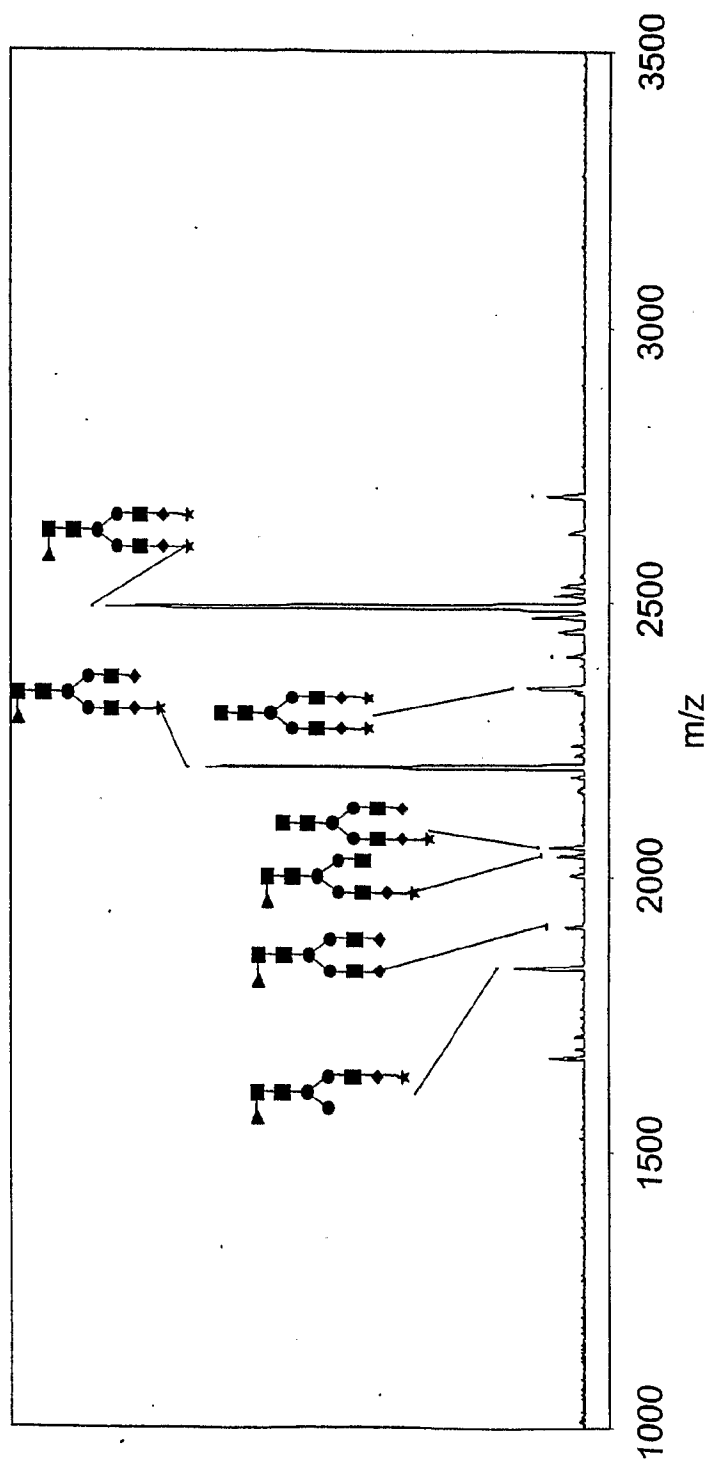


FIG. 114C

403/498

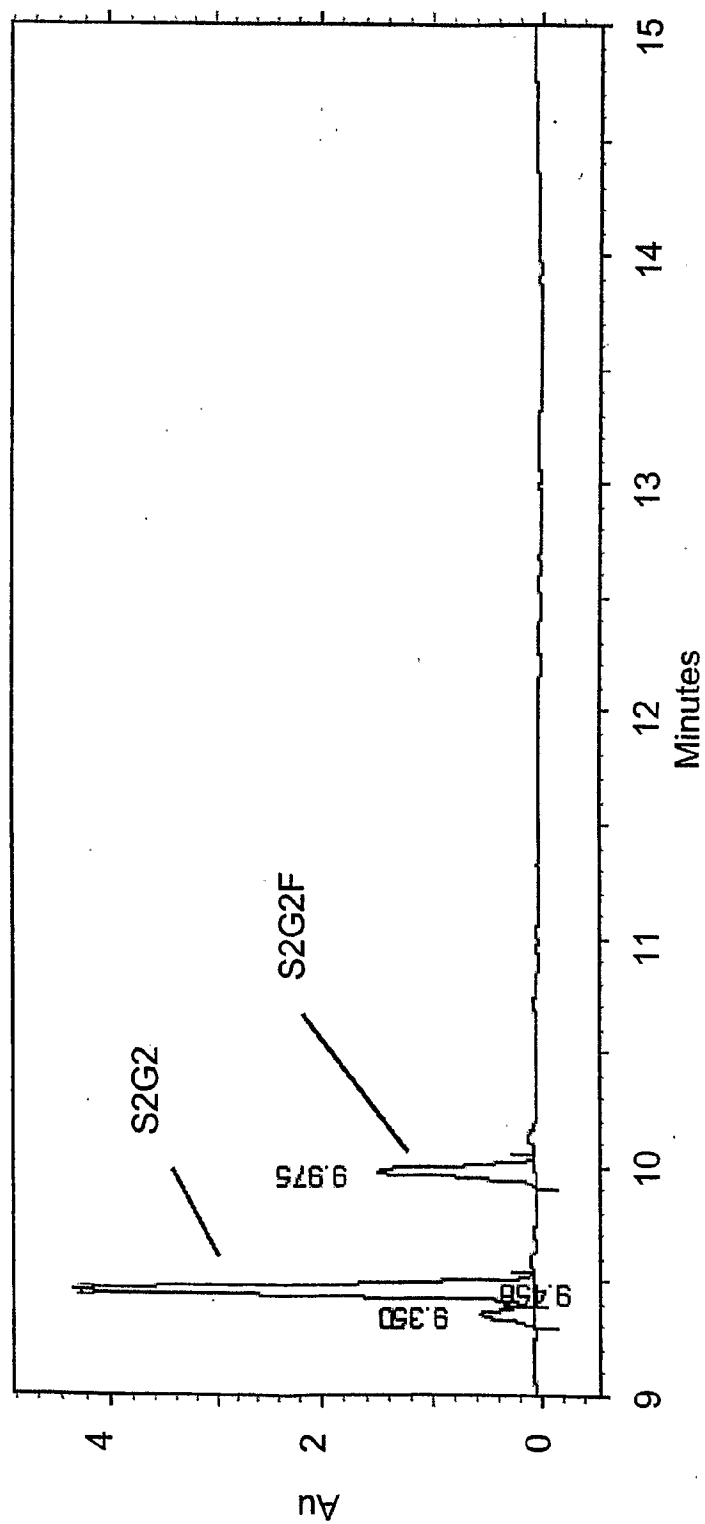


FIG. 115A

404/498

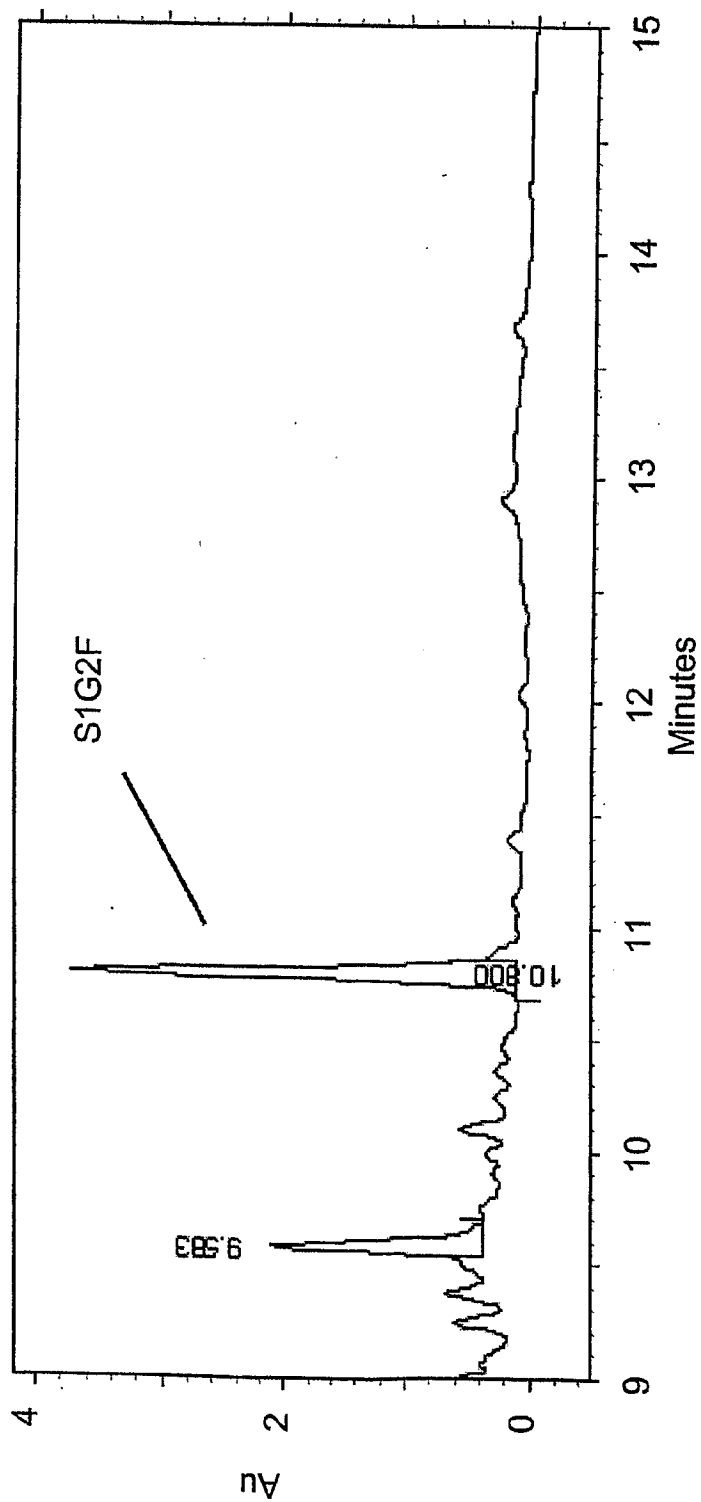


FIG. 115B

405/498

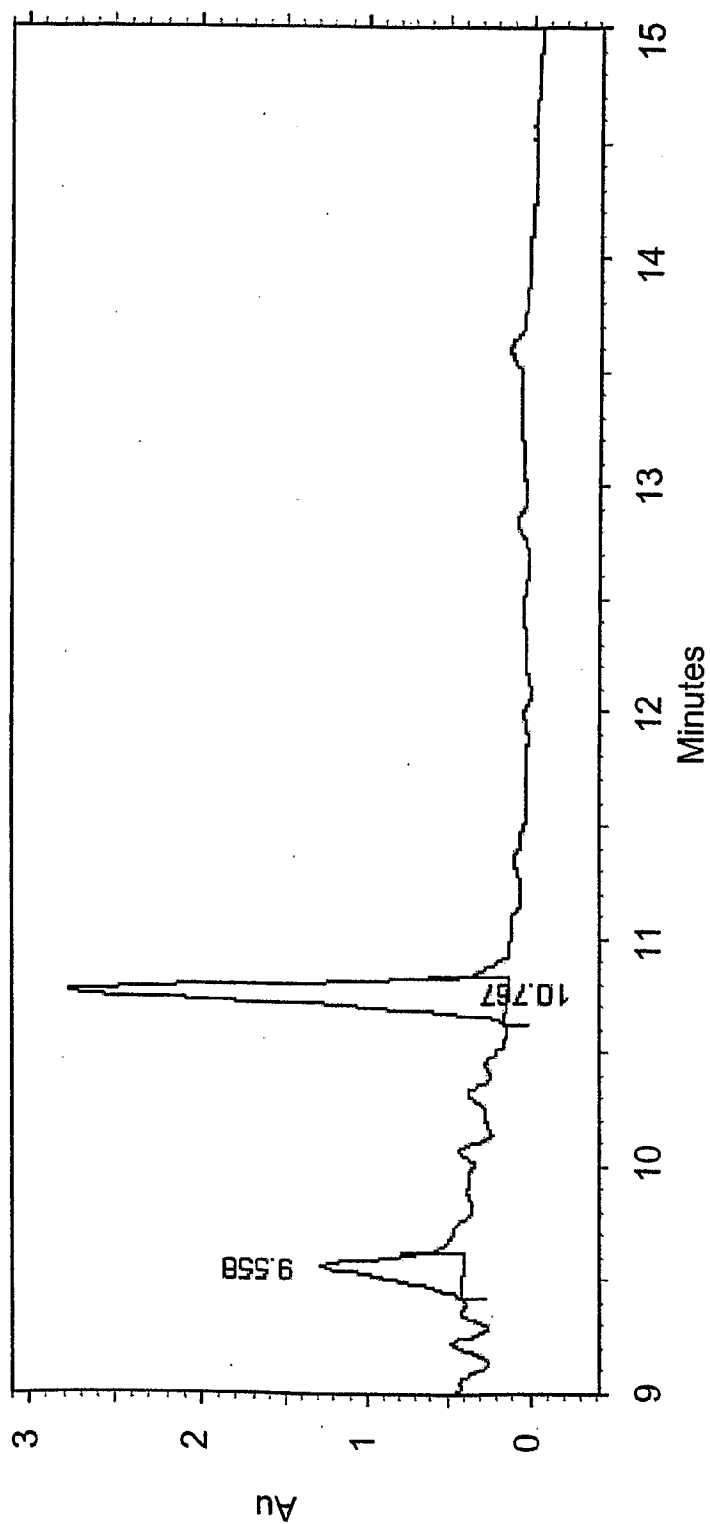


FIG. 115C

406/498

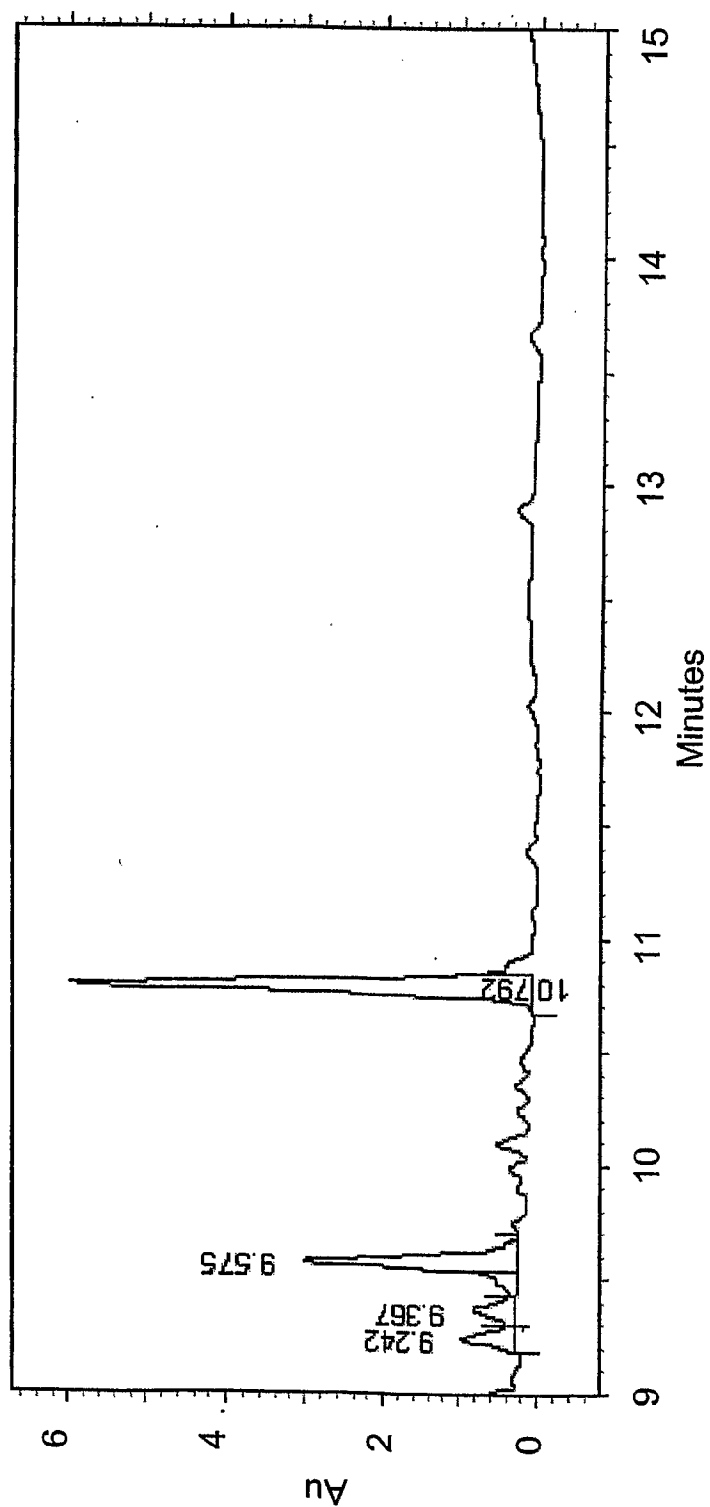


FIG. 115D

407/498

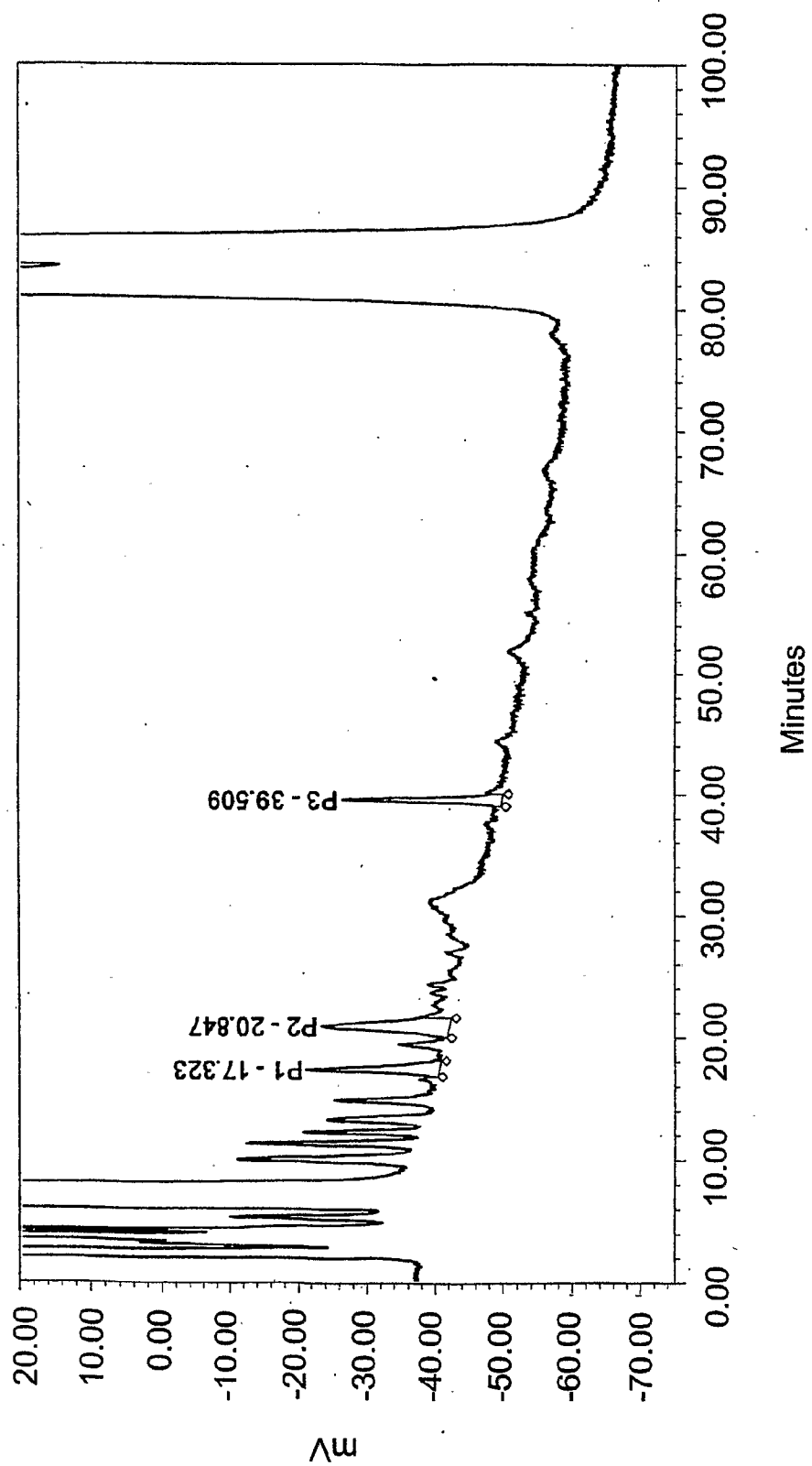


FIG. 116A

408/498

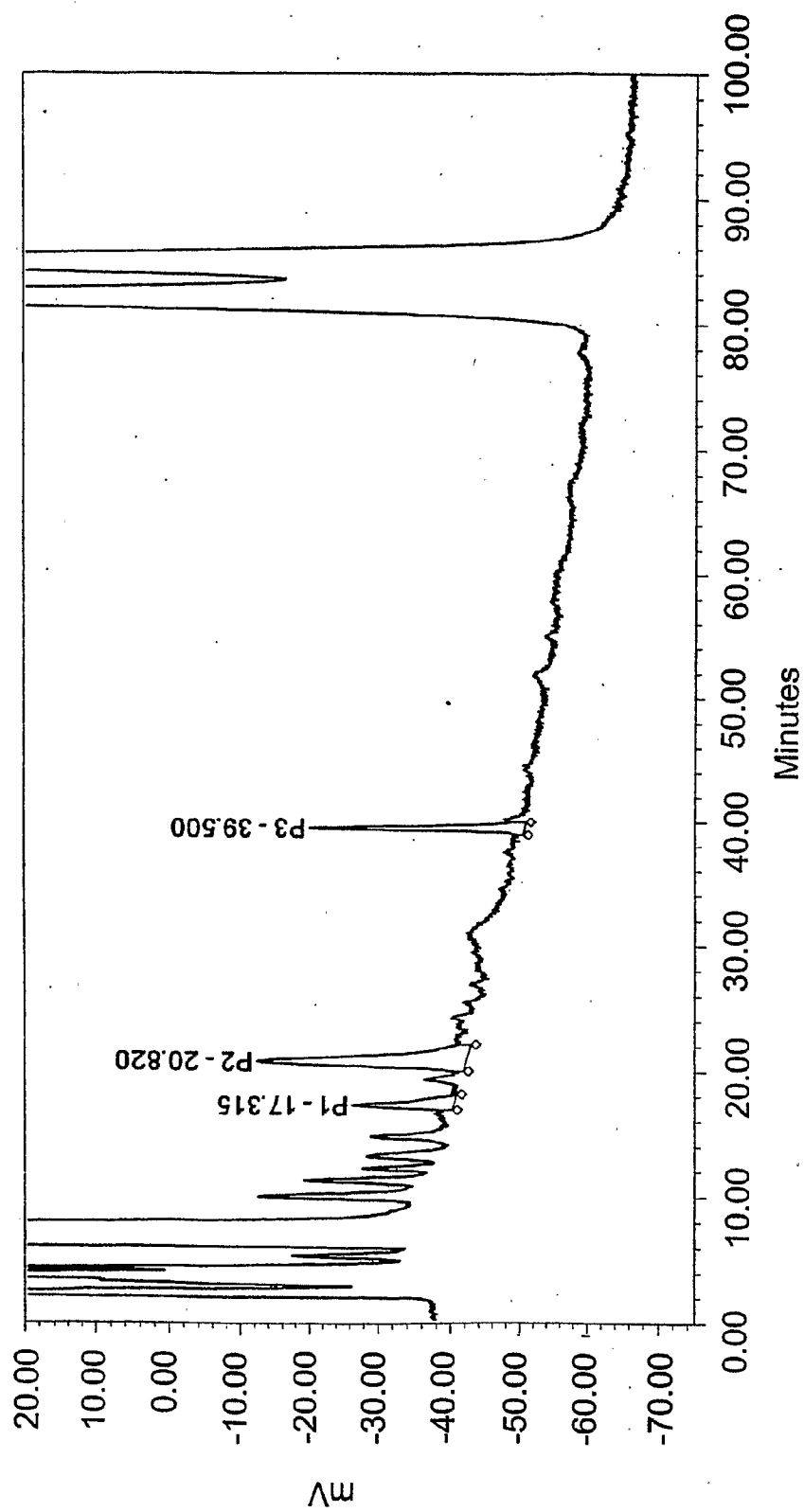


FIG. 116B

409/498

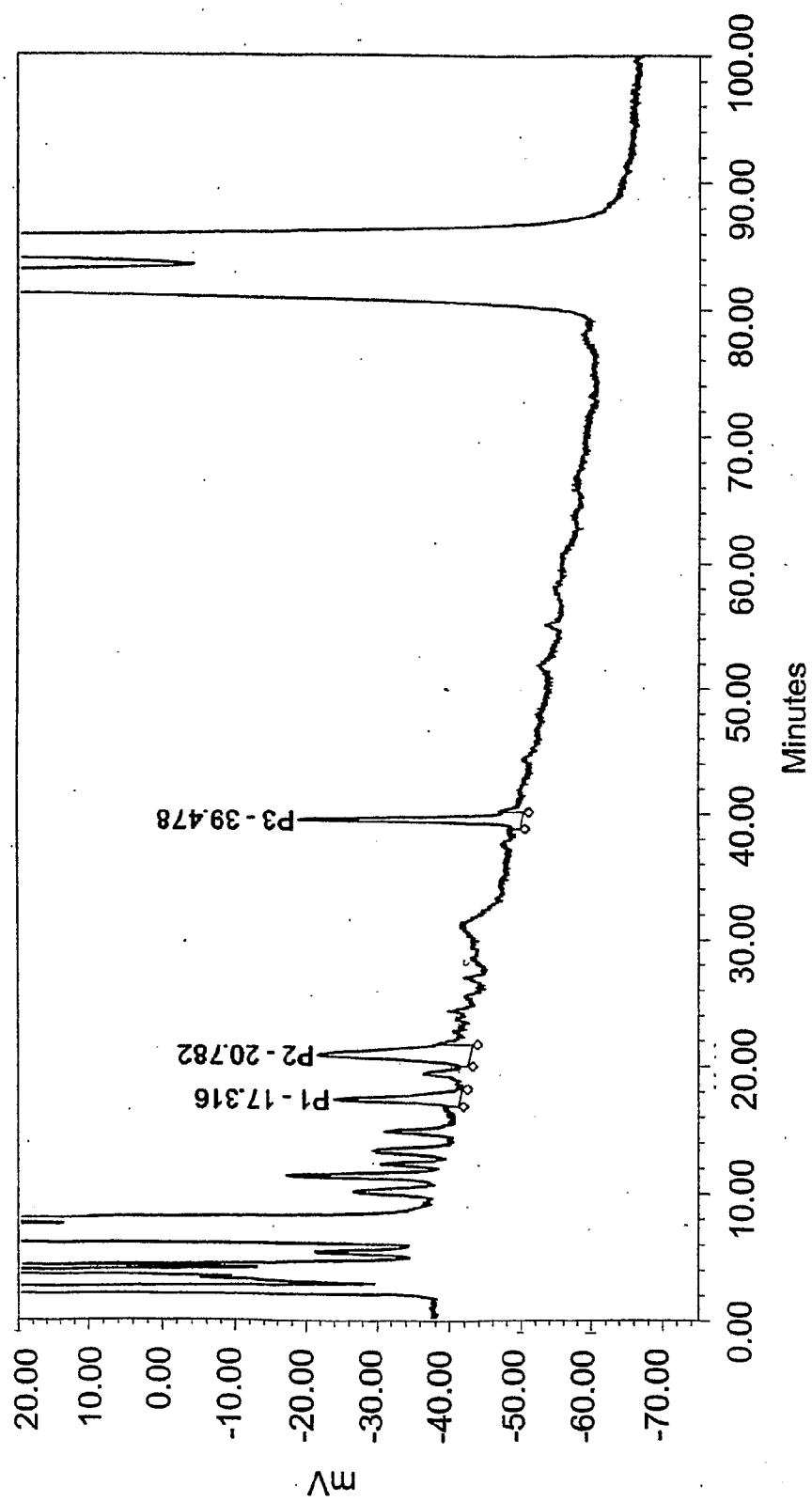


FIG. 116C

410/498

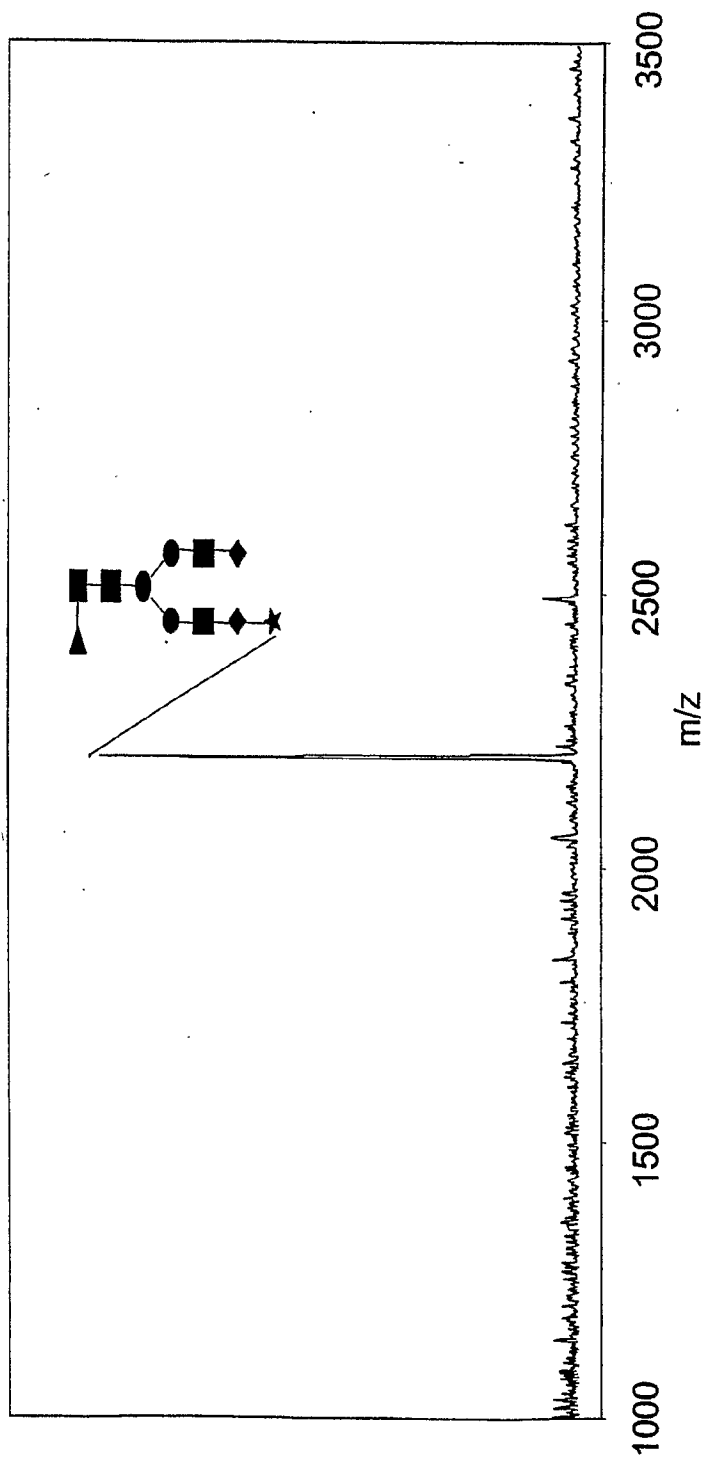


FIG. 117A

411/498

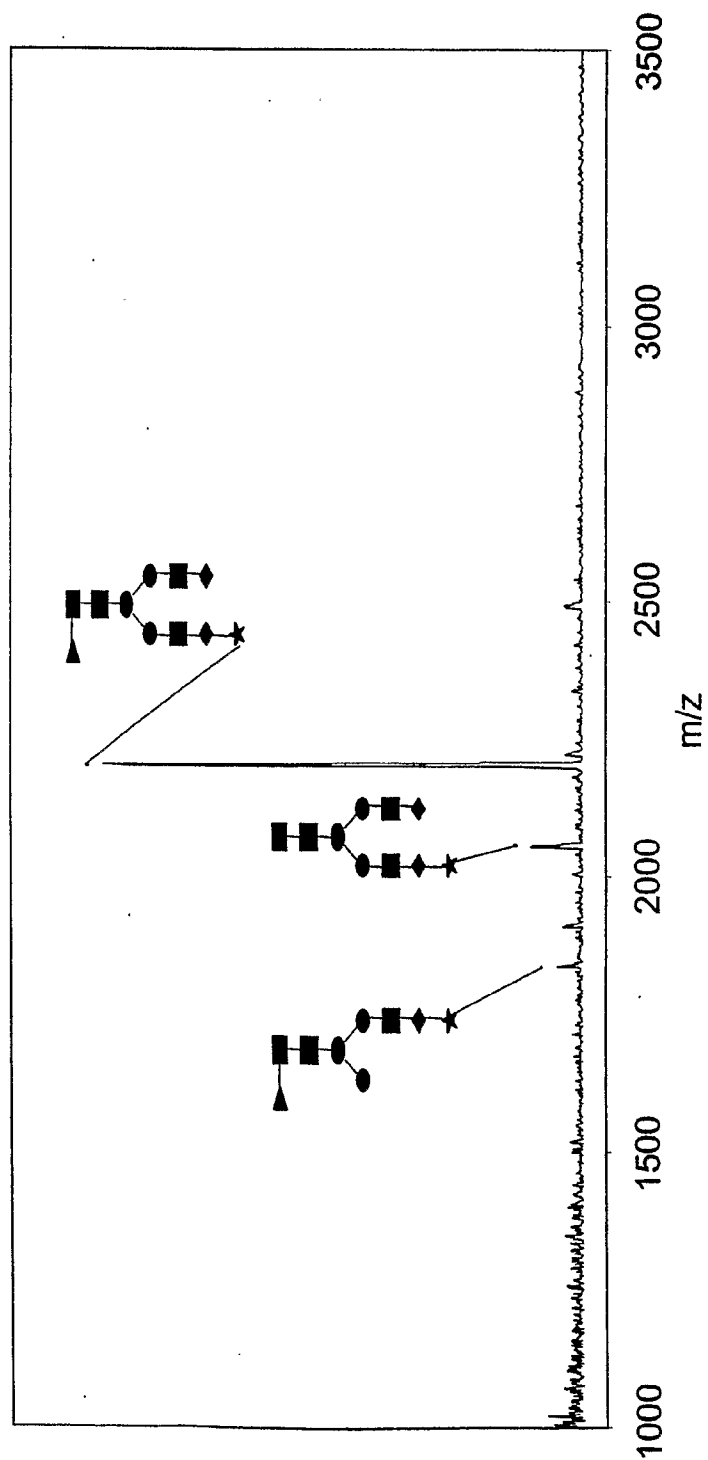


FIG. 117B

412/498

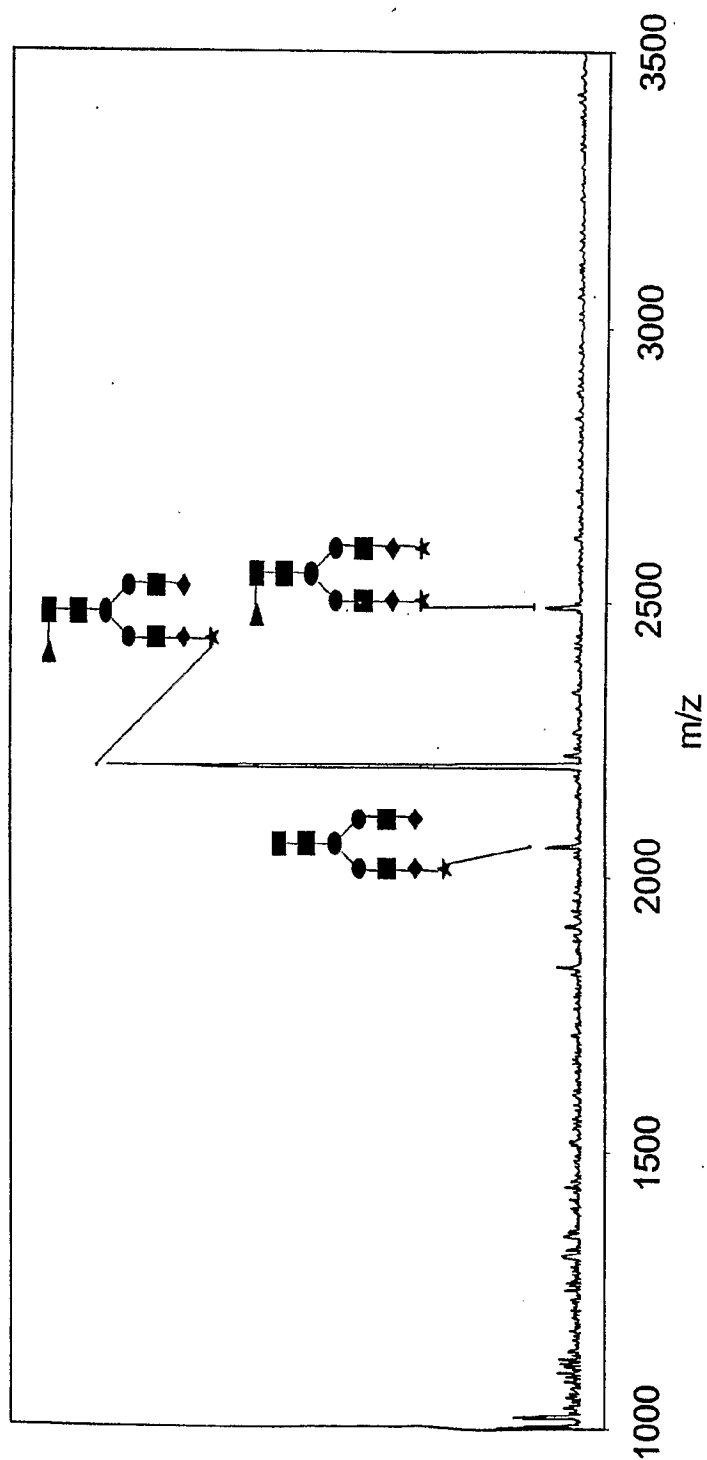


FIG. 117C

413/498

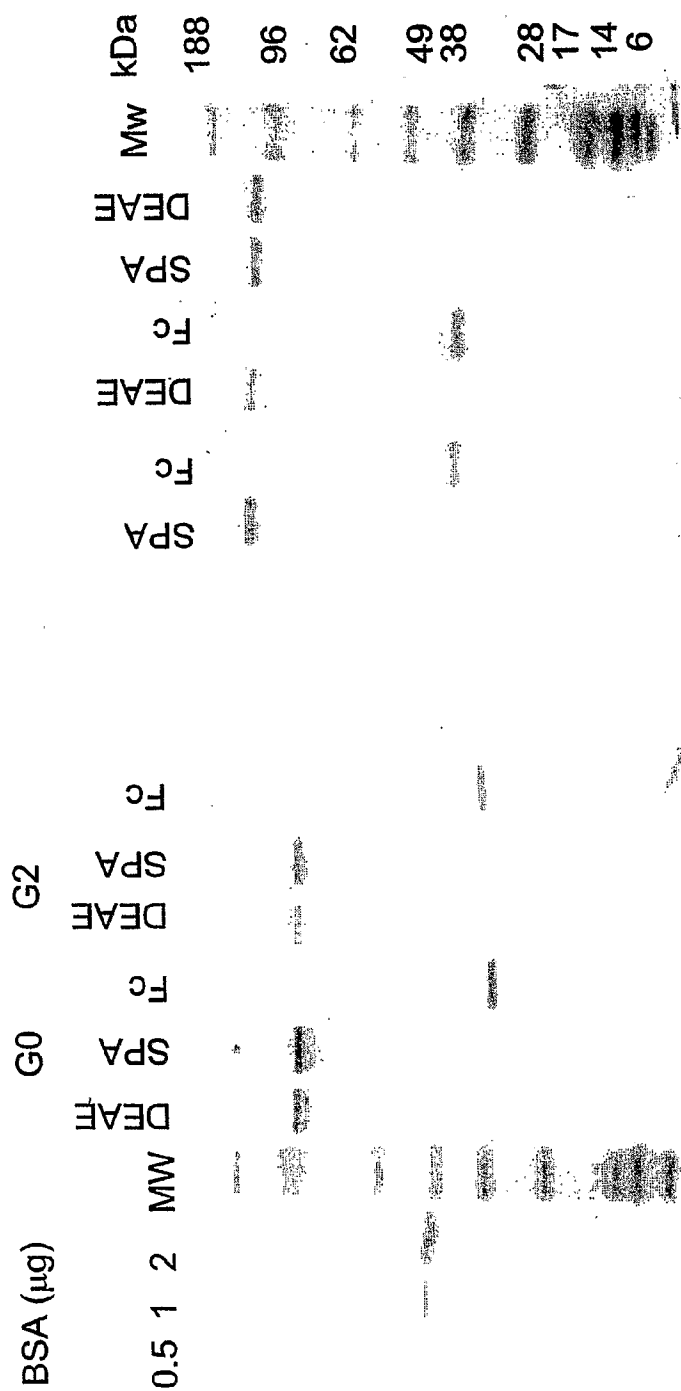


FIG. 118B

FIG. 118A

414/498

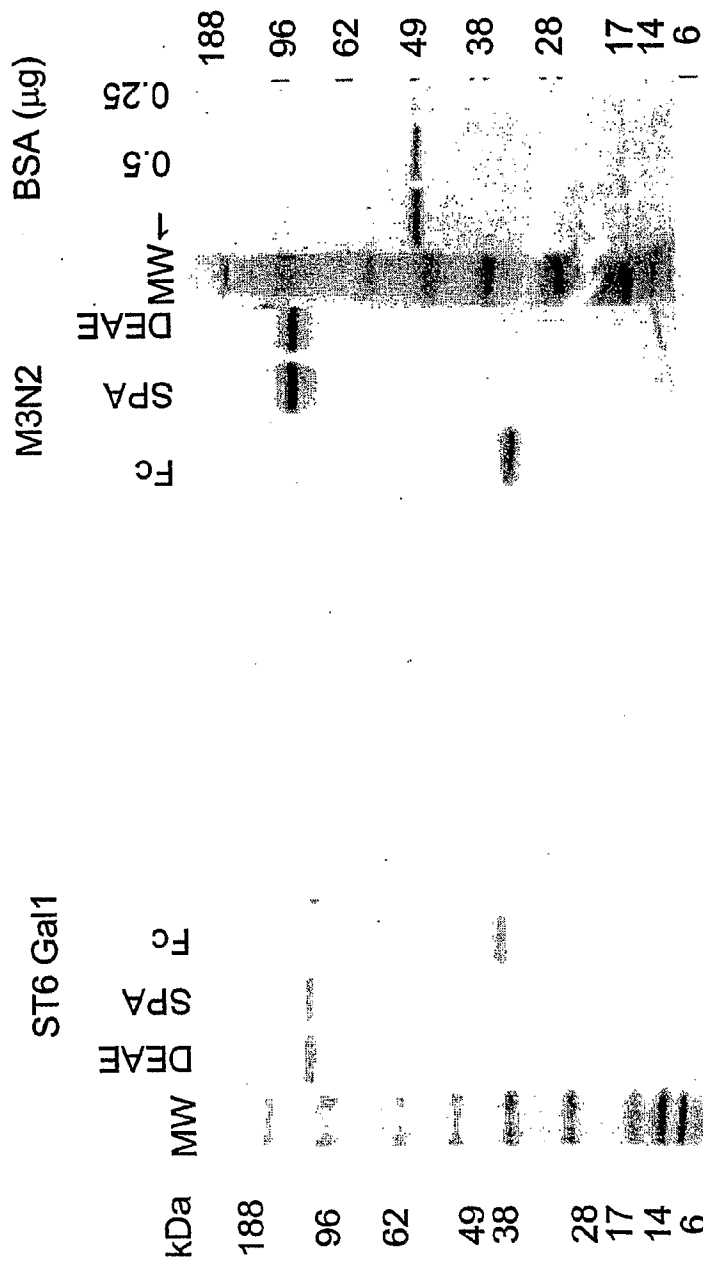


FIG. 118D

FIG. 118C

415/498

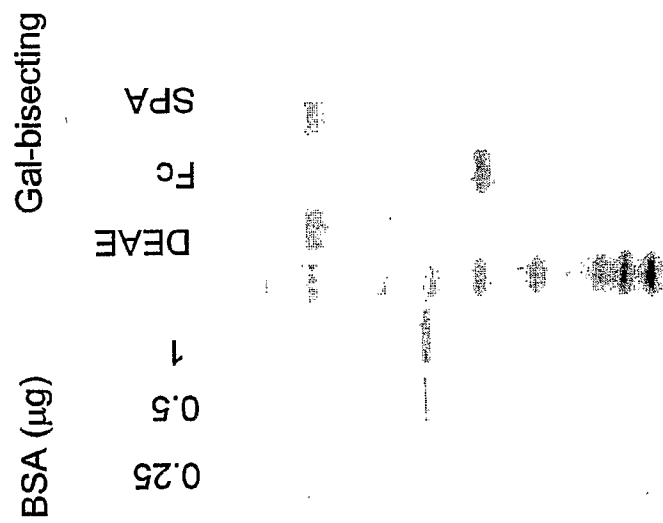


FIG. 118E

416/498

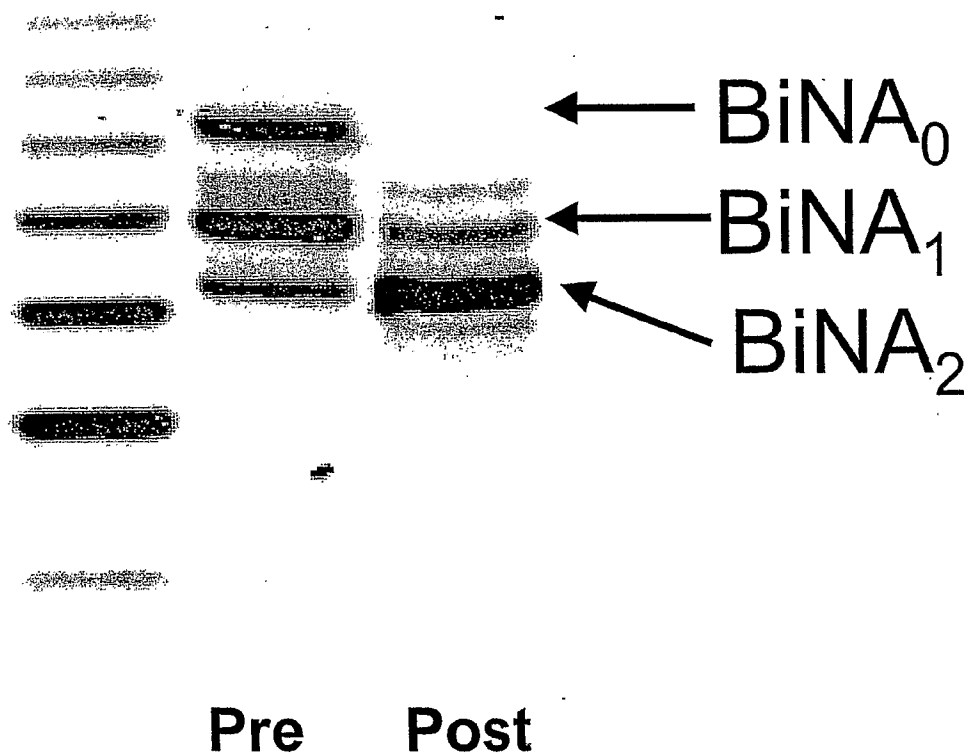


FIG. 119

417/498

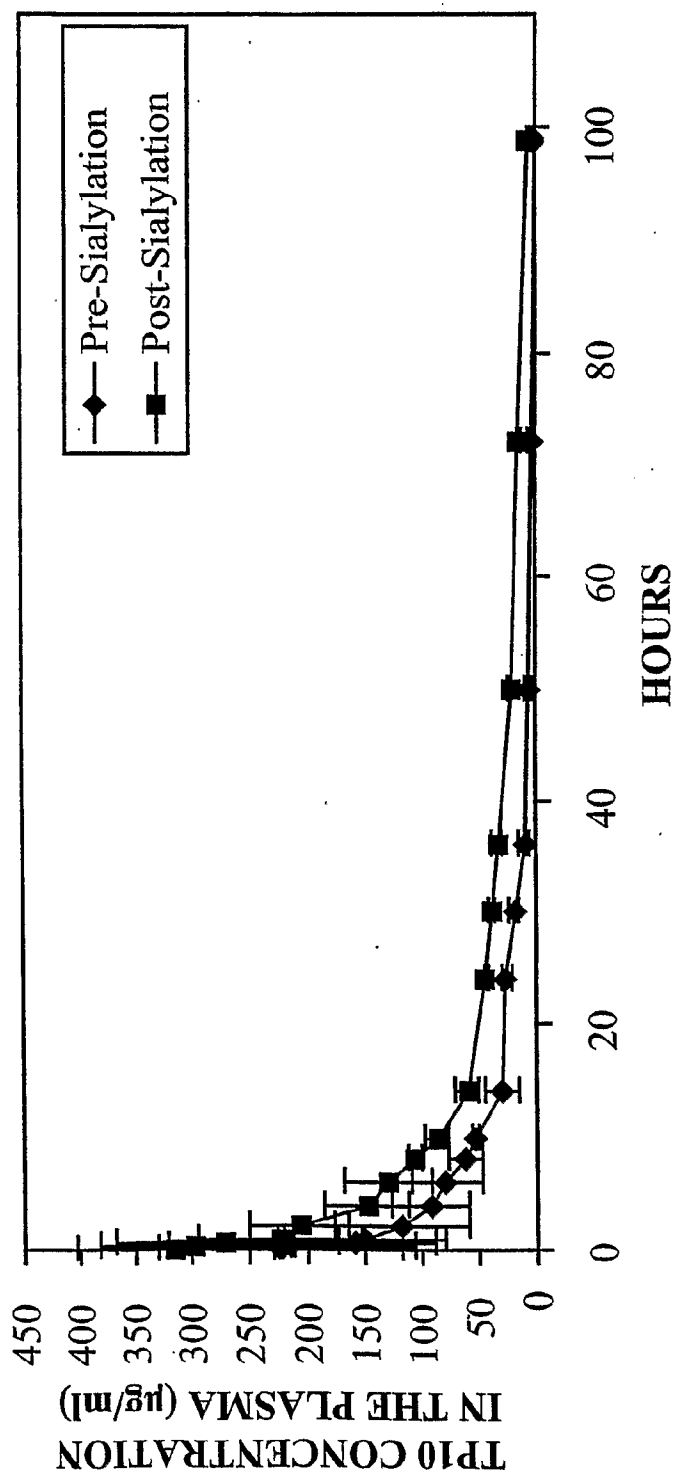


FIG. 120

418/498

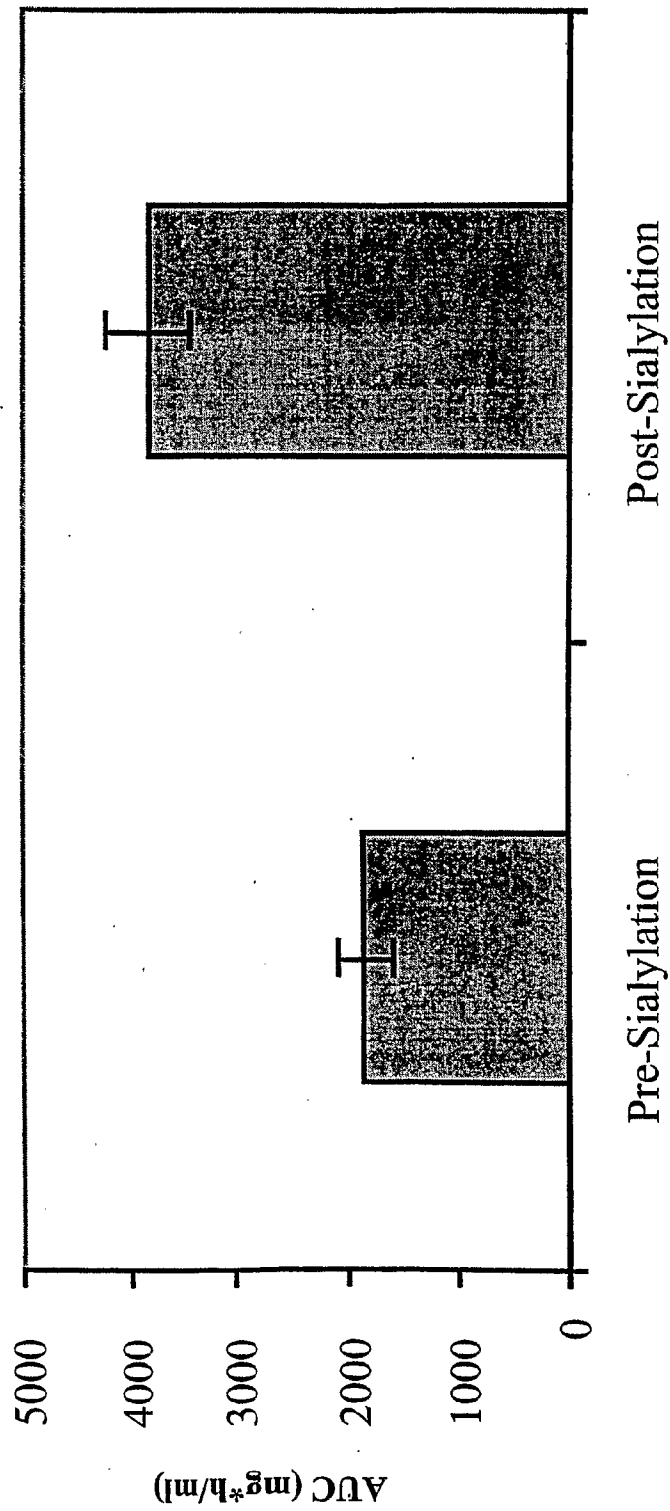


FIG. 121

419/498

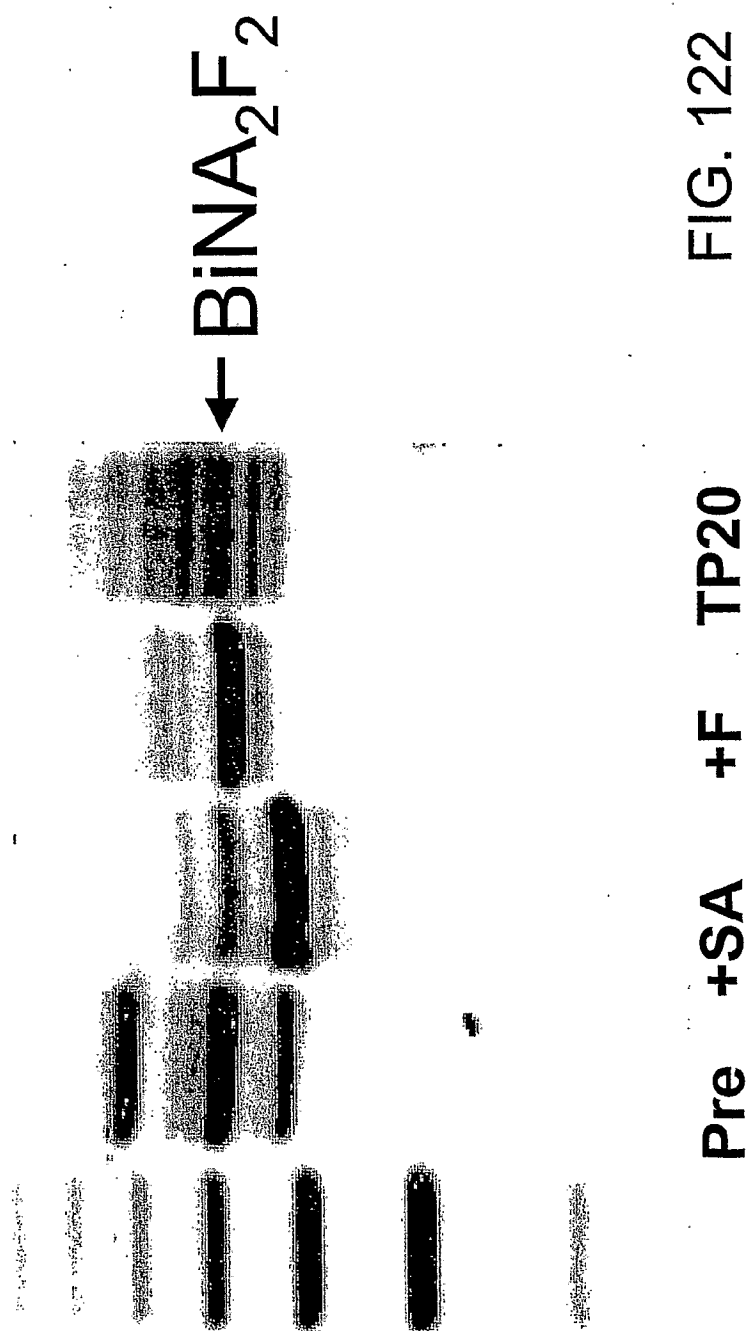


FIG. 122

420/498

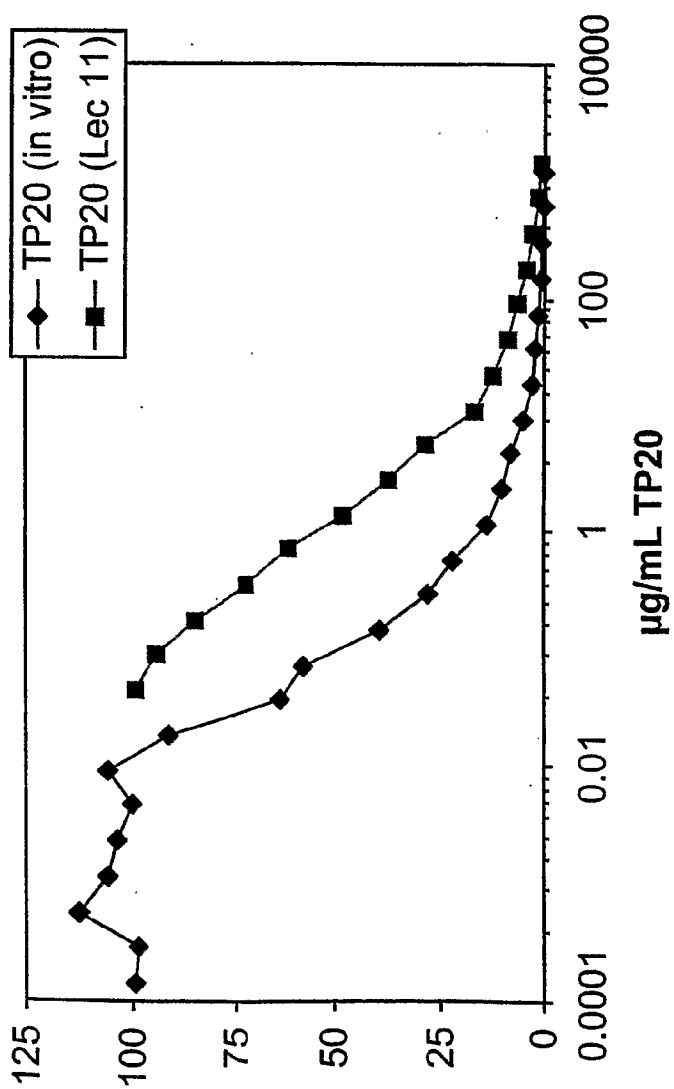


FIG. 123

421/498

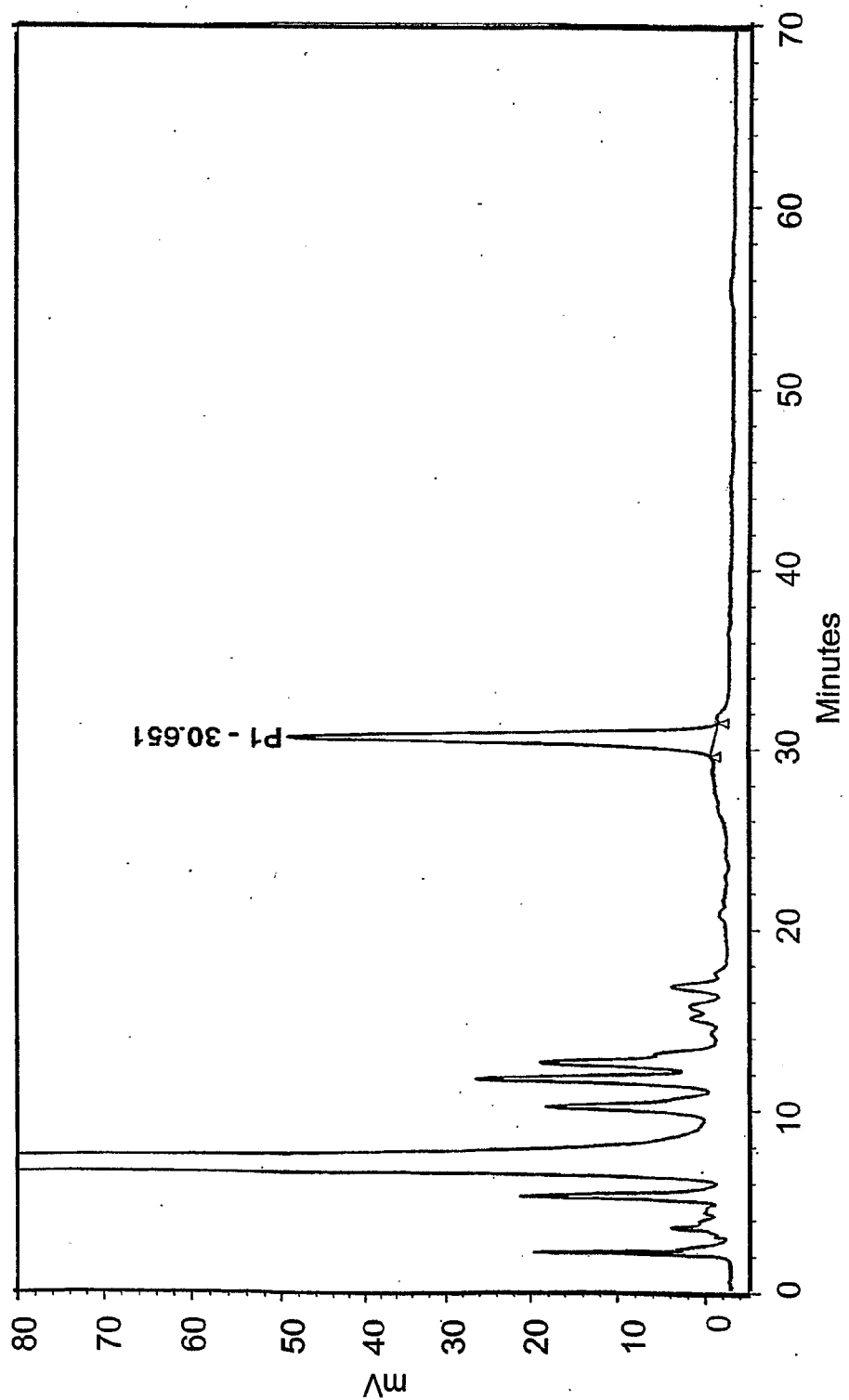


FIG. 124

422/498

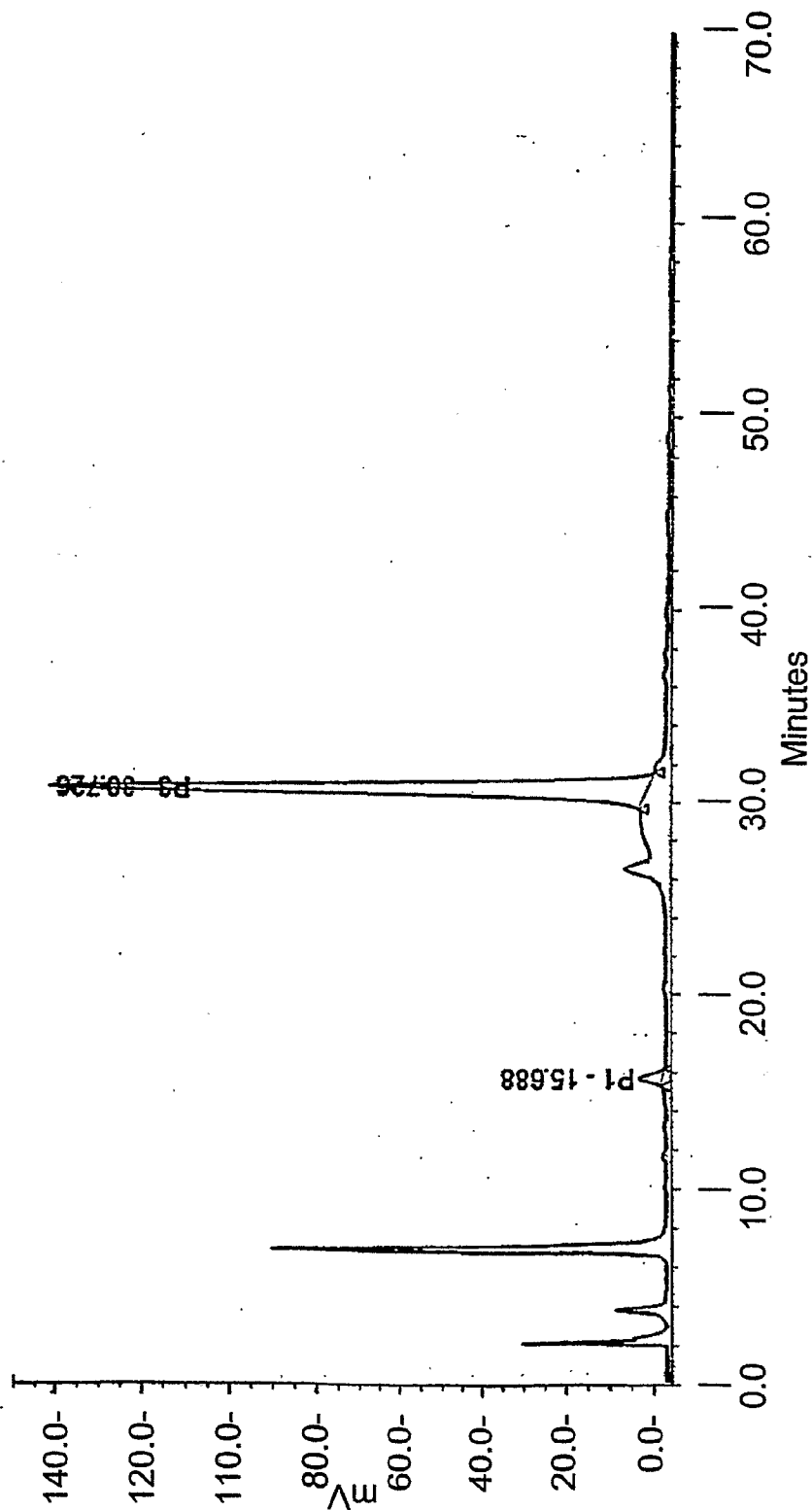


FIG. 125A

423/498

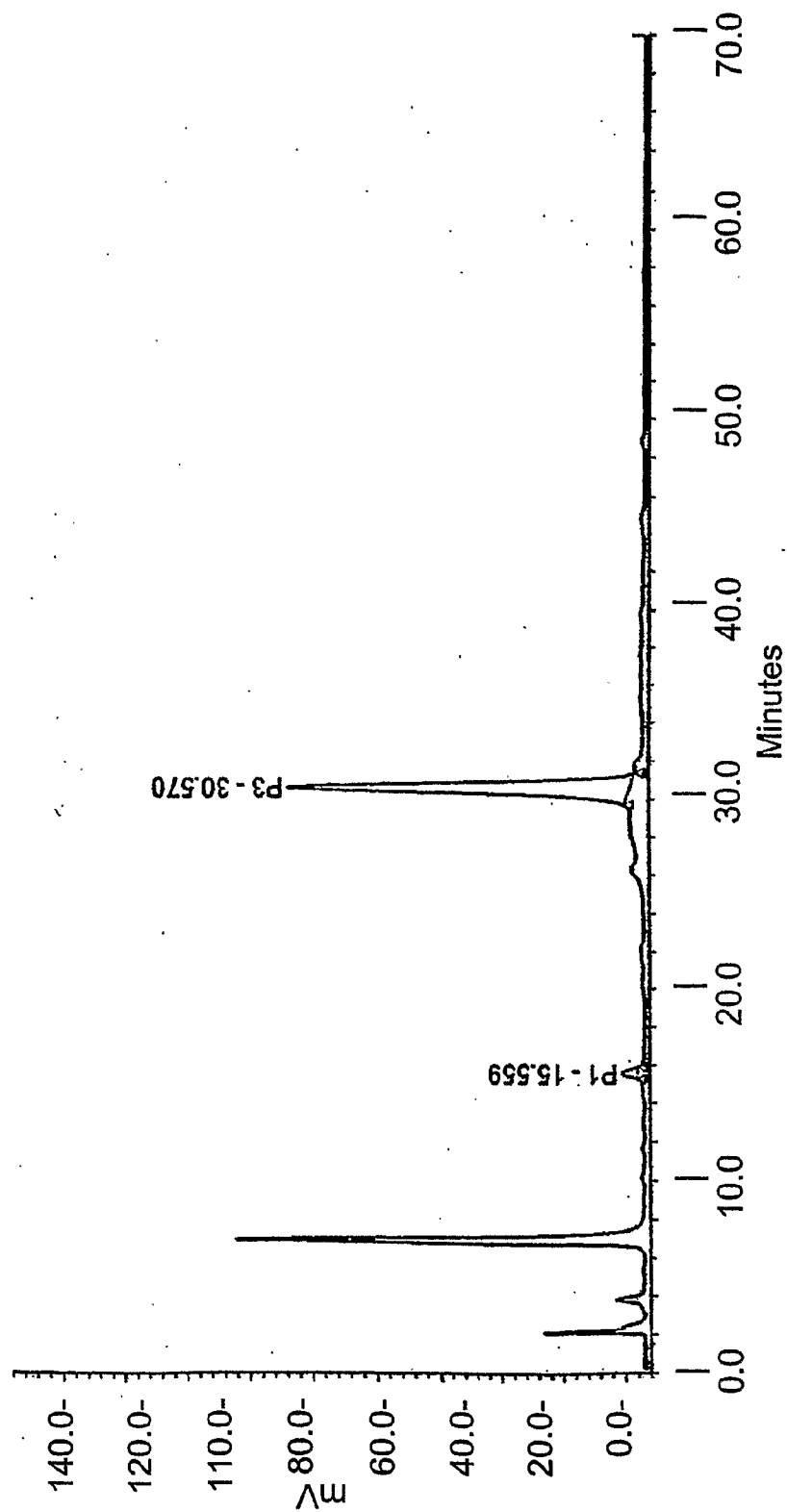


FIG. 125B

424/498

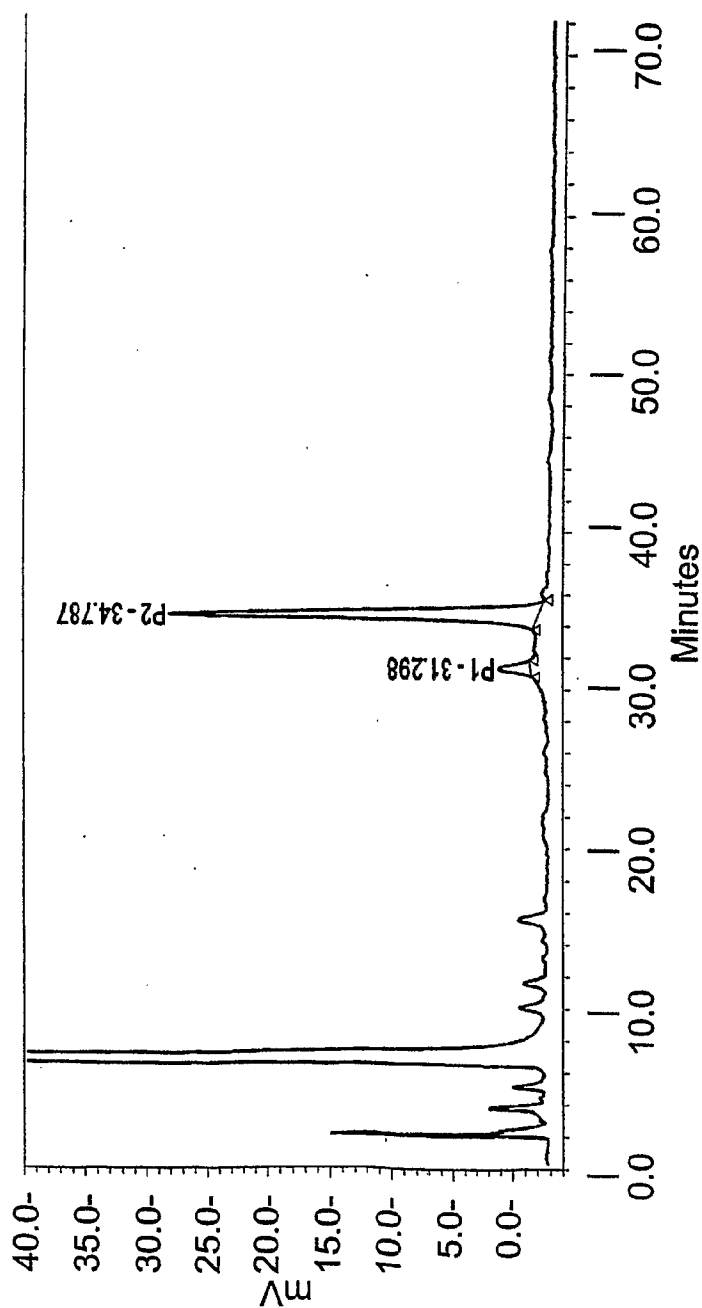


FIG. 126

425/498

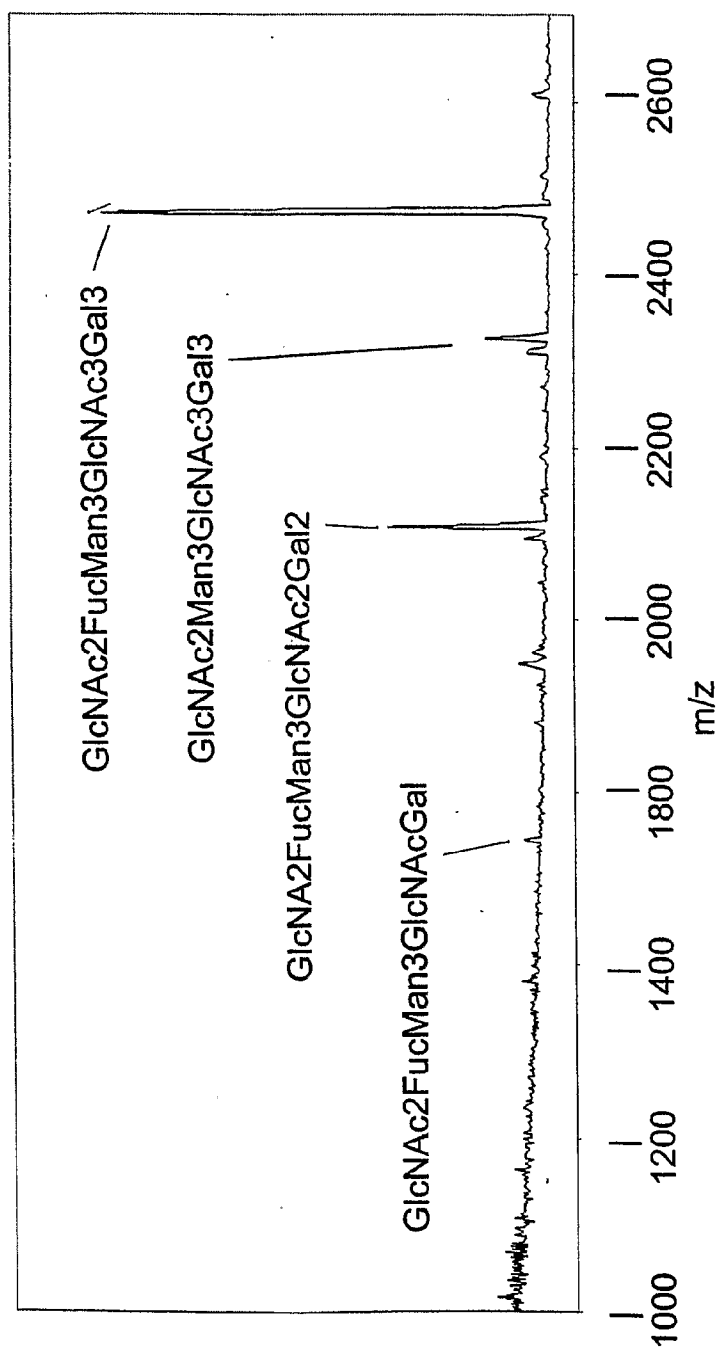


FIG. 127

426/498

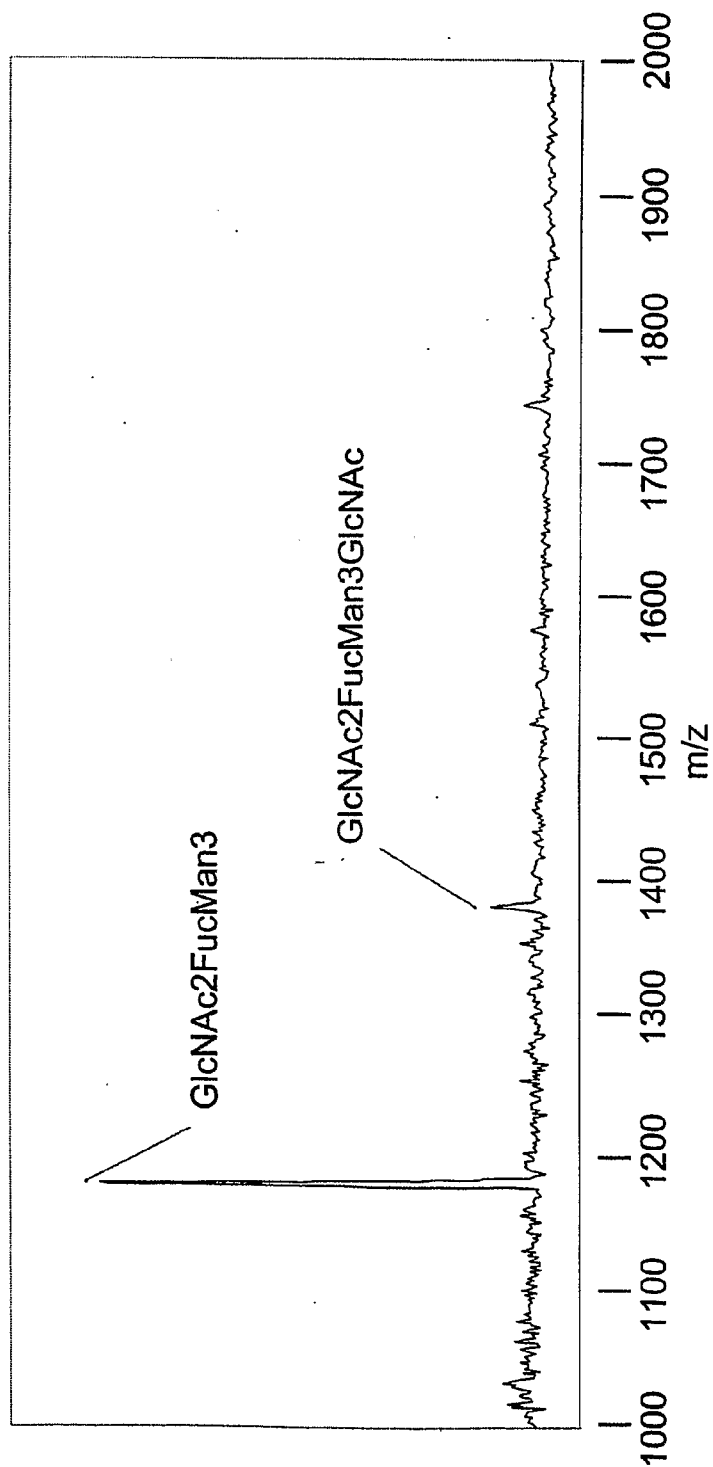


FIG. 128

427/498

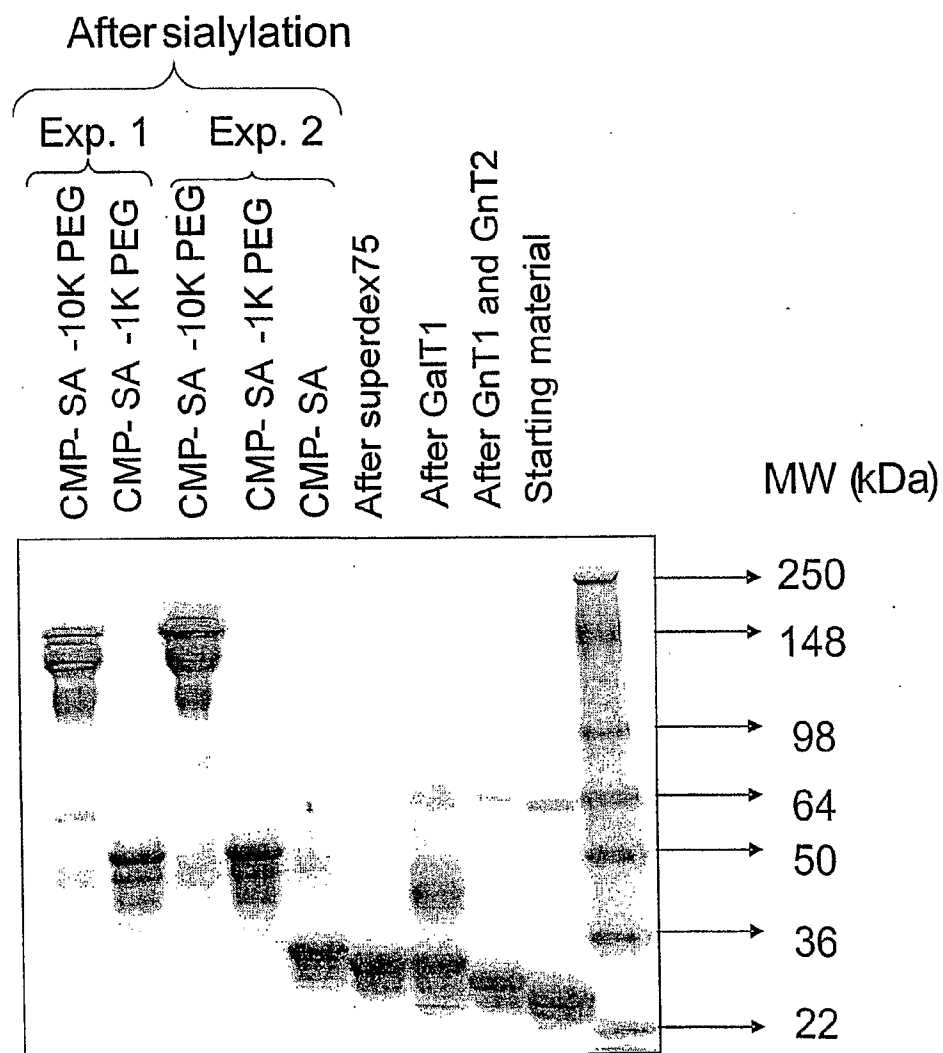


FIG. 129

428/498

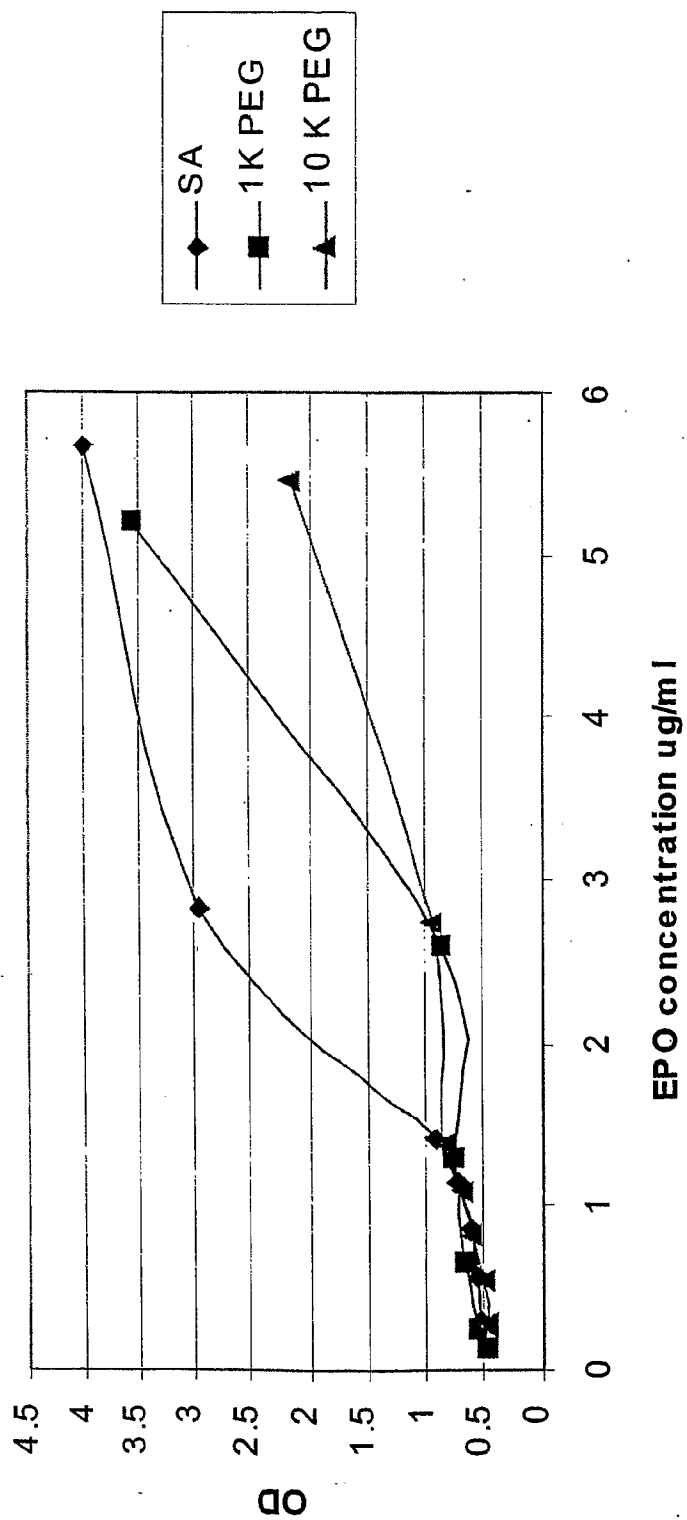
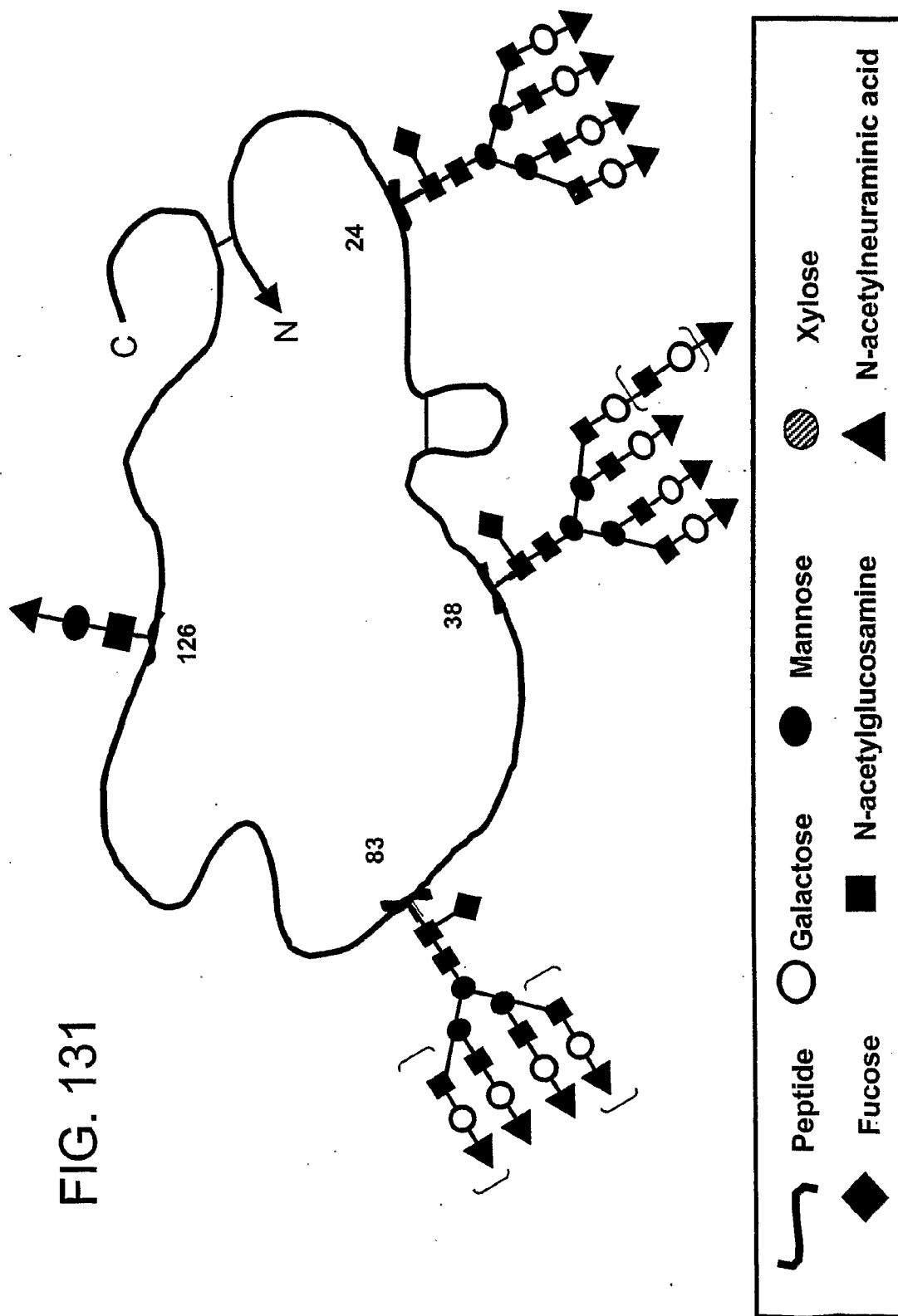


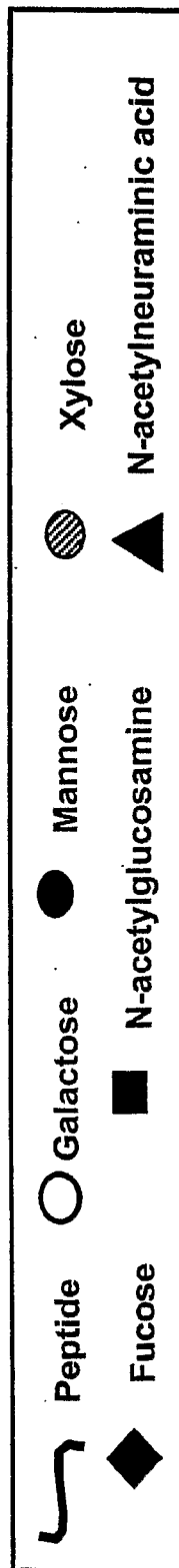
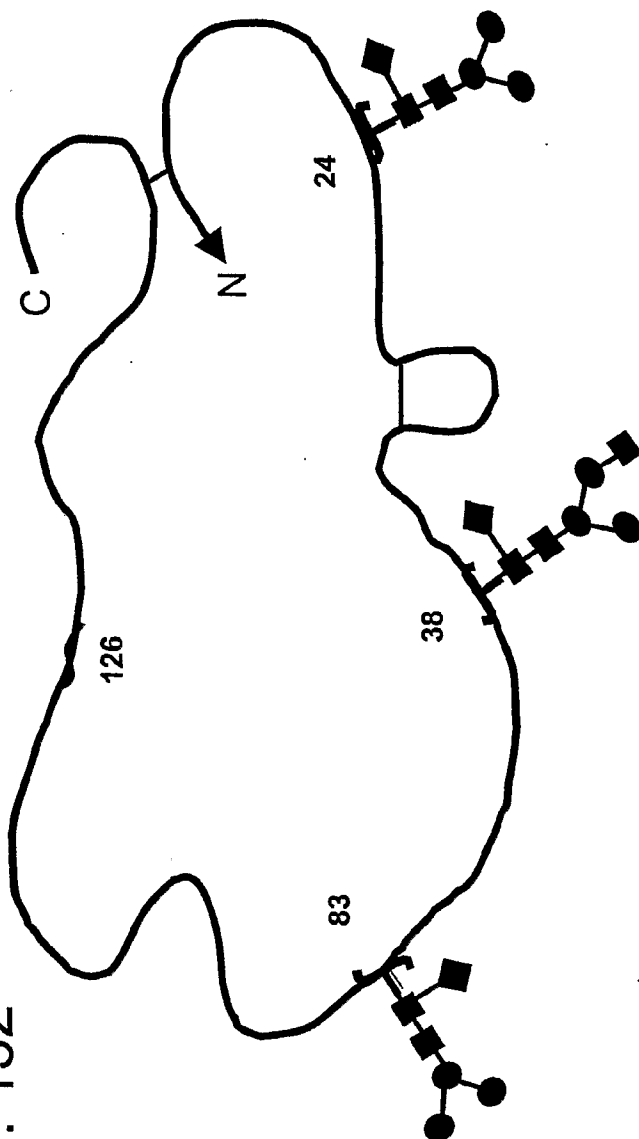
FIG. 130

429/498



430/498

FIG. 132



431/498

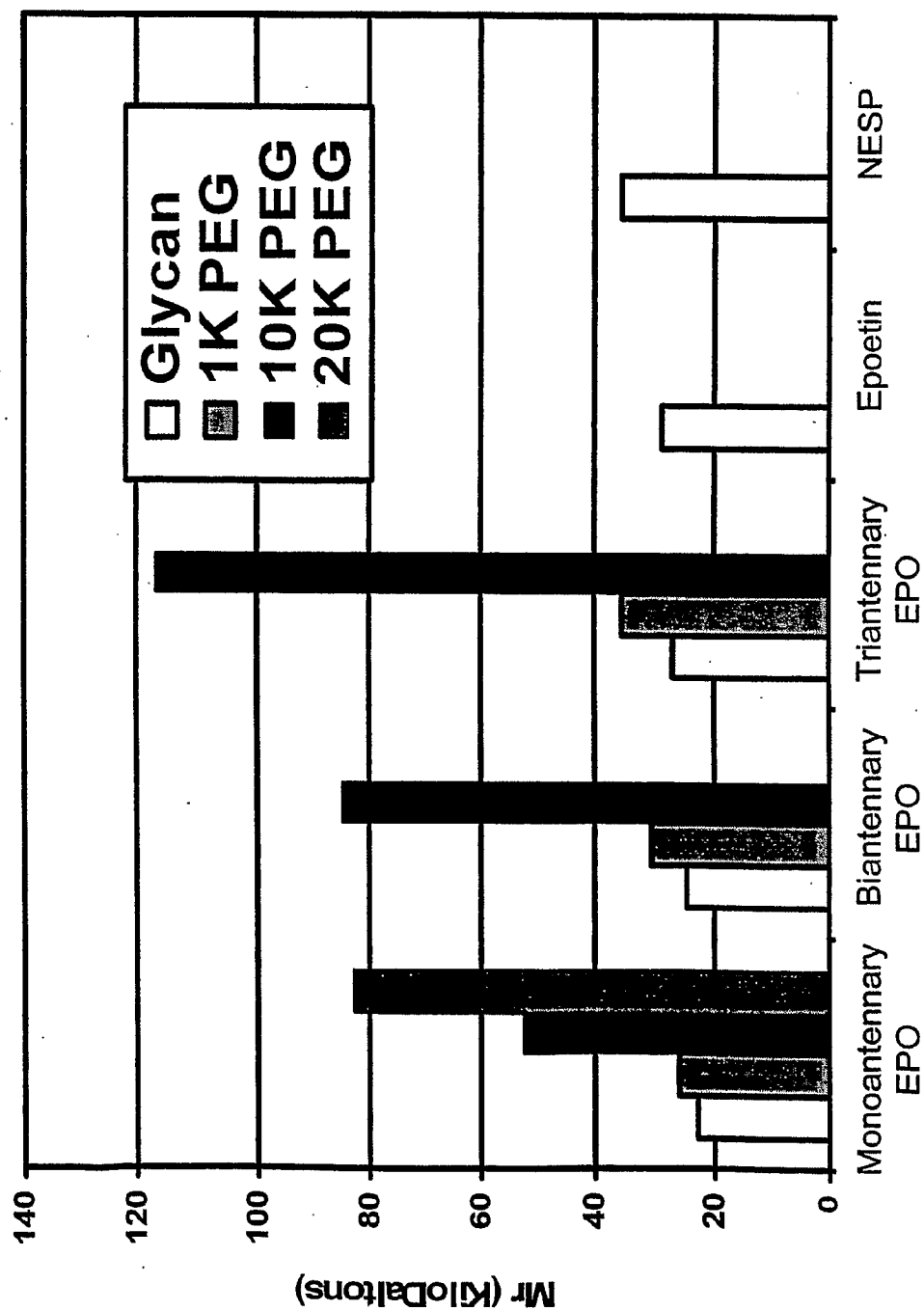
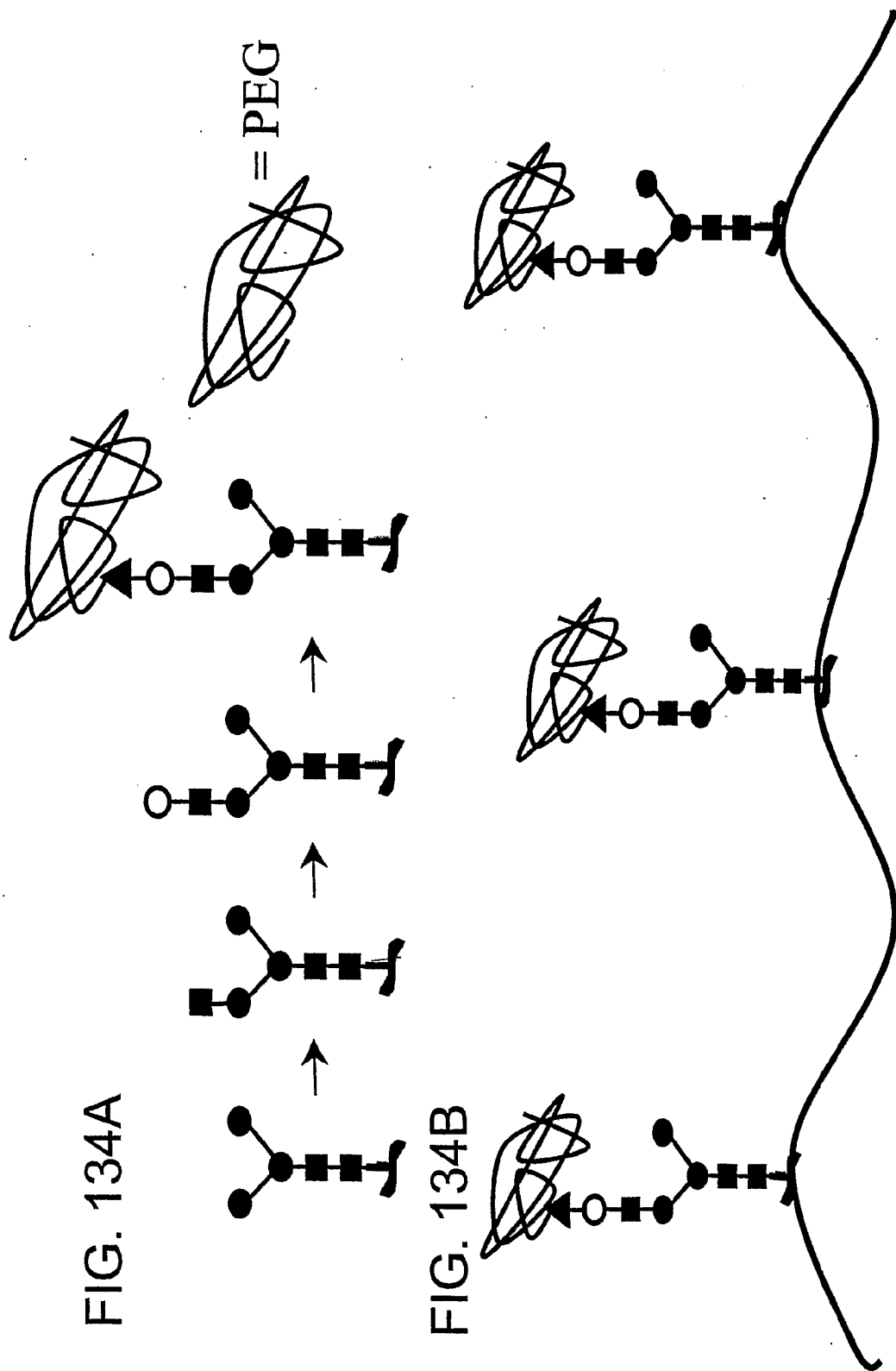


FIG. 133

432/498



433/498

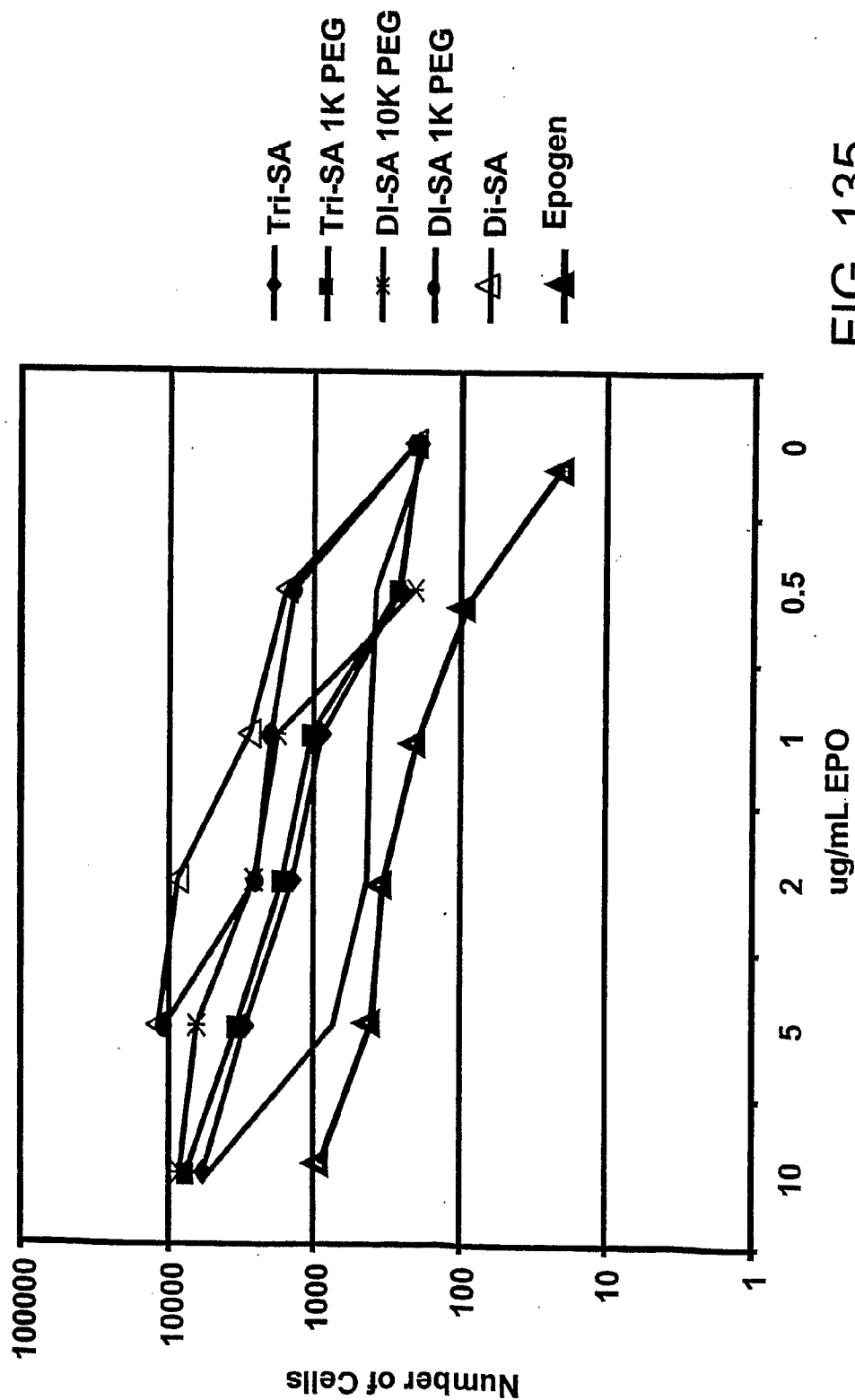


FIG. 135

434/498

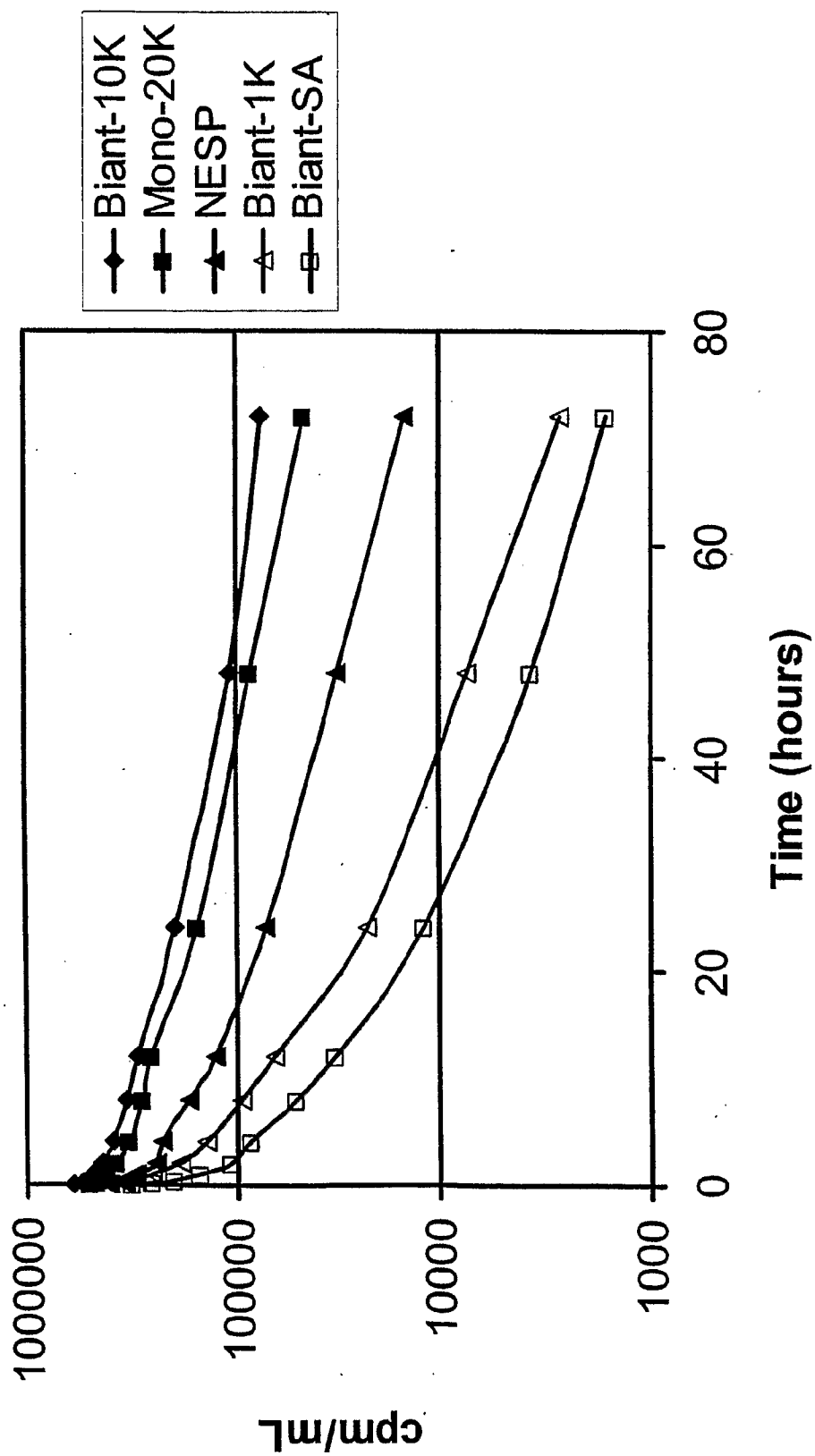


FIG. 136

435/498

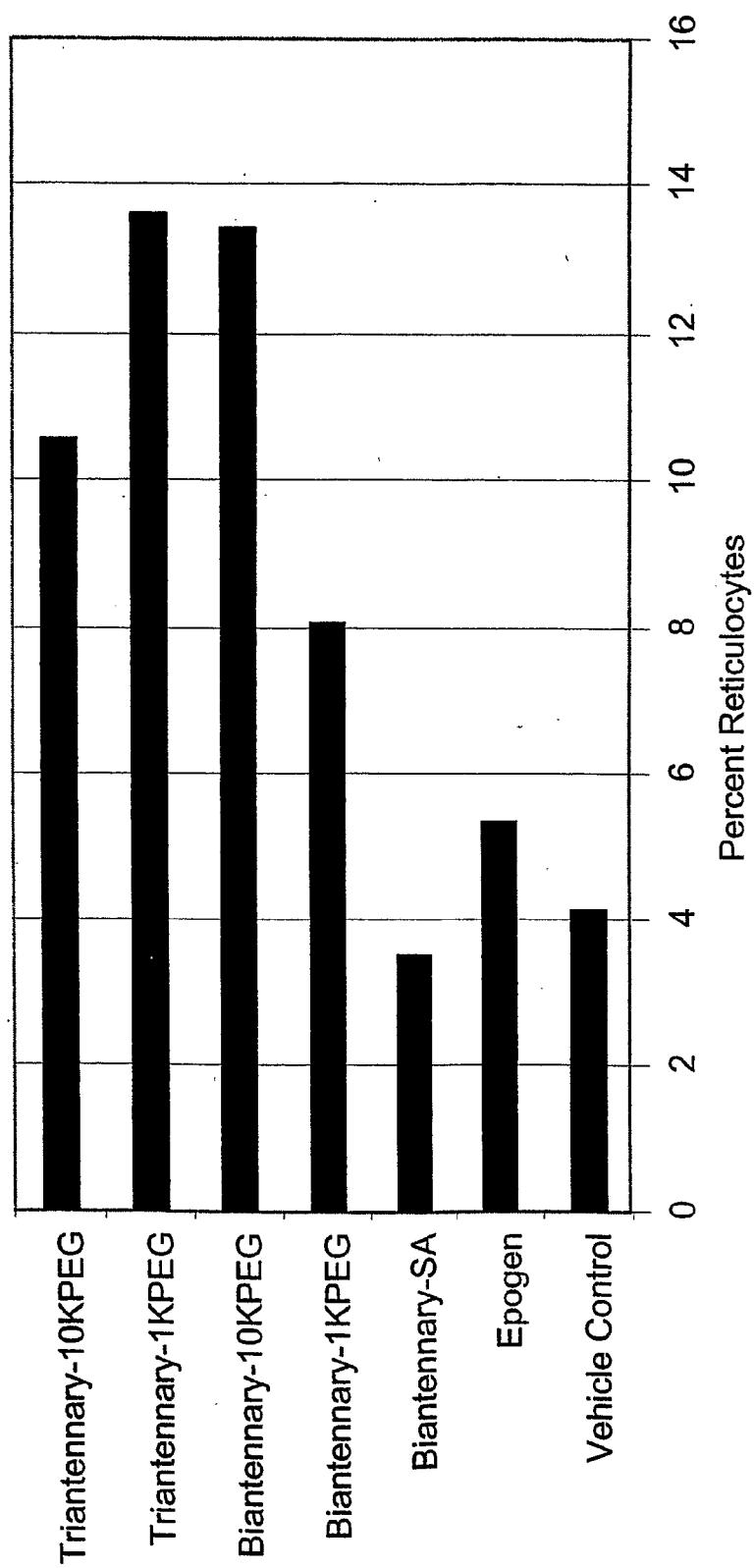


FIG. 137

436/498

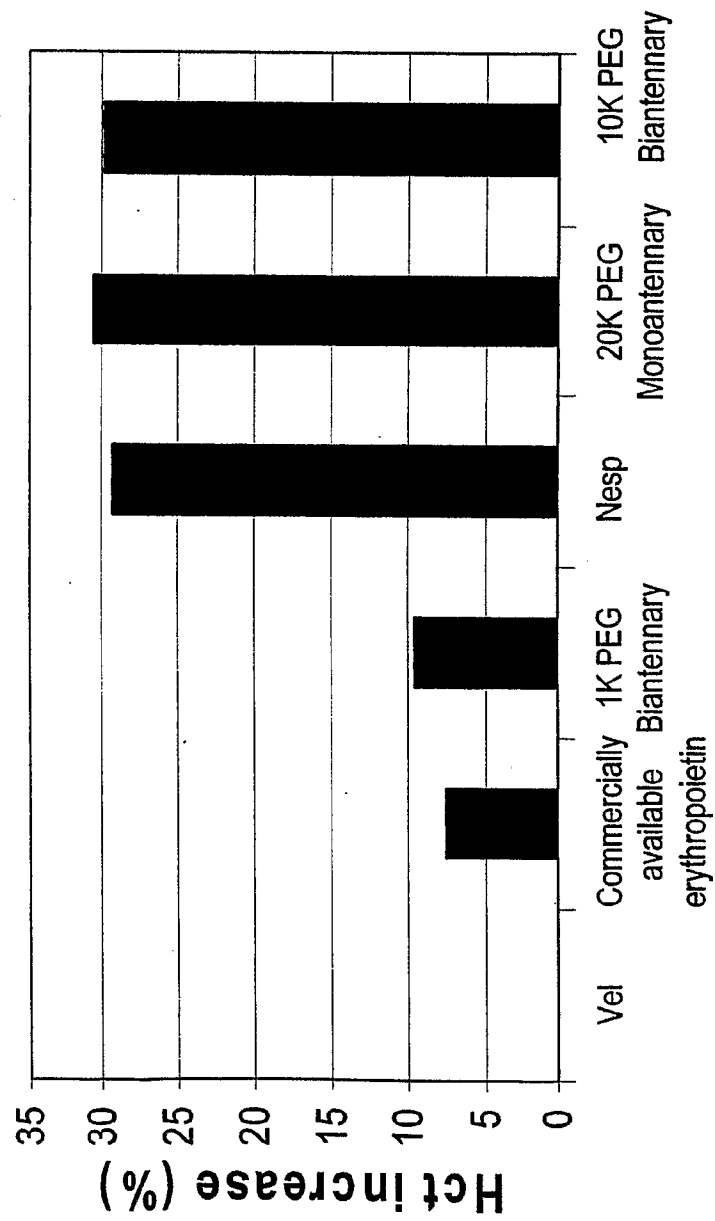


FIG. 138

437/498

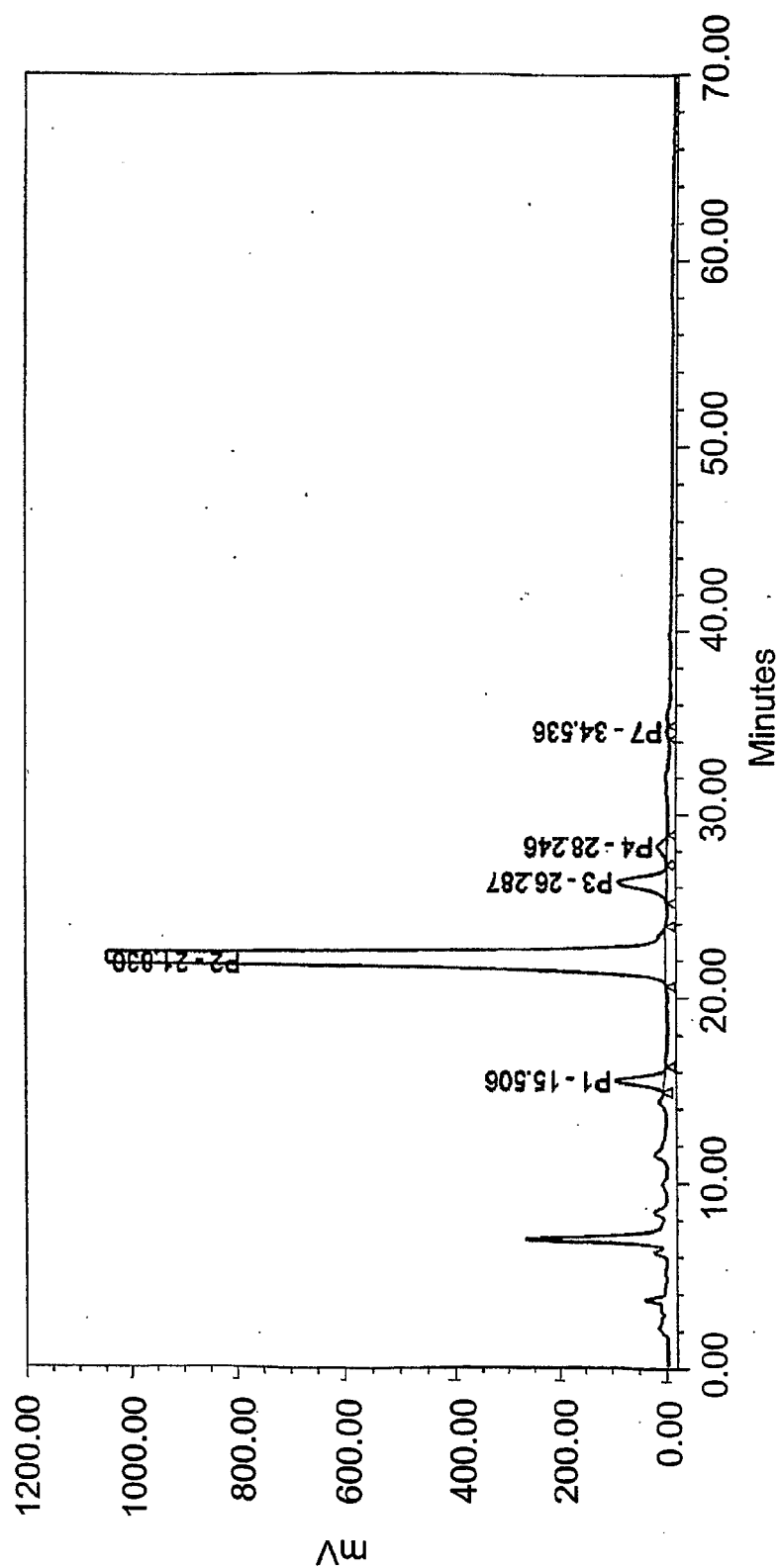


FIG. 139A

438/498

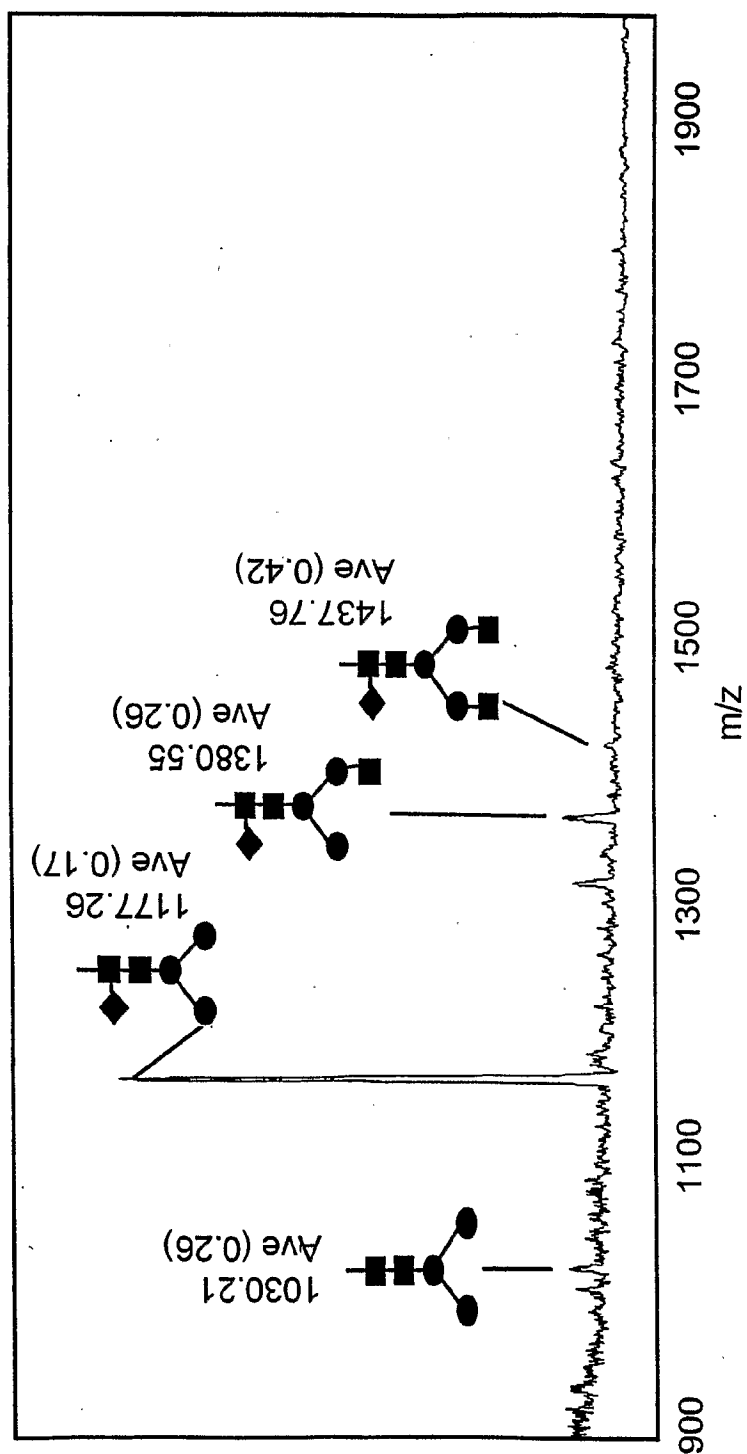


FIG. 139B

439/498

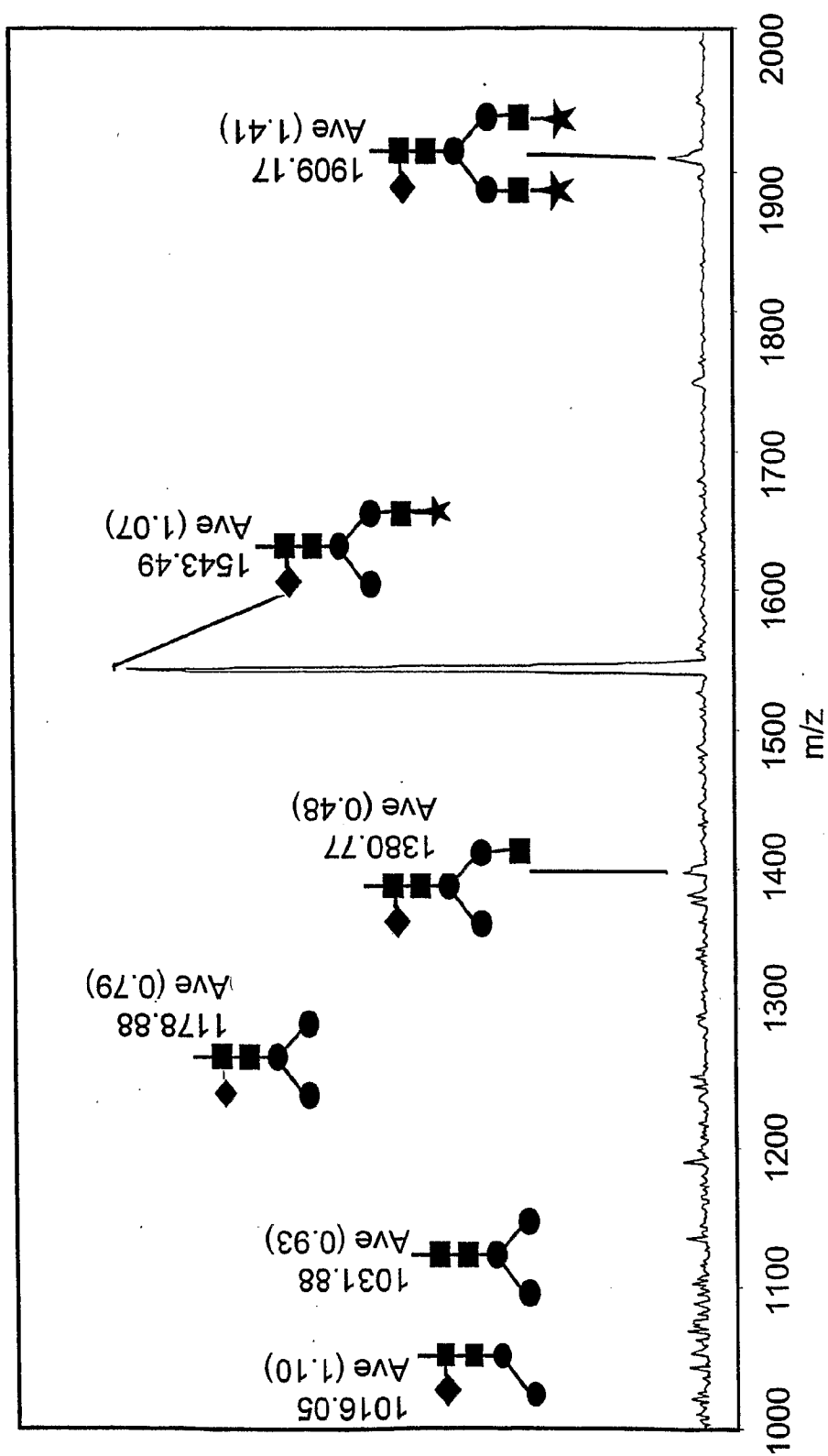


FIG. 140

440/498

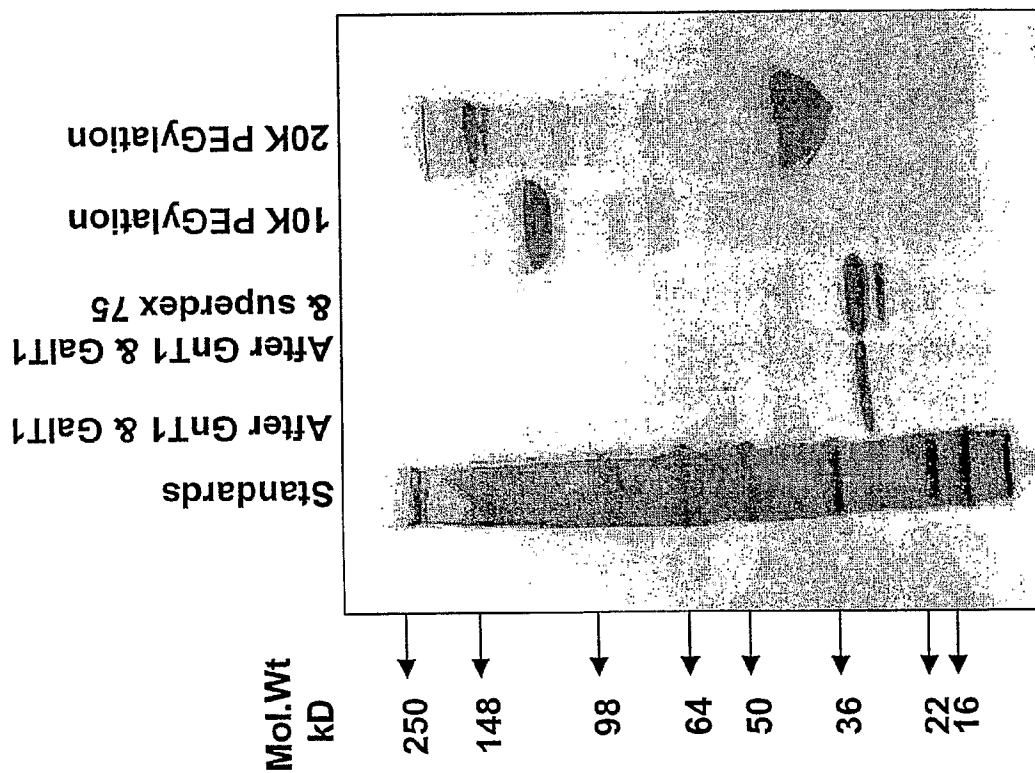


FIG. 141

441/498

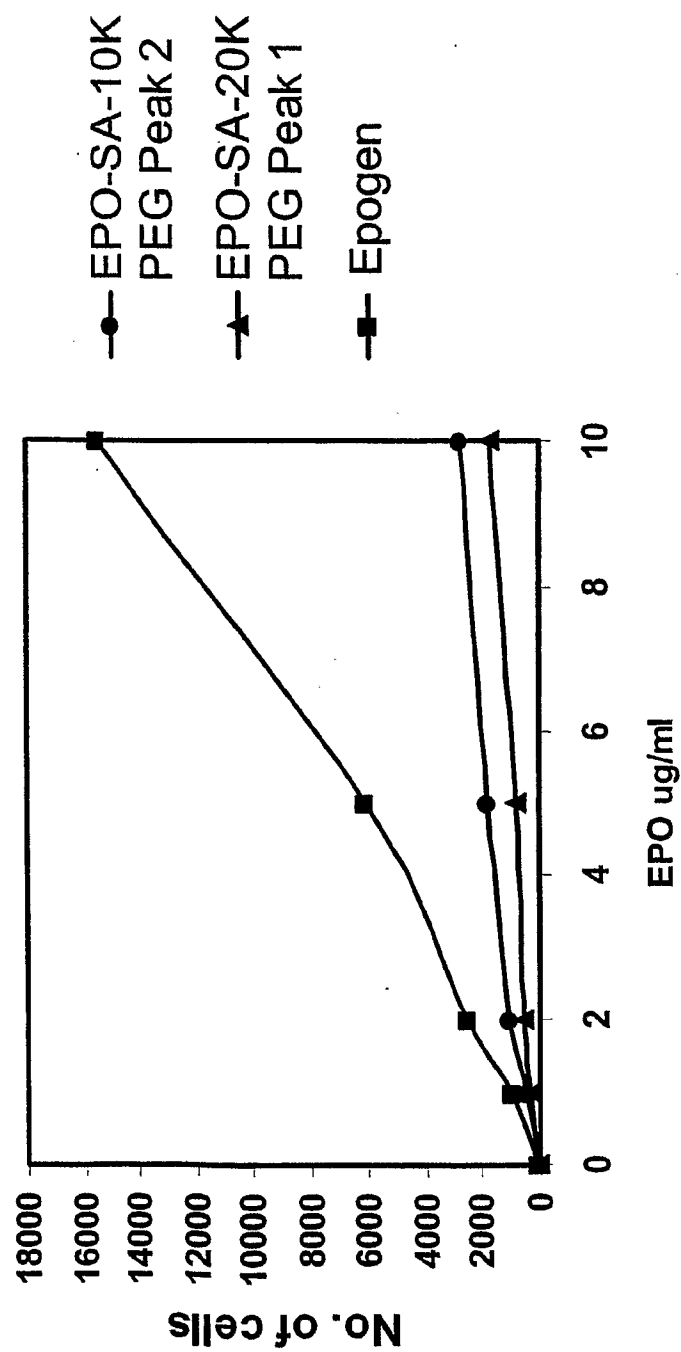


FIG. 142

442/498

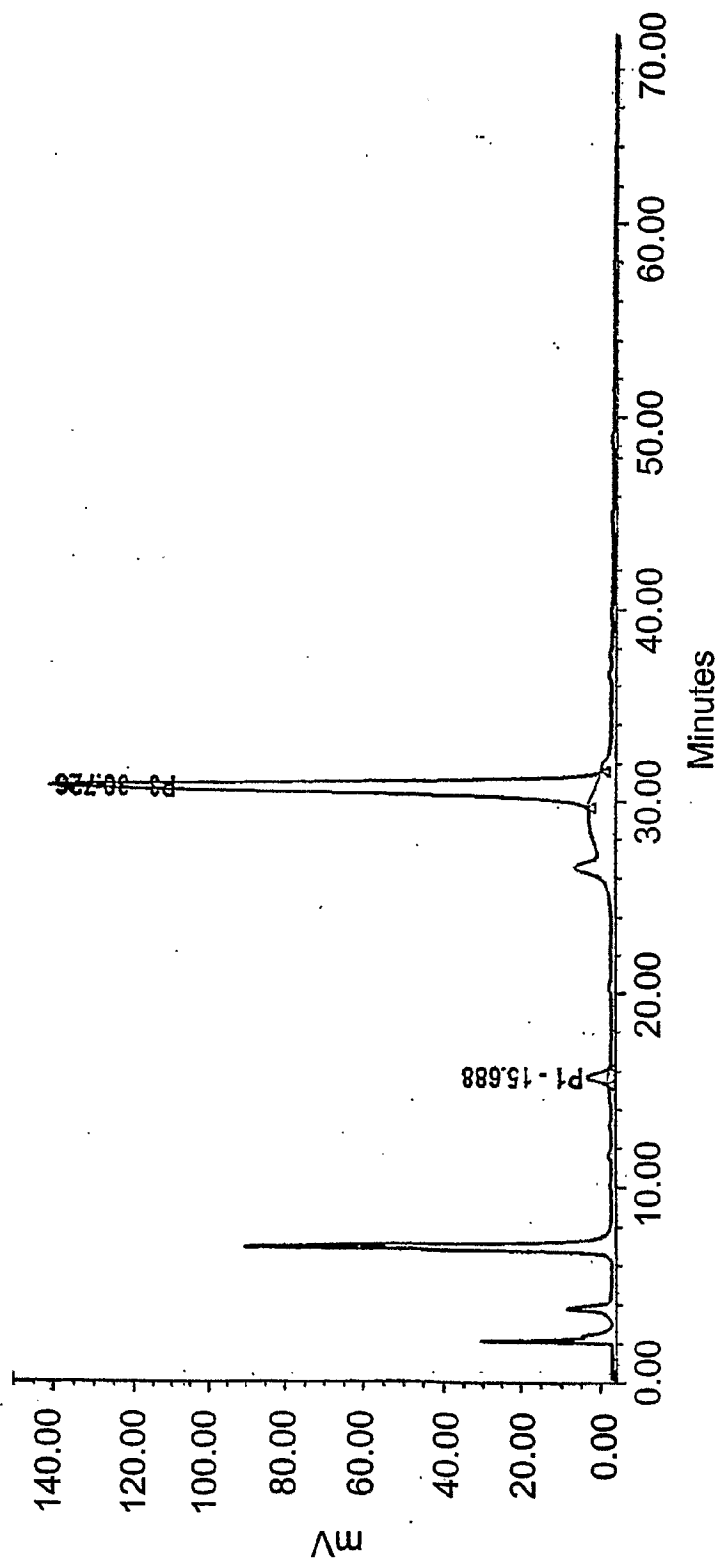


FIG. 143A

443/498

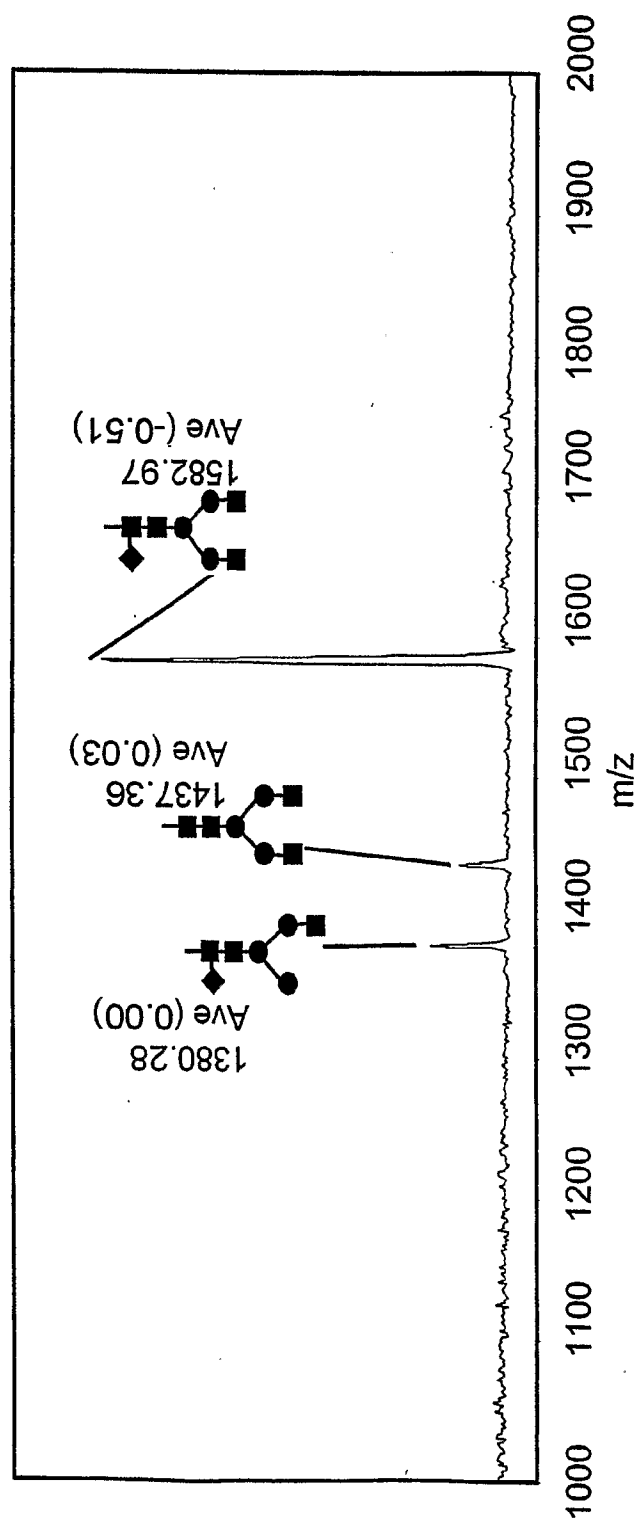


FIG. 143B

444/498

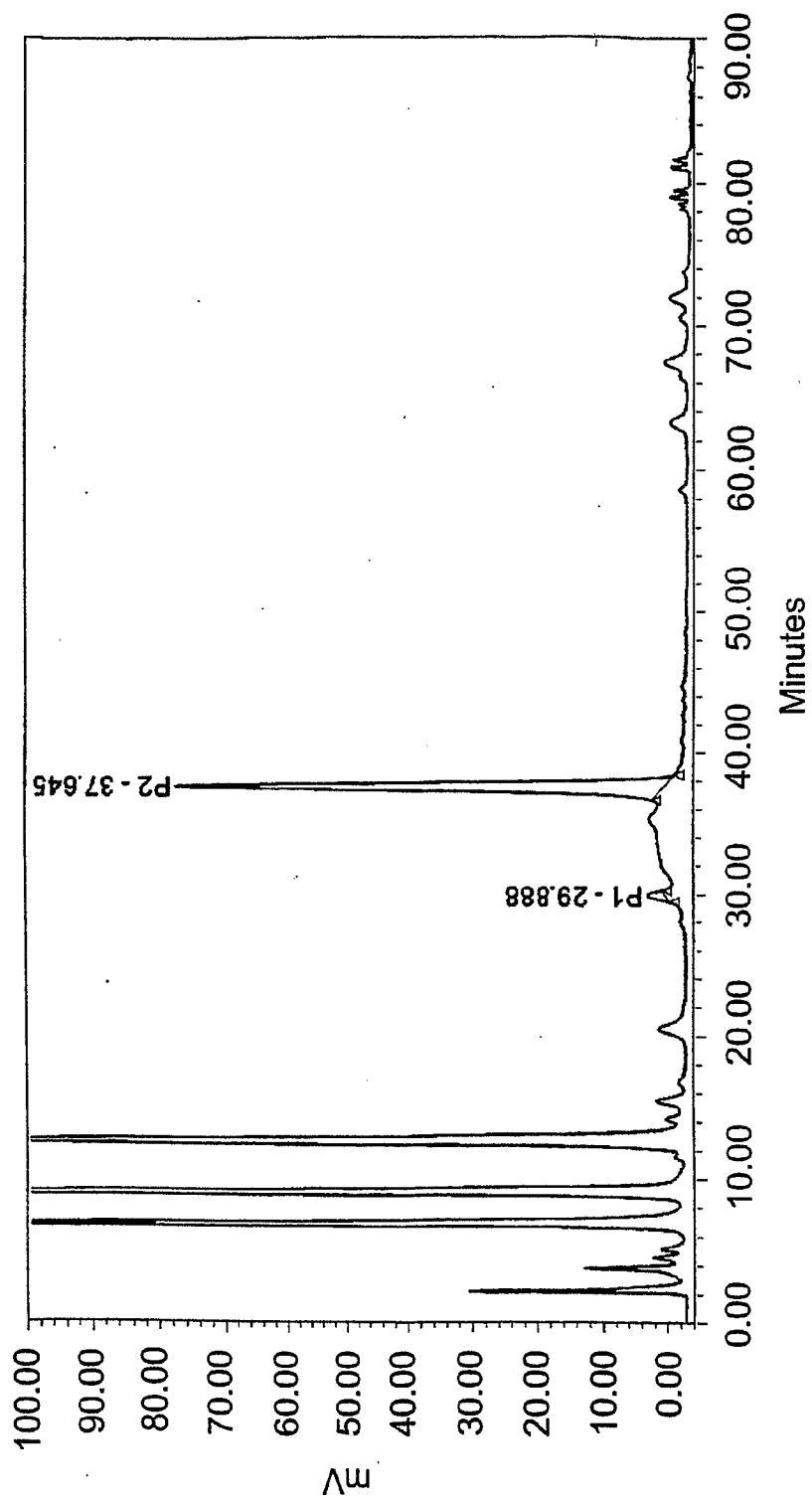


FIG. 144A

445/498

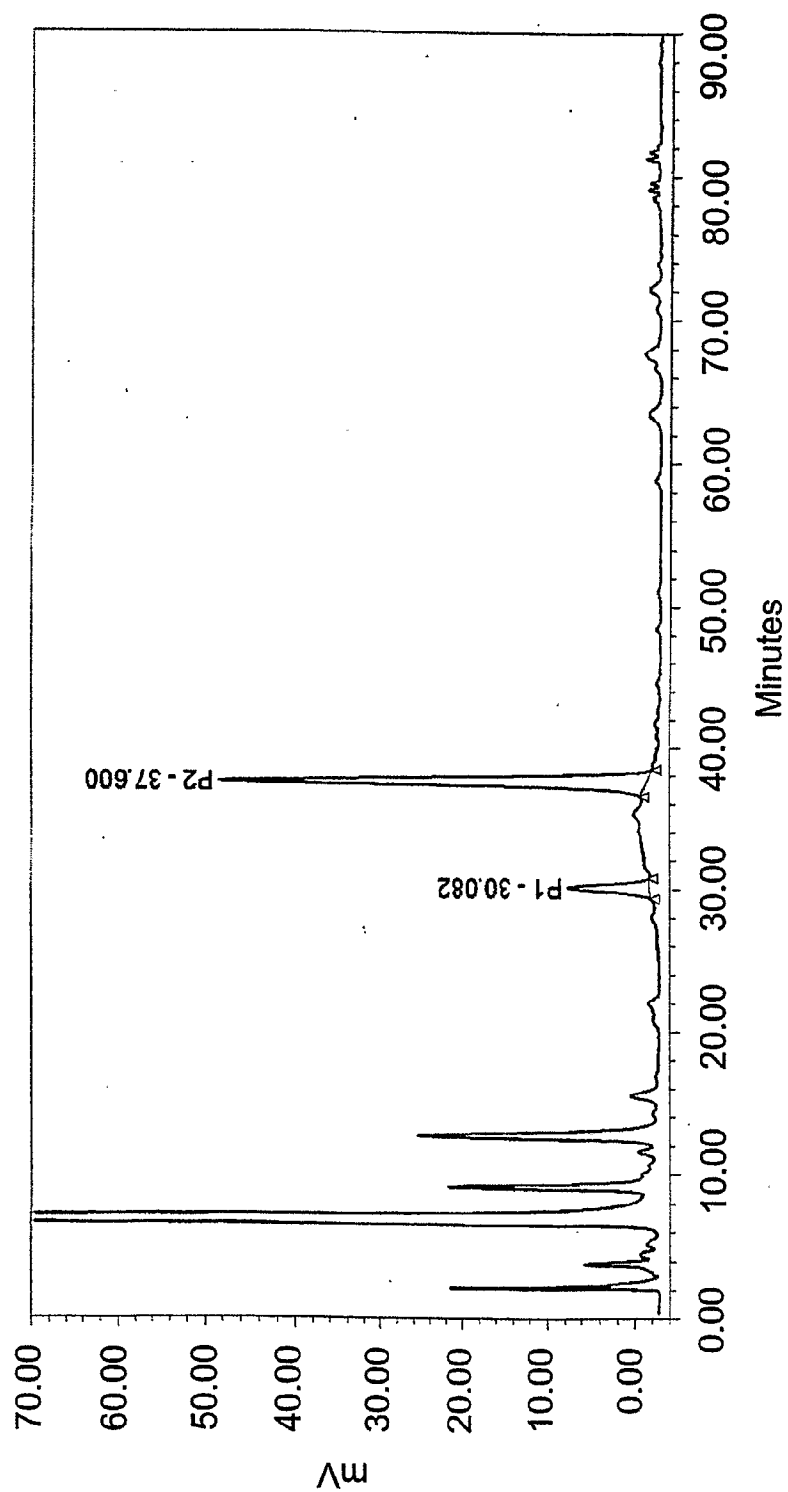


FIG. 144B

446/498

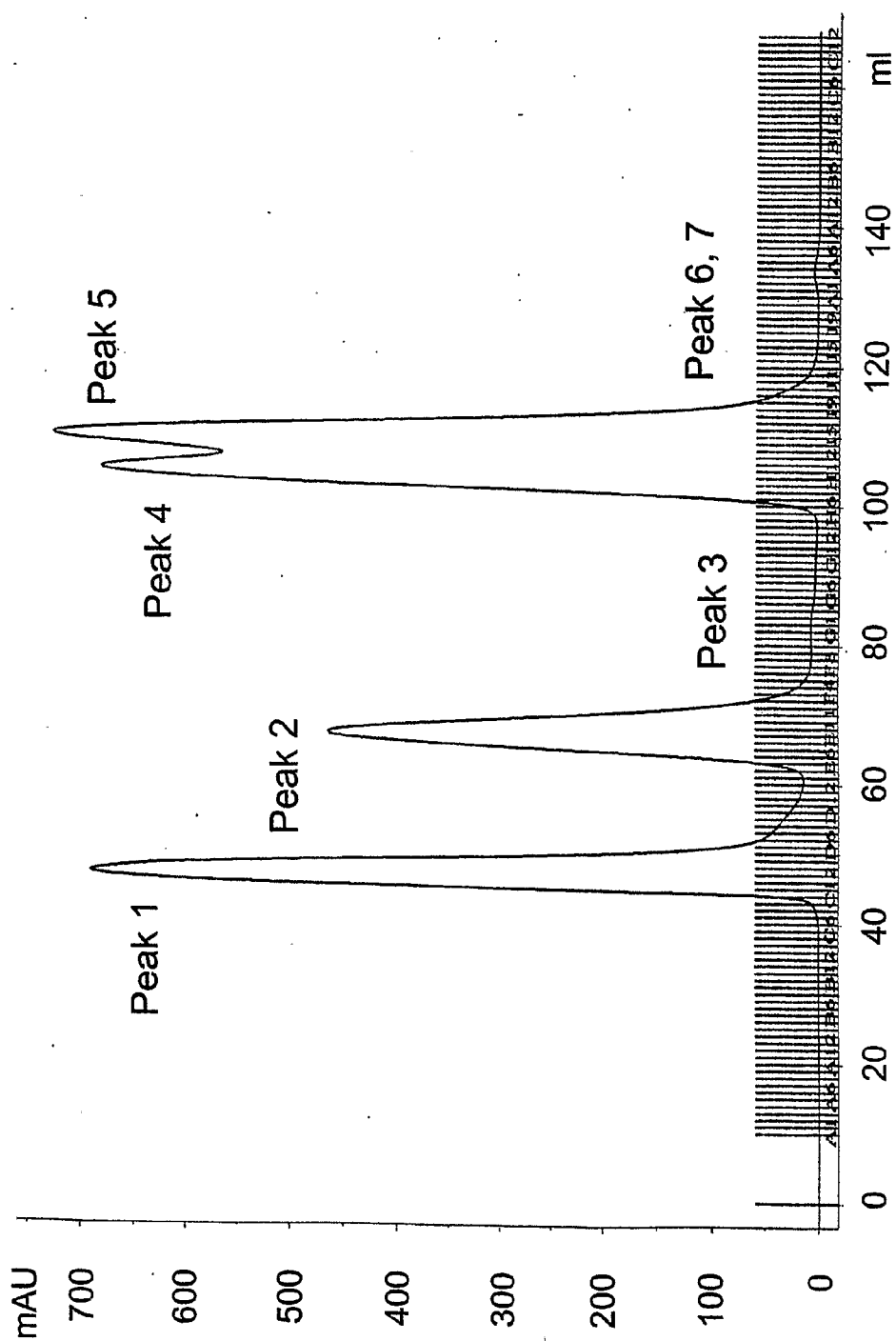


FIG. 145

447/498

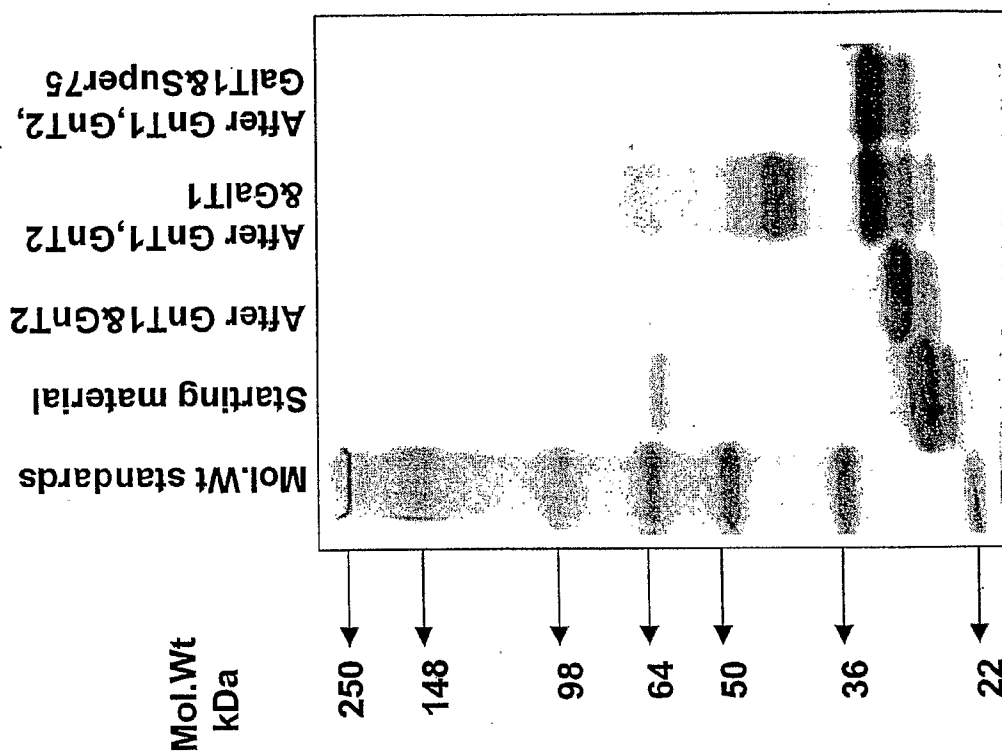


FIG. 146

448/498

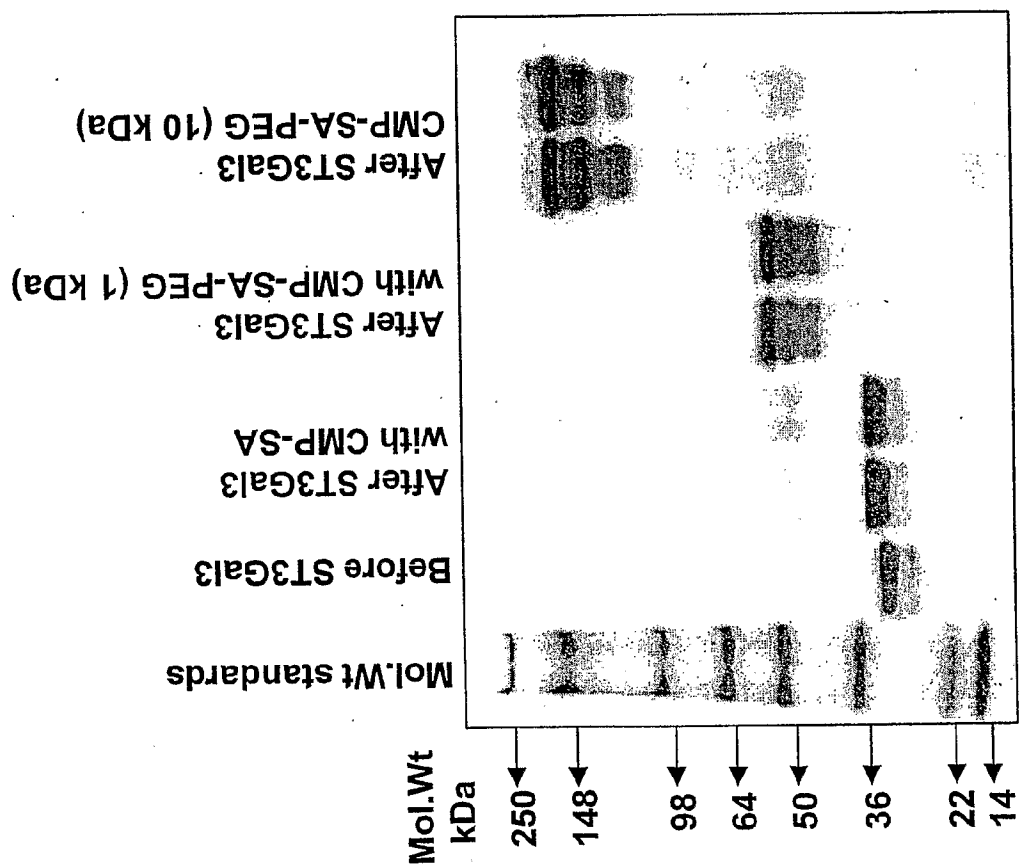


FIG. 147

449/498

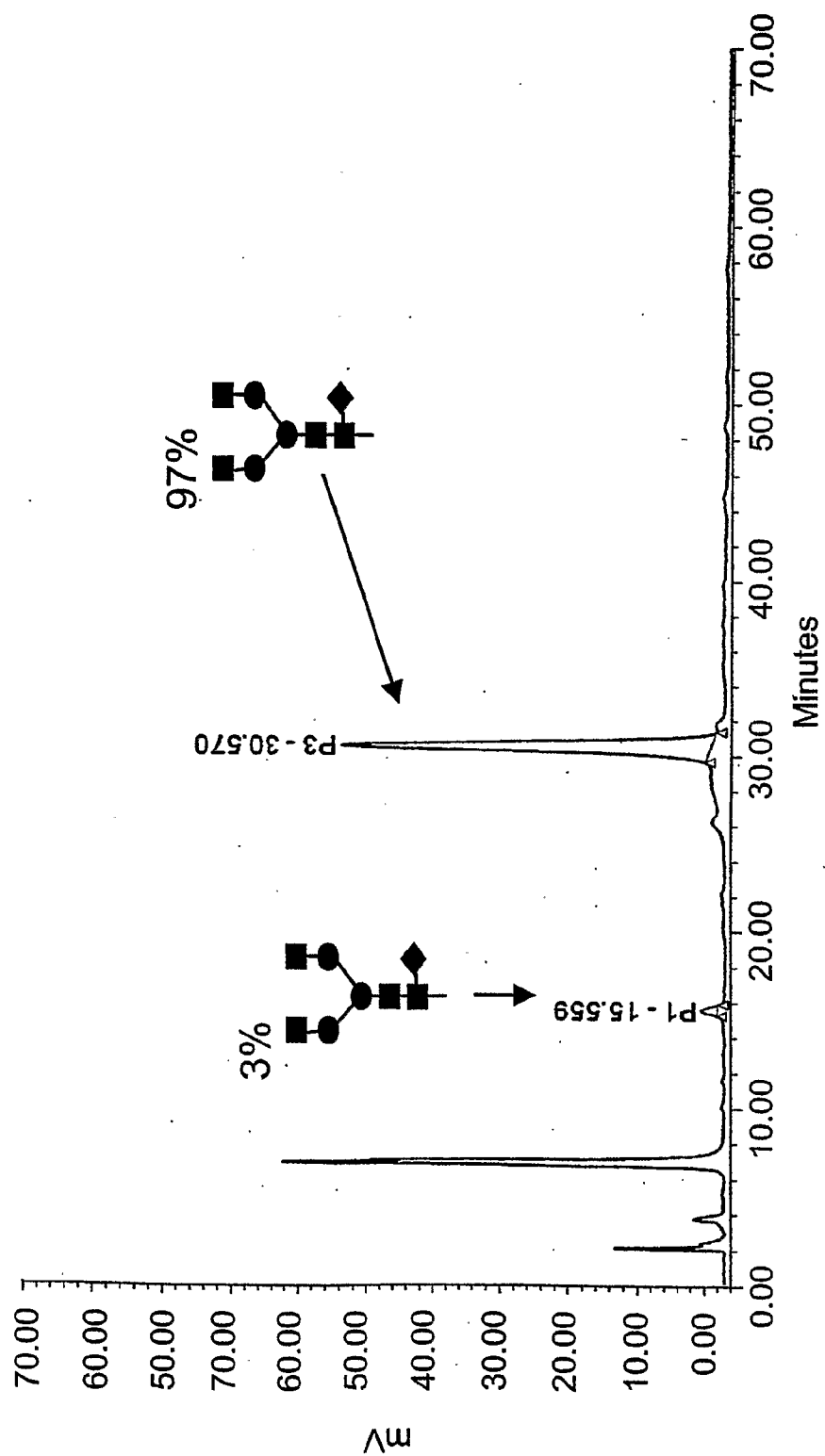


FIG. 148

450/498

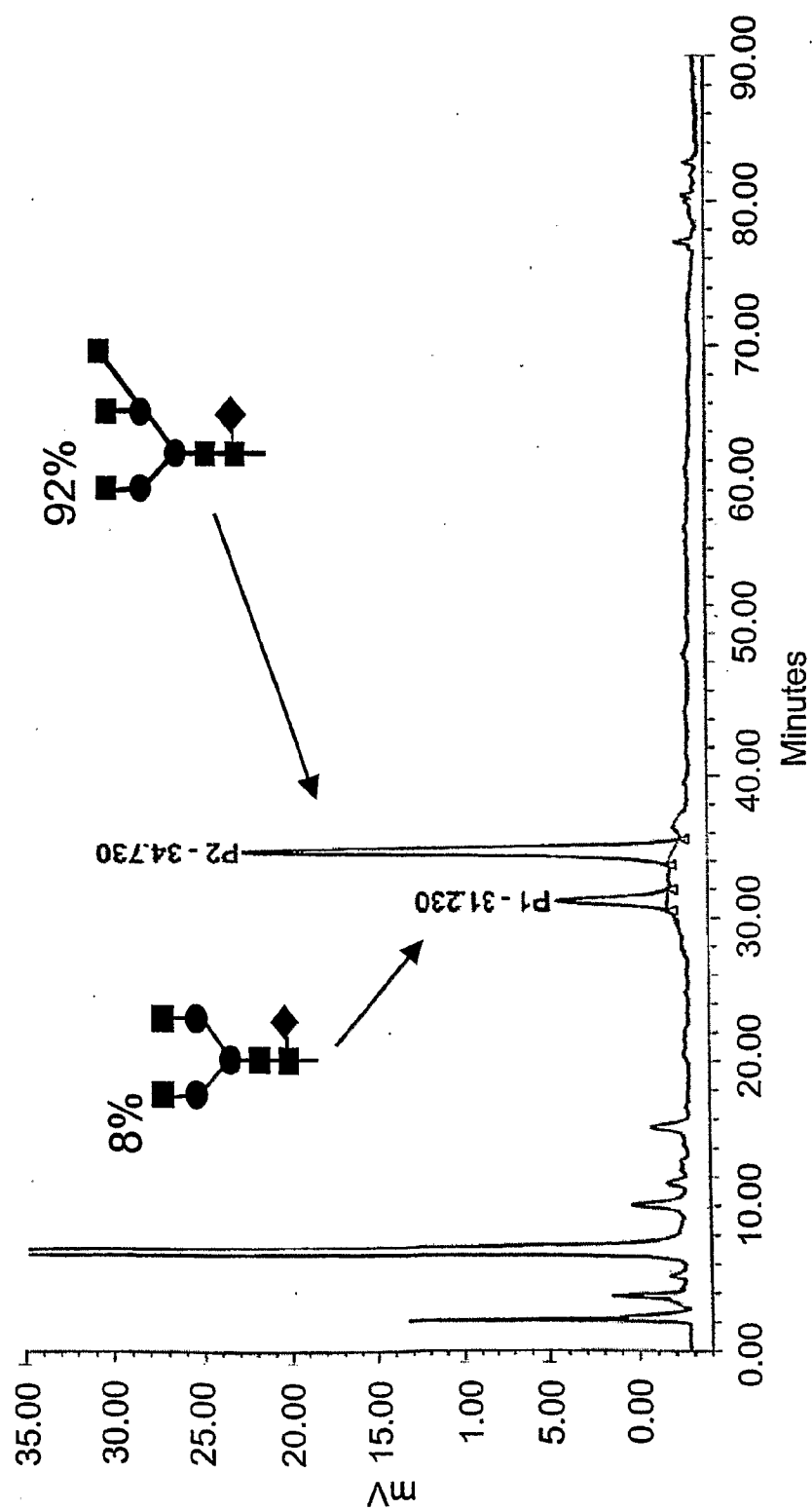


FIG. 149

451/498

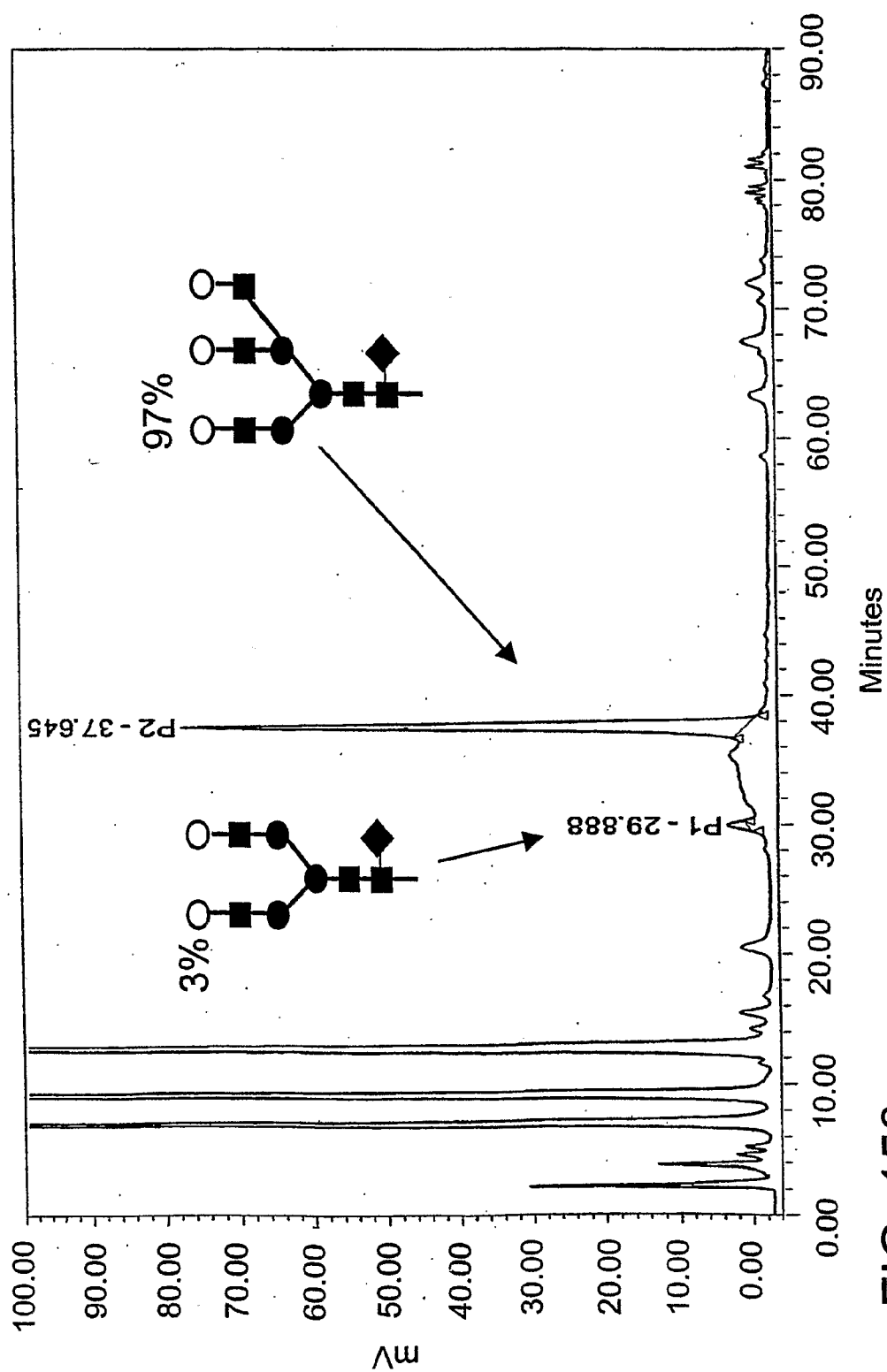


FIG. 150

452/498

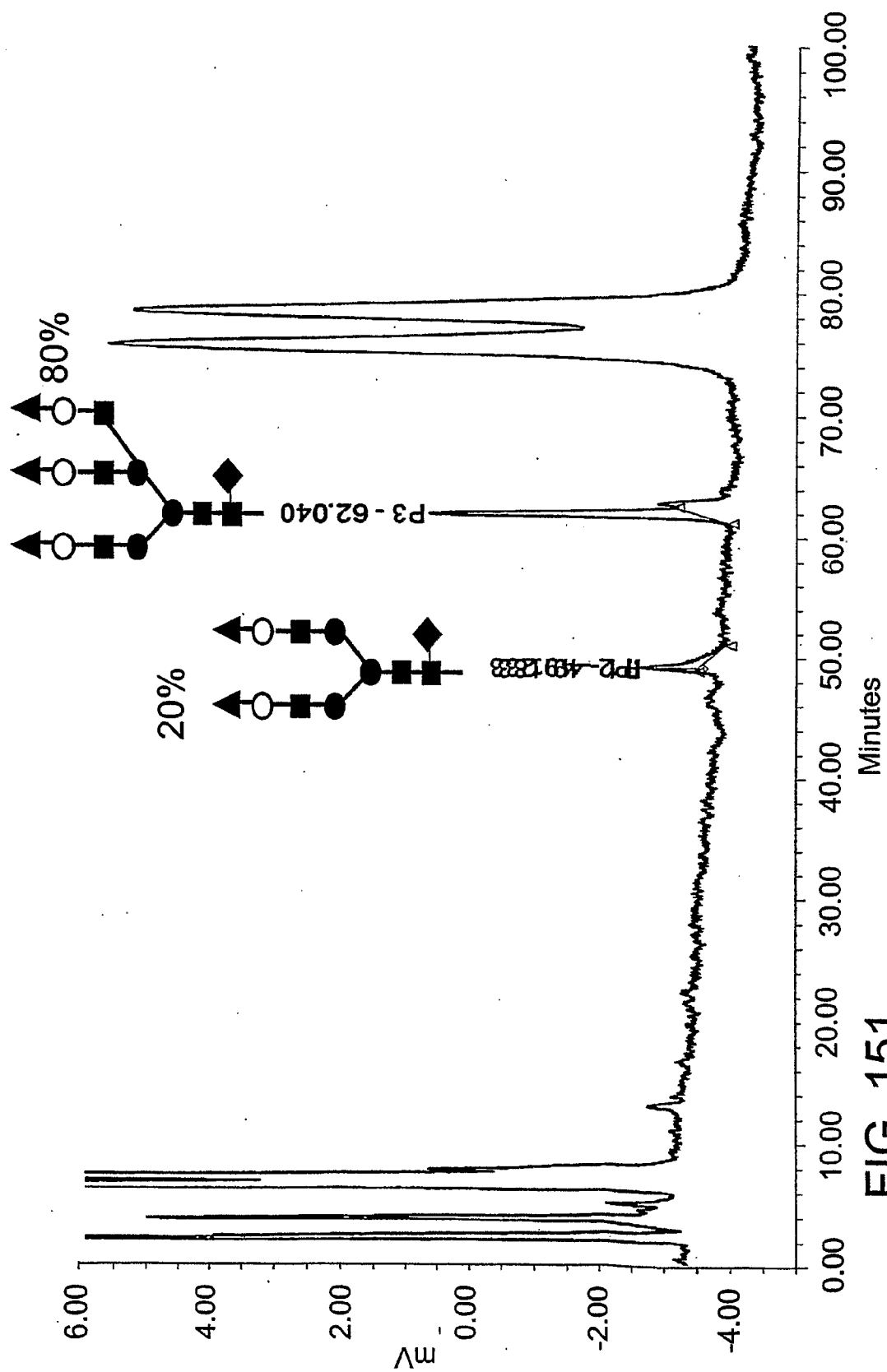


FIG. 151

453/498

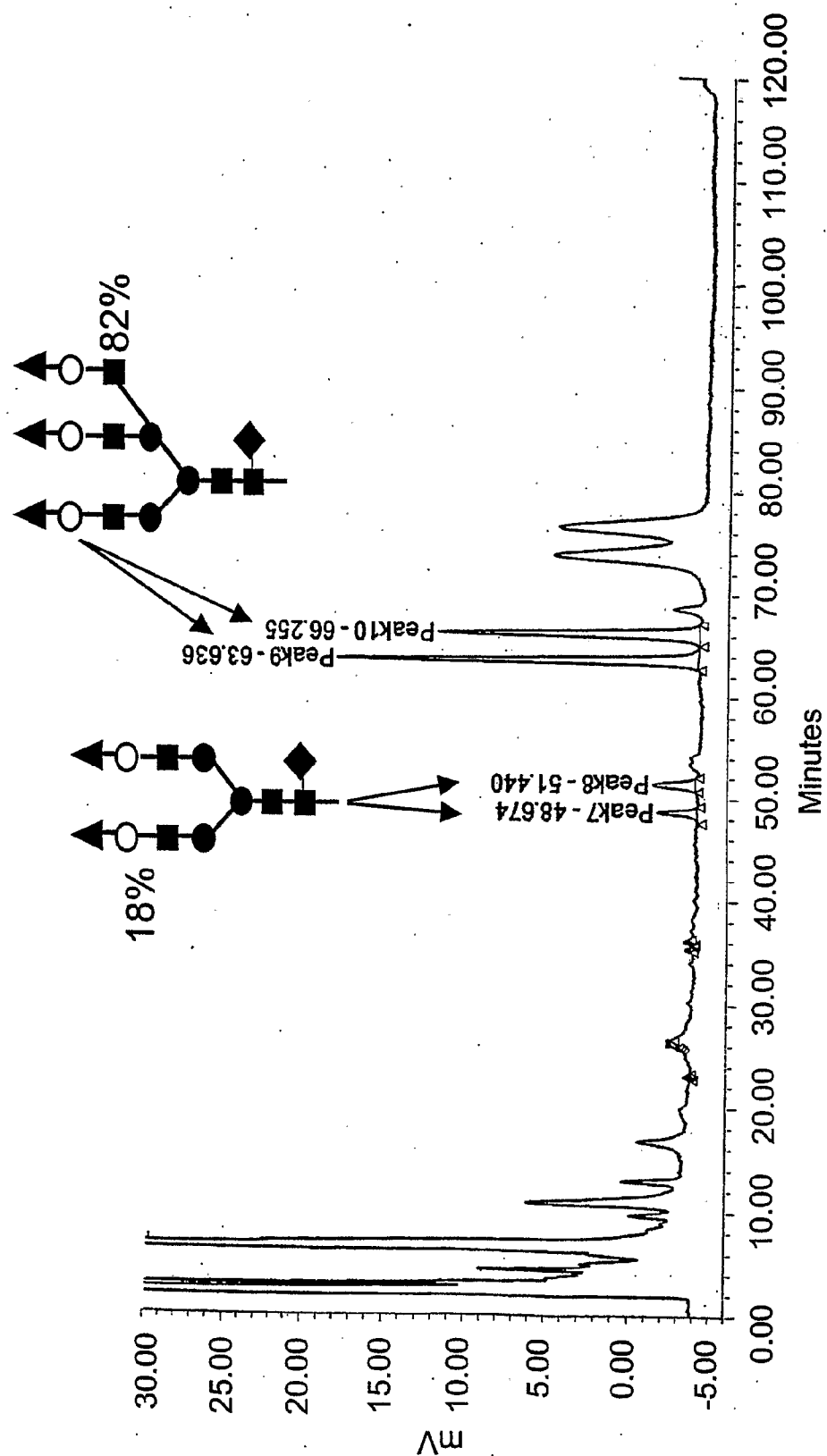


FIG. 152

454/498

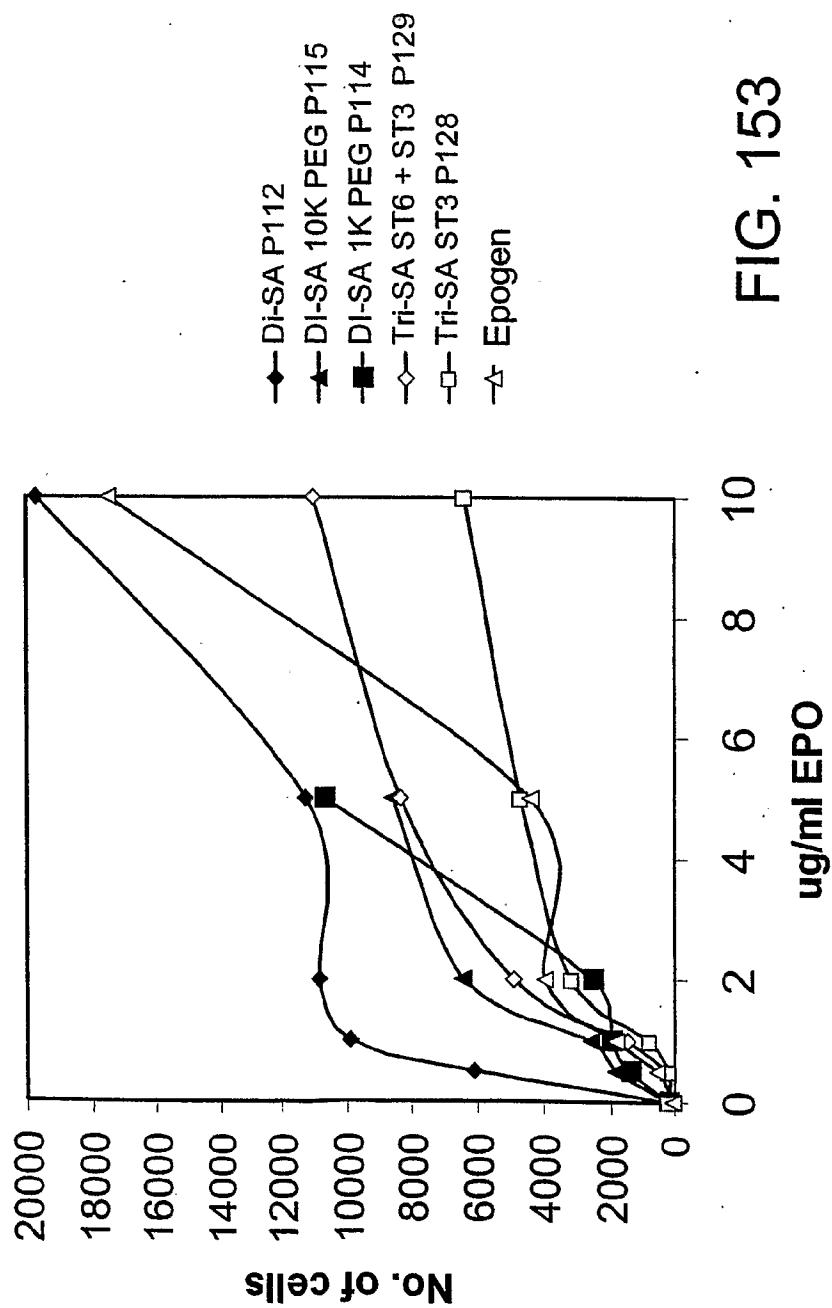


FIG. 153

455/498

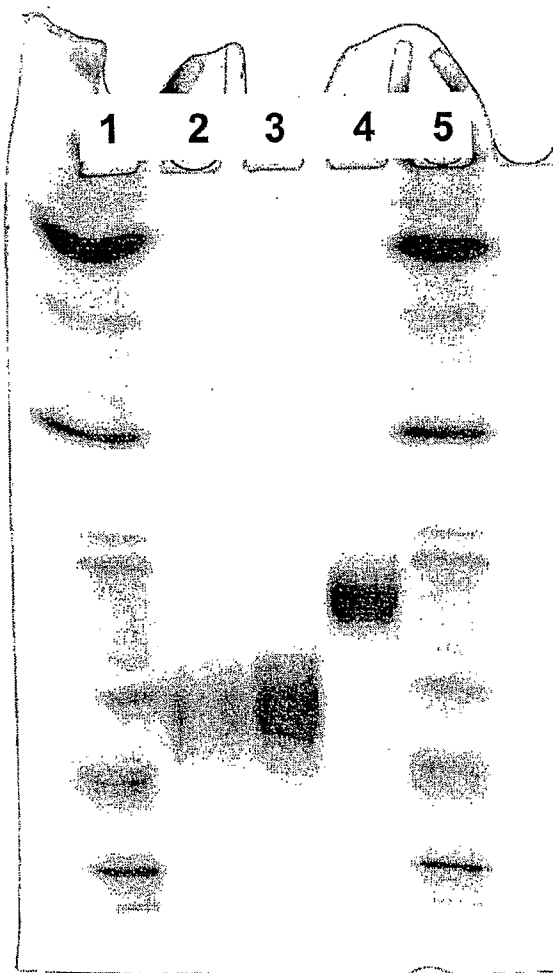


FIG. 154

456/498

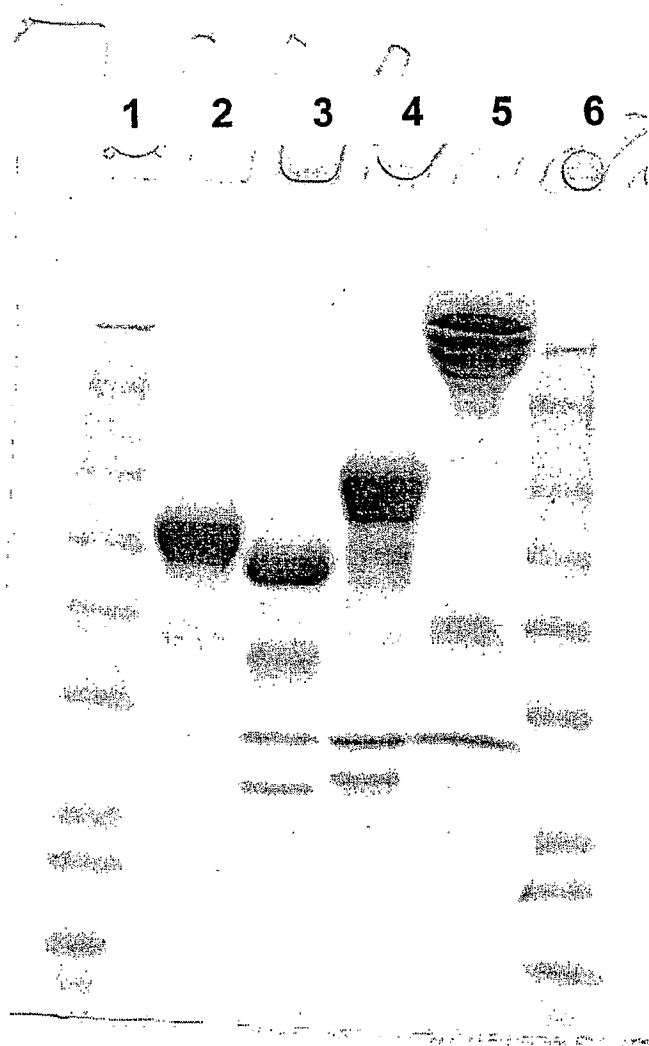


FIG. 155

457/498

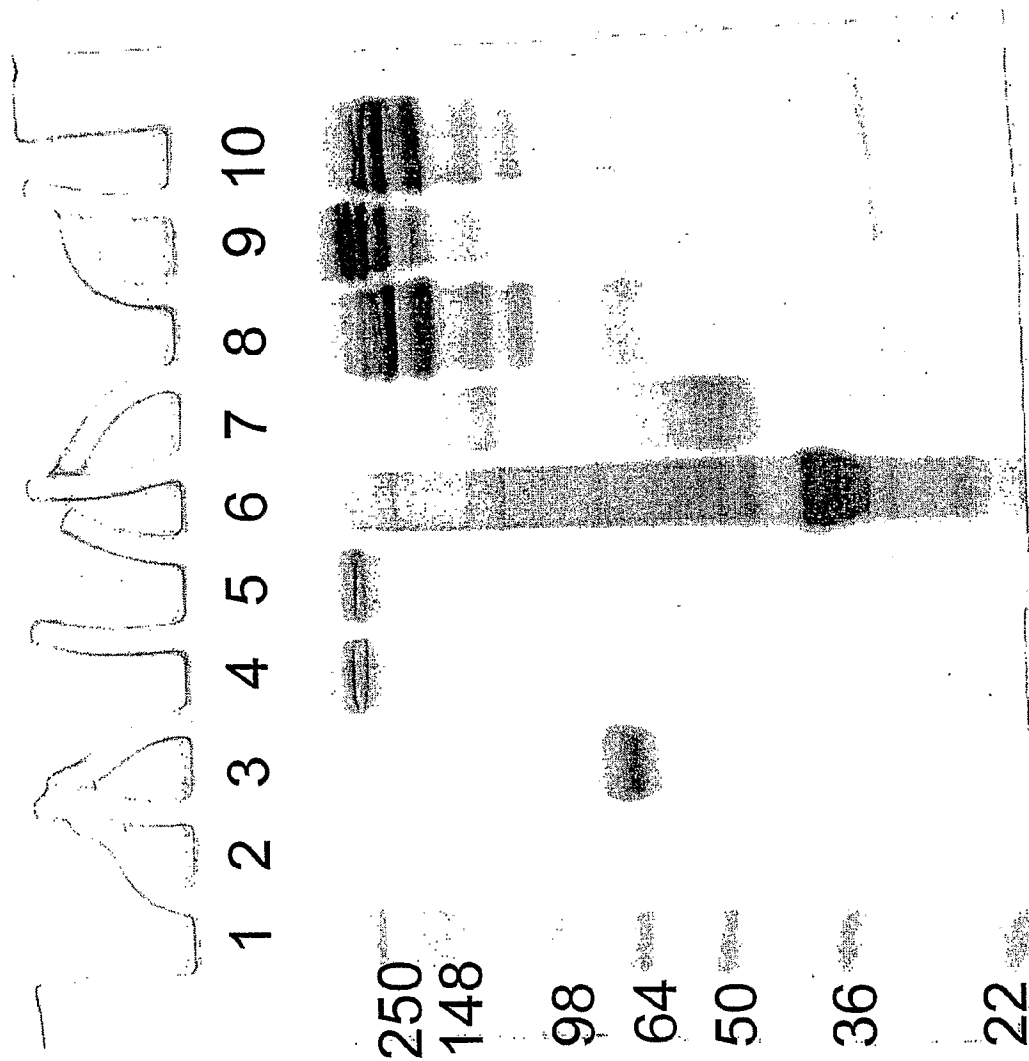


FIG. 156

458/498

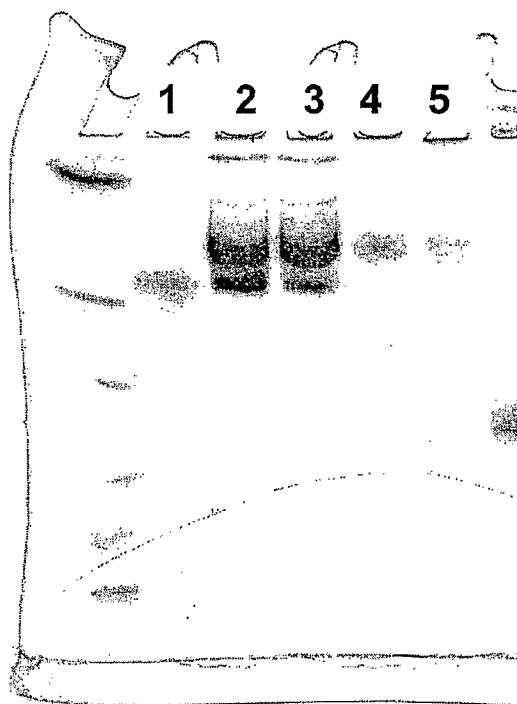


FIG. 157

459/498

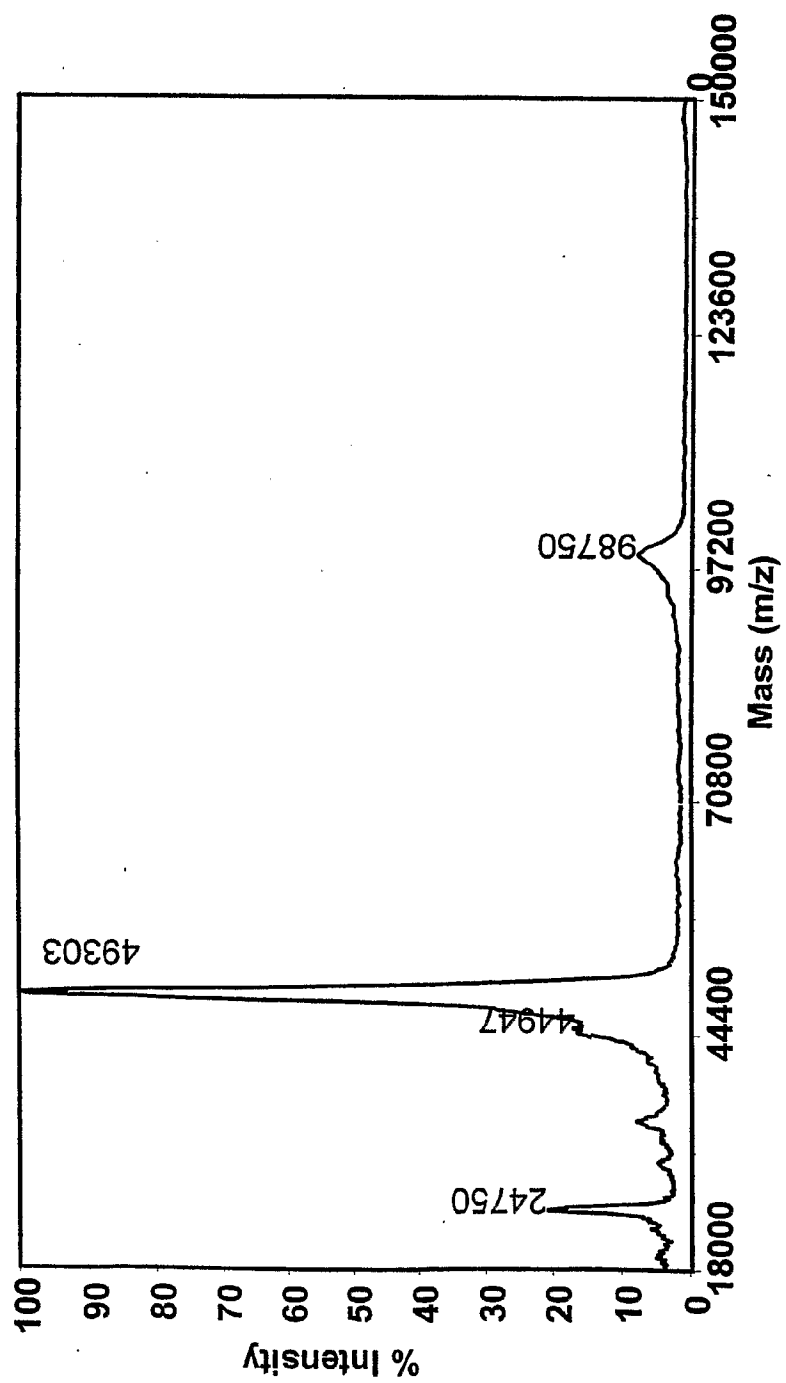


FIG. 158

460/498

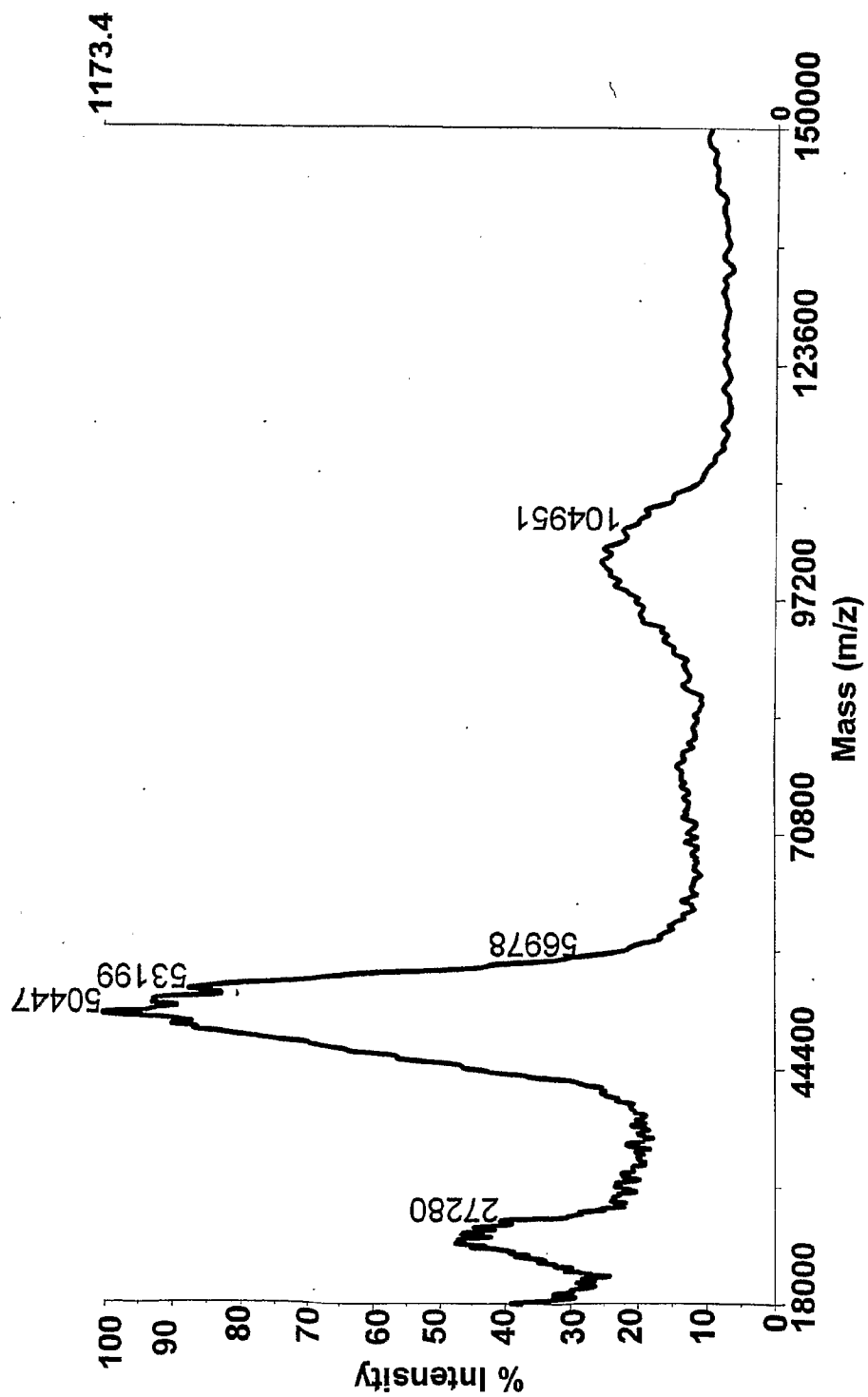


FIG. 159

461/498

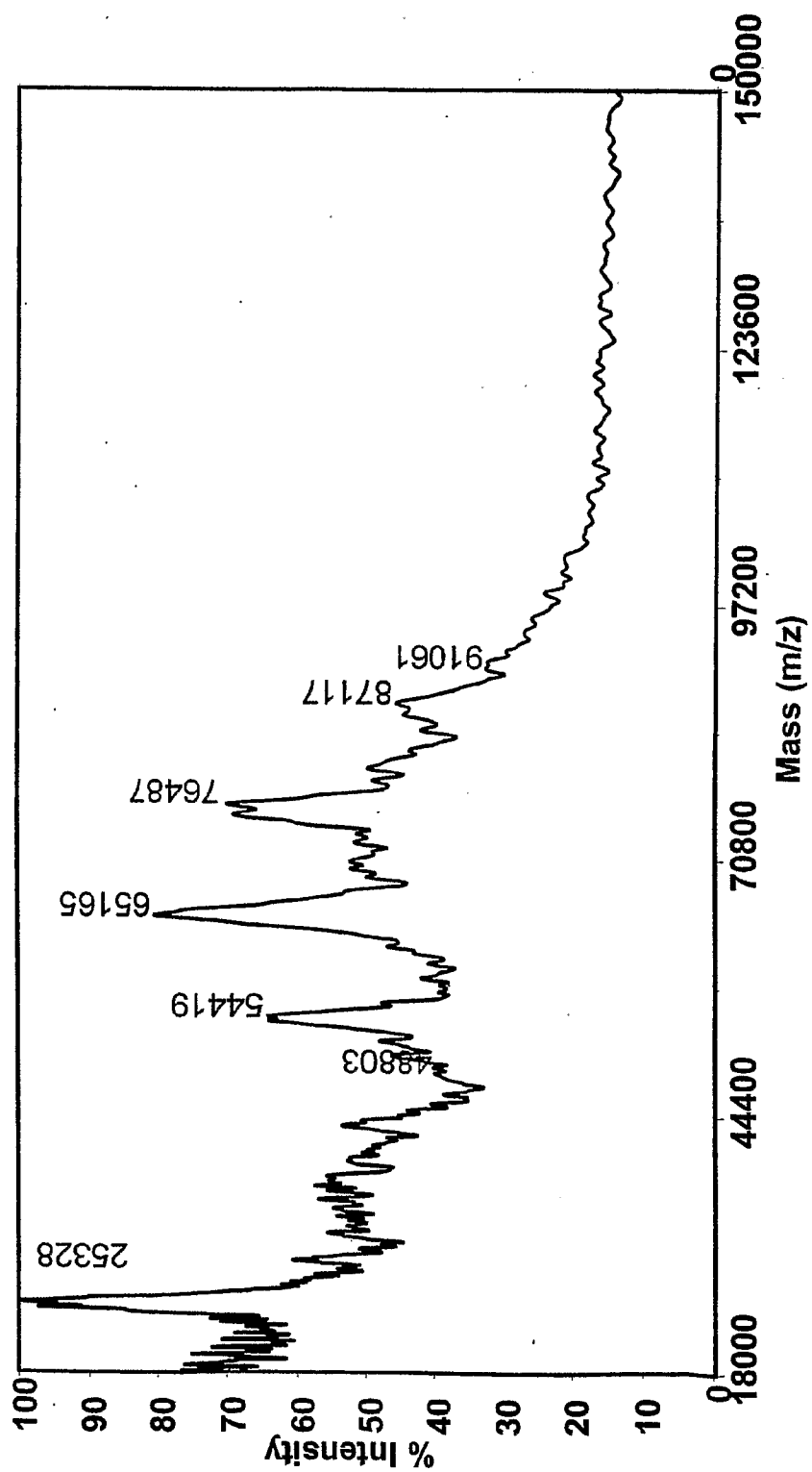


FIG. 160

462/498

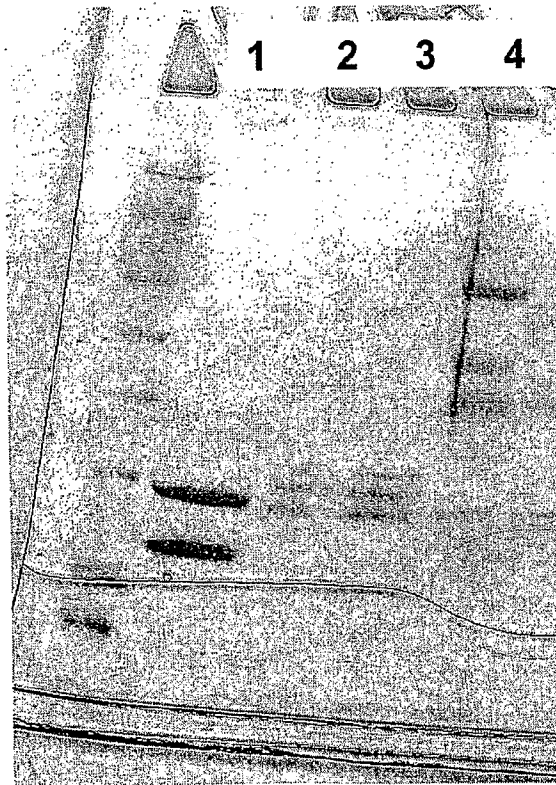


FIG. 161

463/498

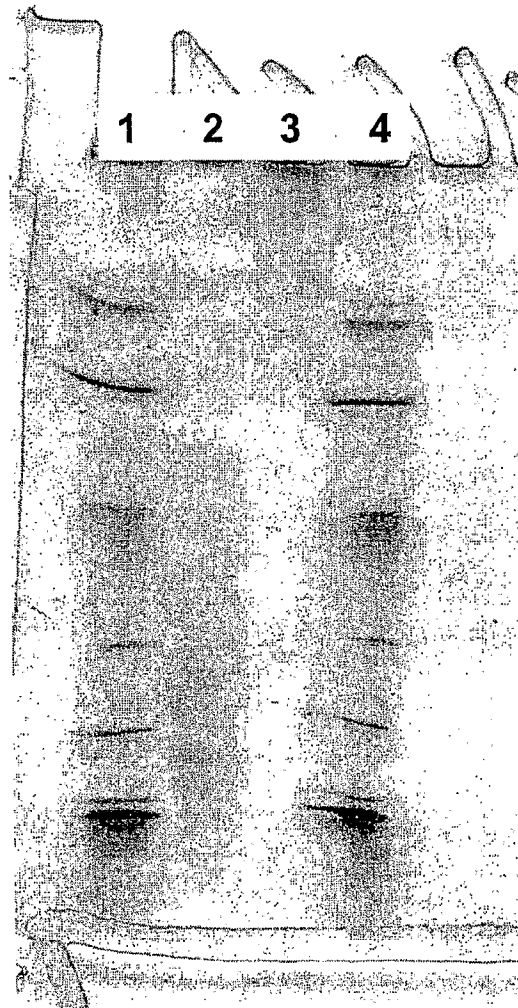


FIG. 162

464/498

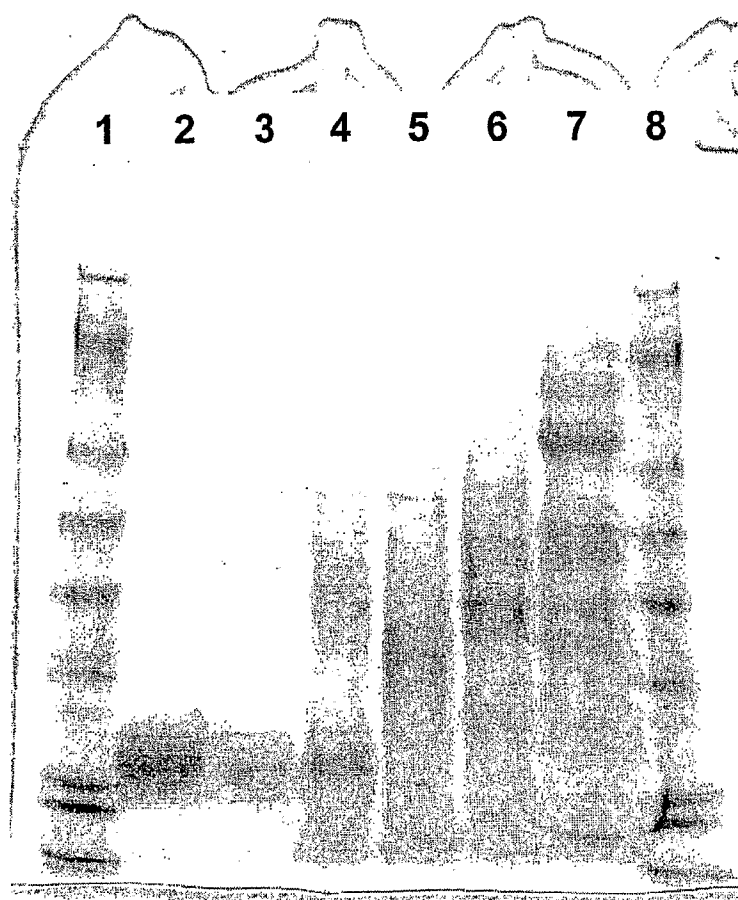


FIG. 163

465/498



FIG. 164

466/498

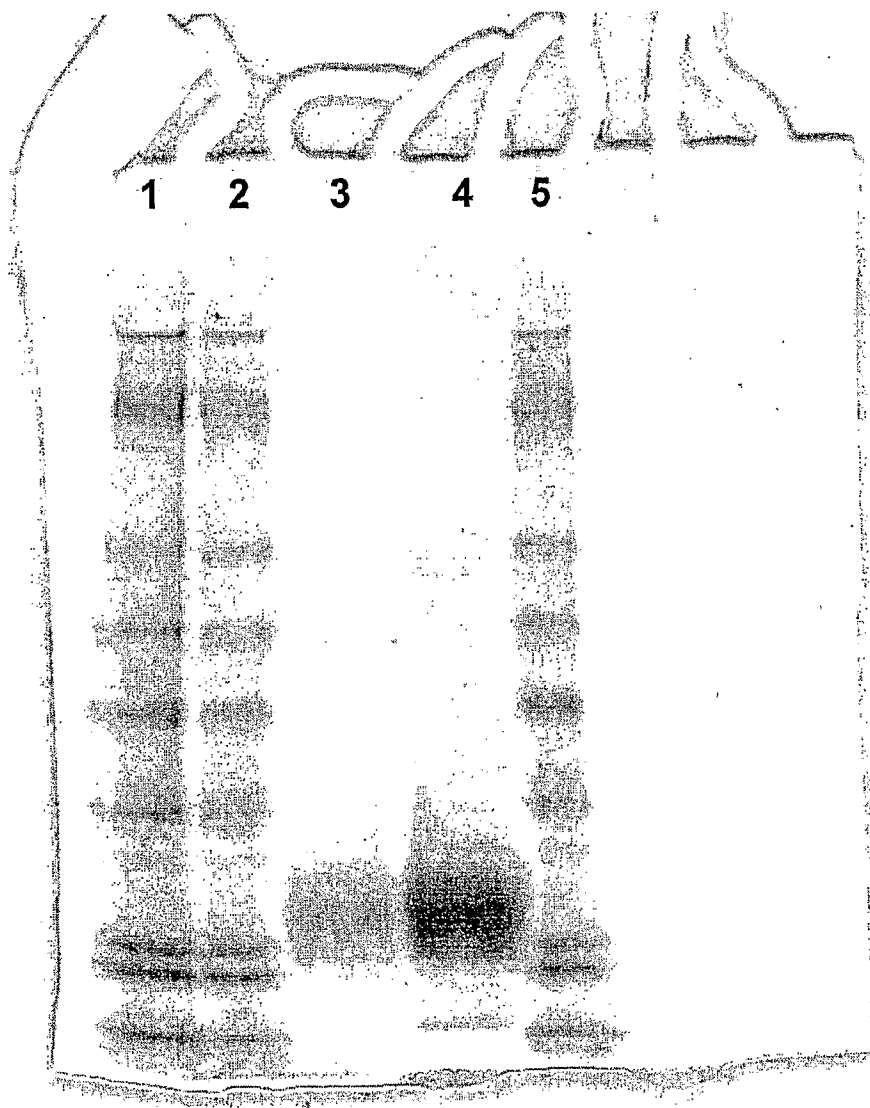


FIG. 165

467/498

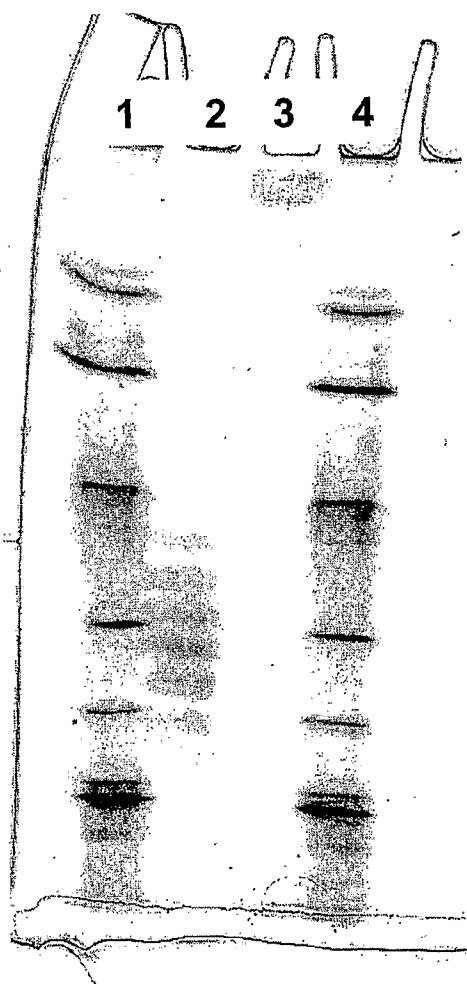


FIG. 166

468/498

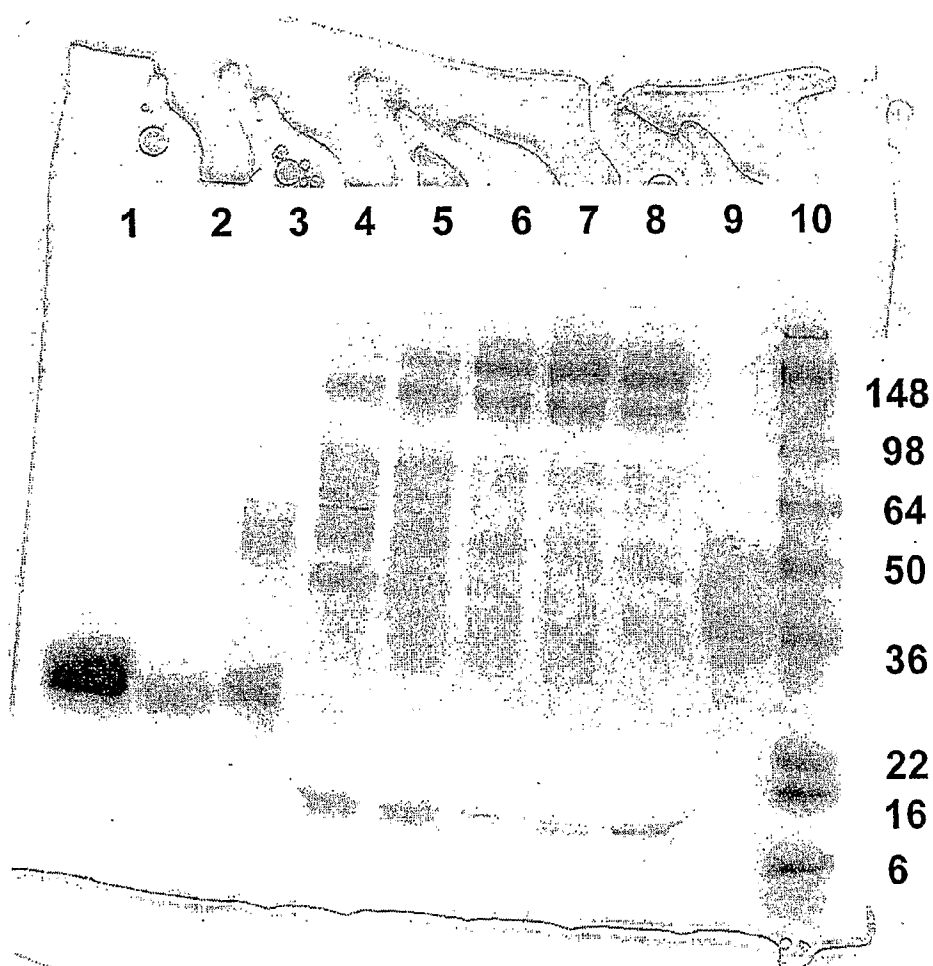


FIG. 167

469/498

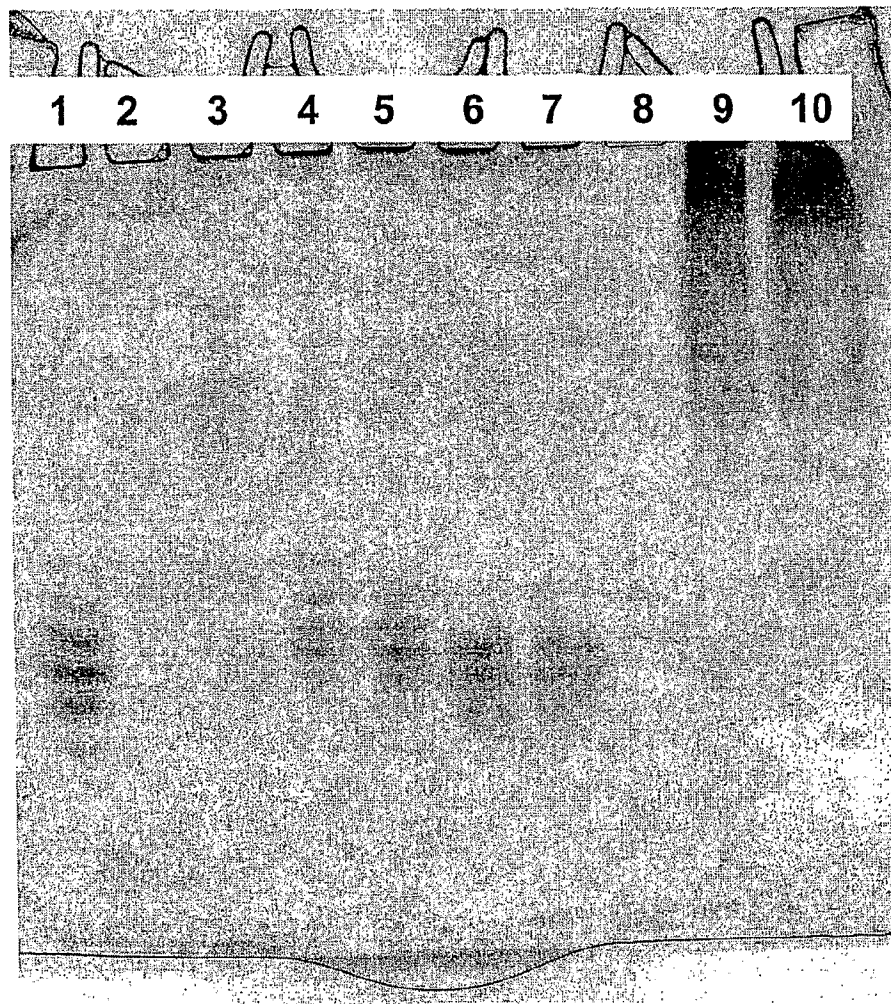


FIG. 168

470/498

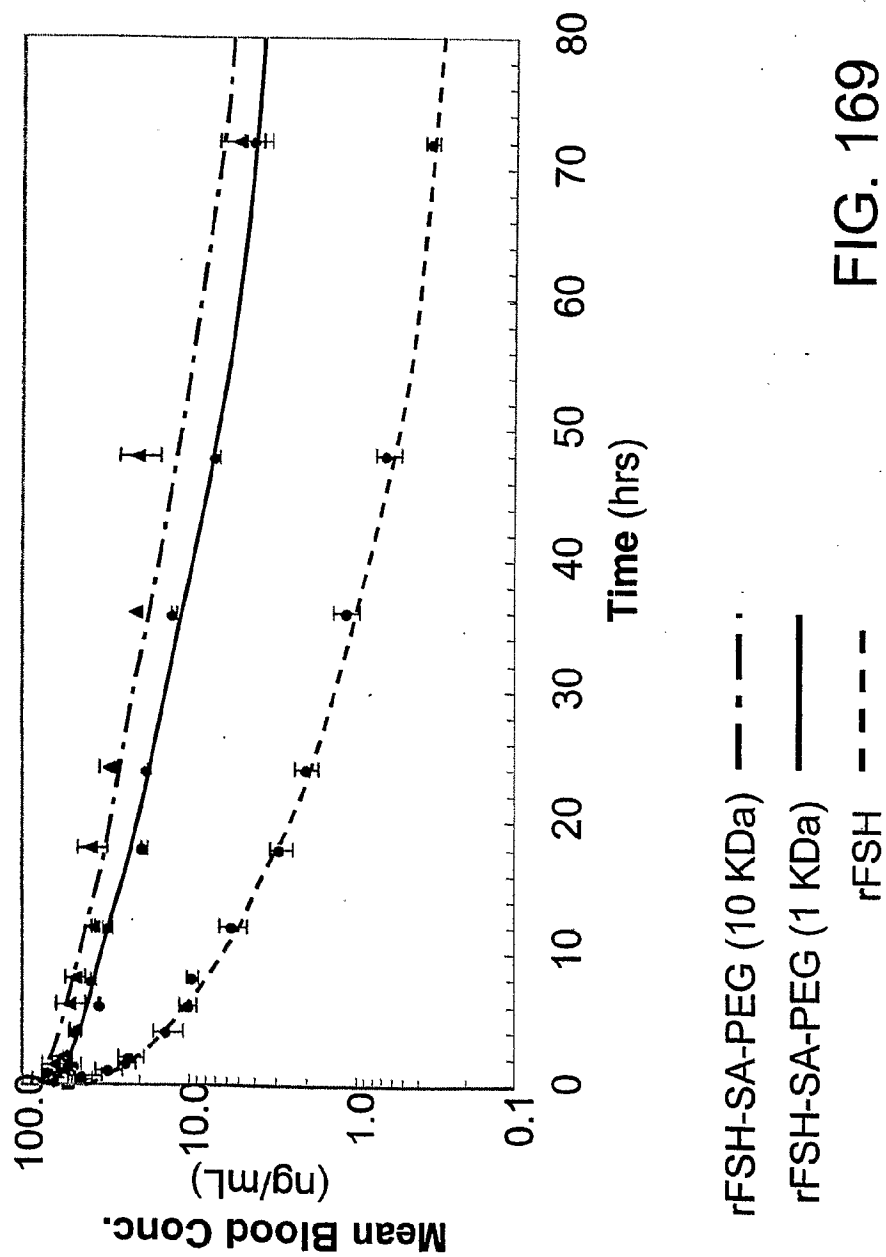


FIG. 169

471/498

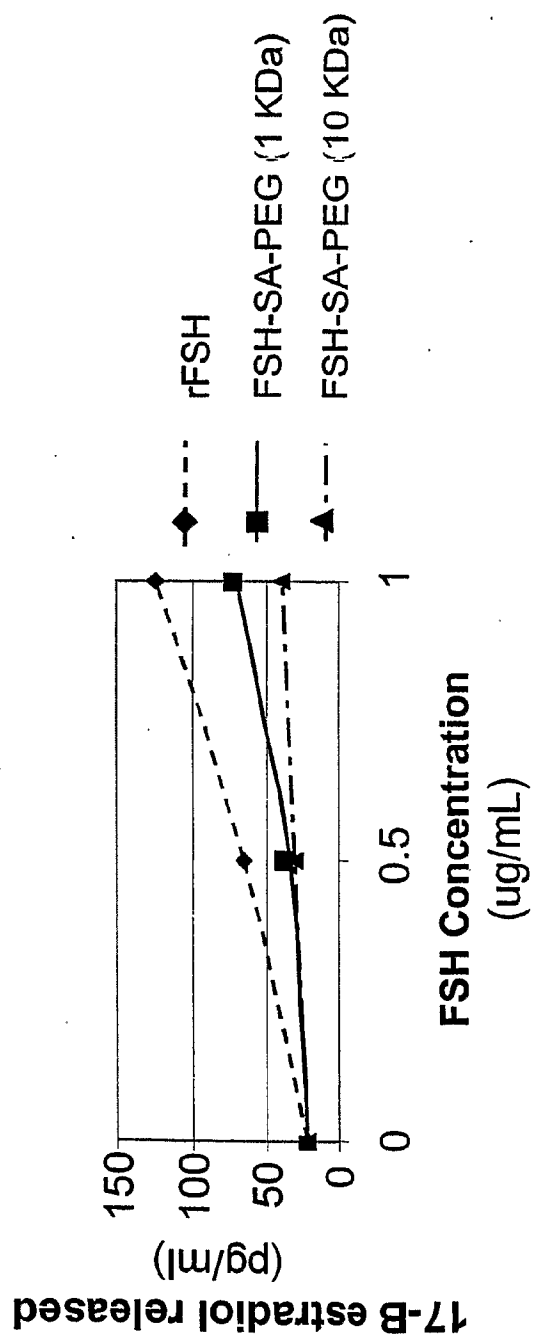


FIG. 170

472/498

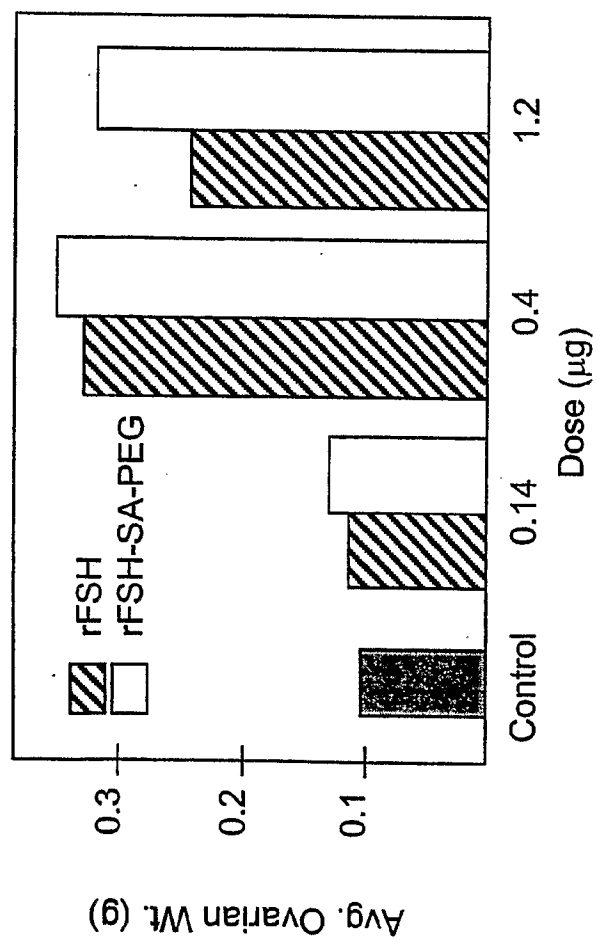


FIG. 171

473/498

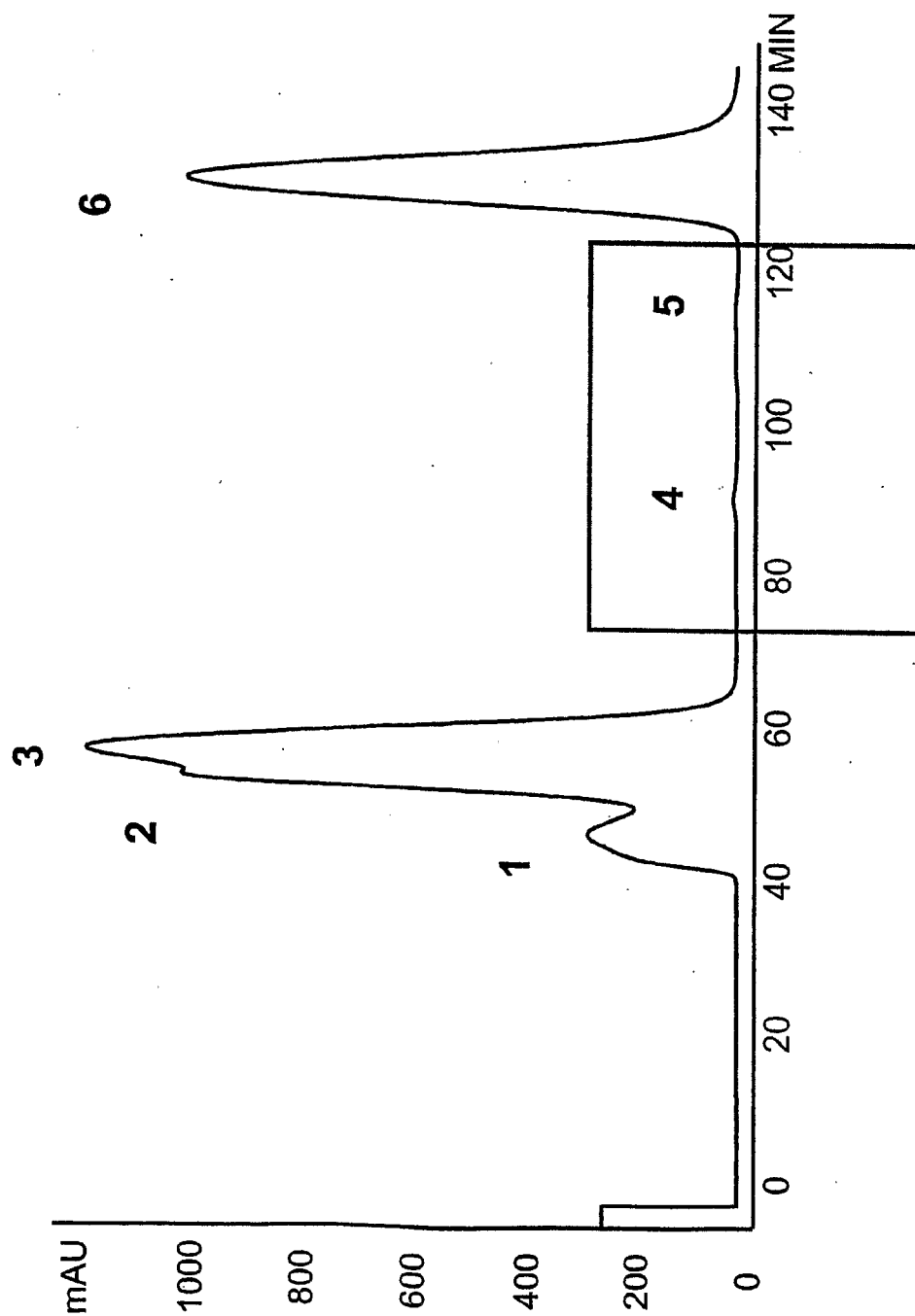


FIG. 172A

474/498

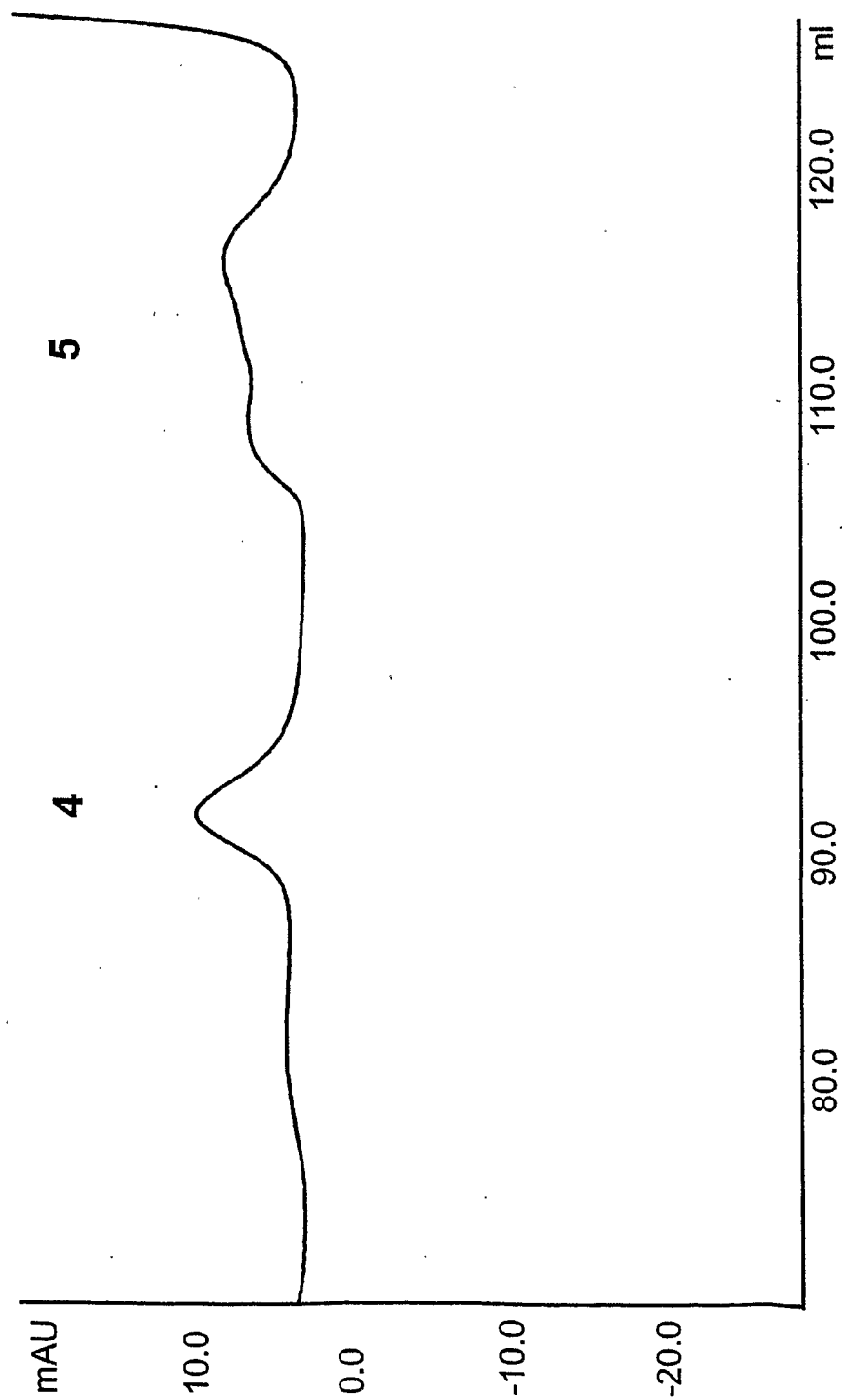


FIG. 172B

475/498

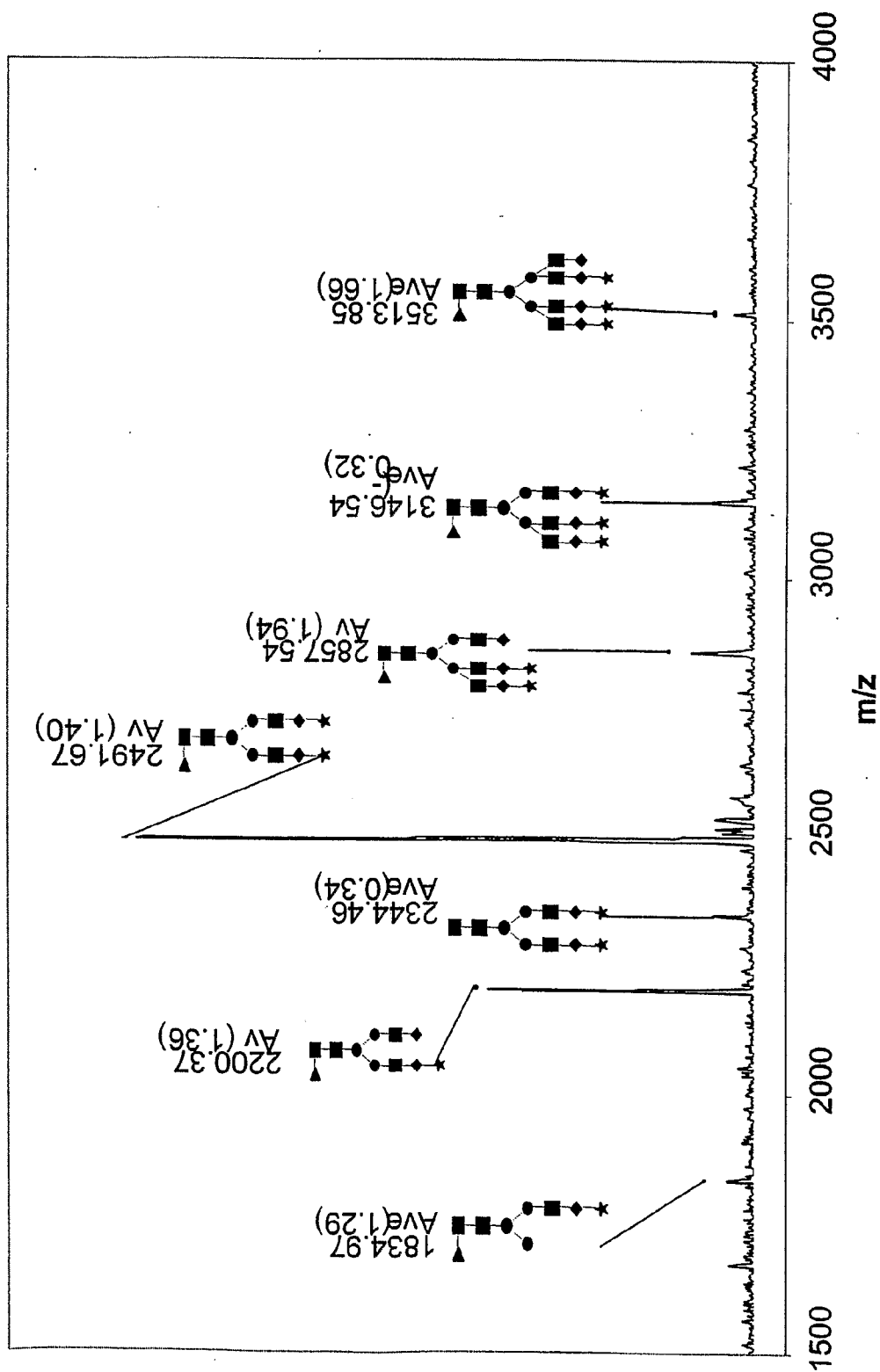


FIG. 173A

476/498

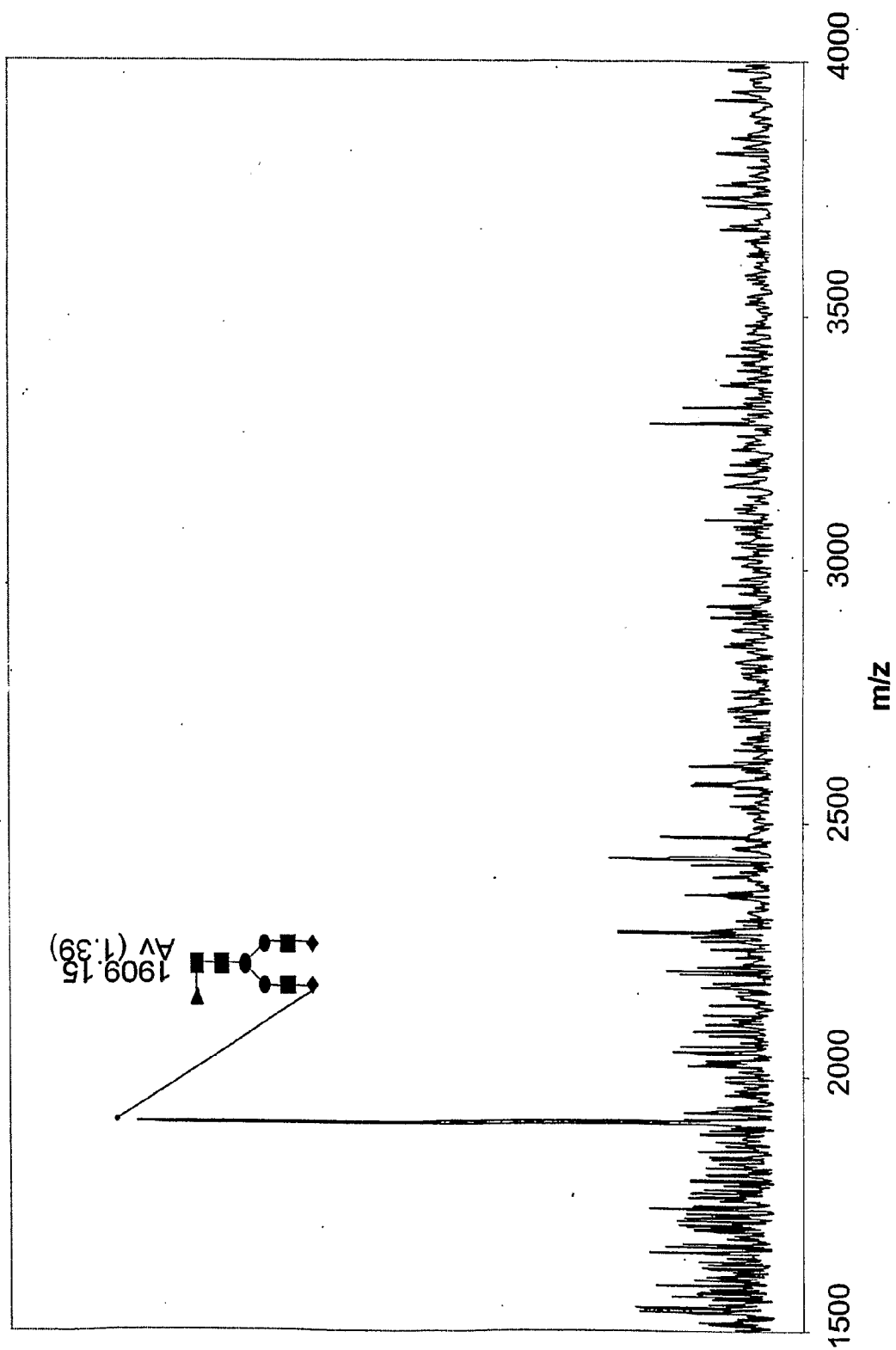


FIG. 173B

477/498

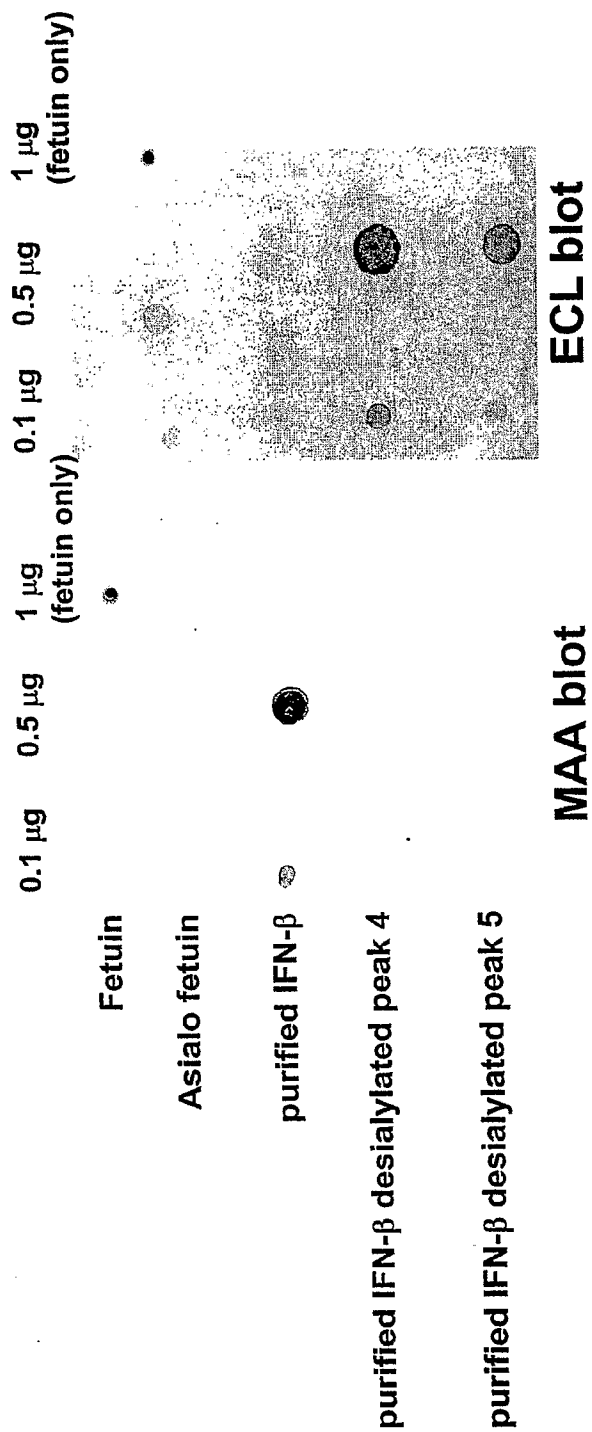


FIG. 174

478/498

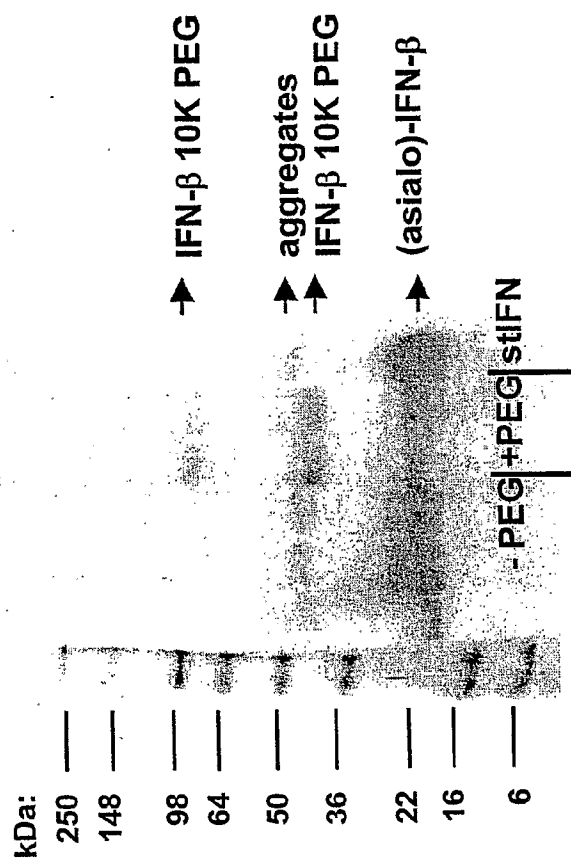


FIG. 175

479/498

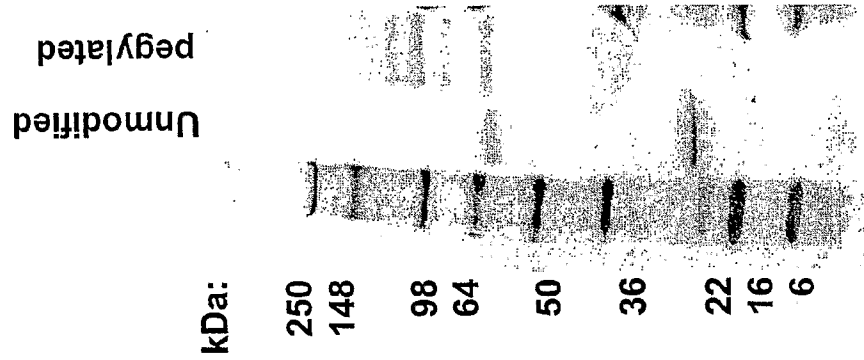


FIG. 176

480/498

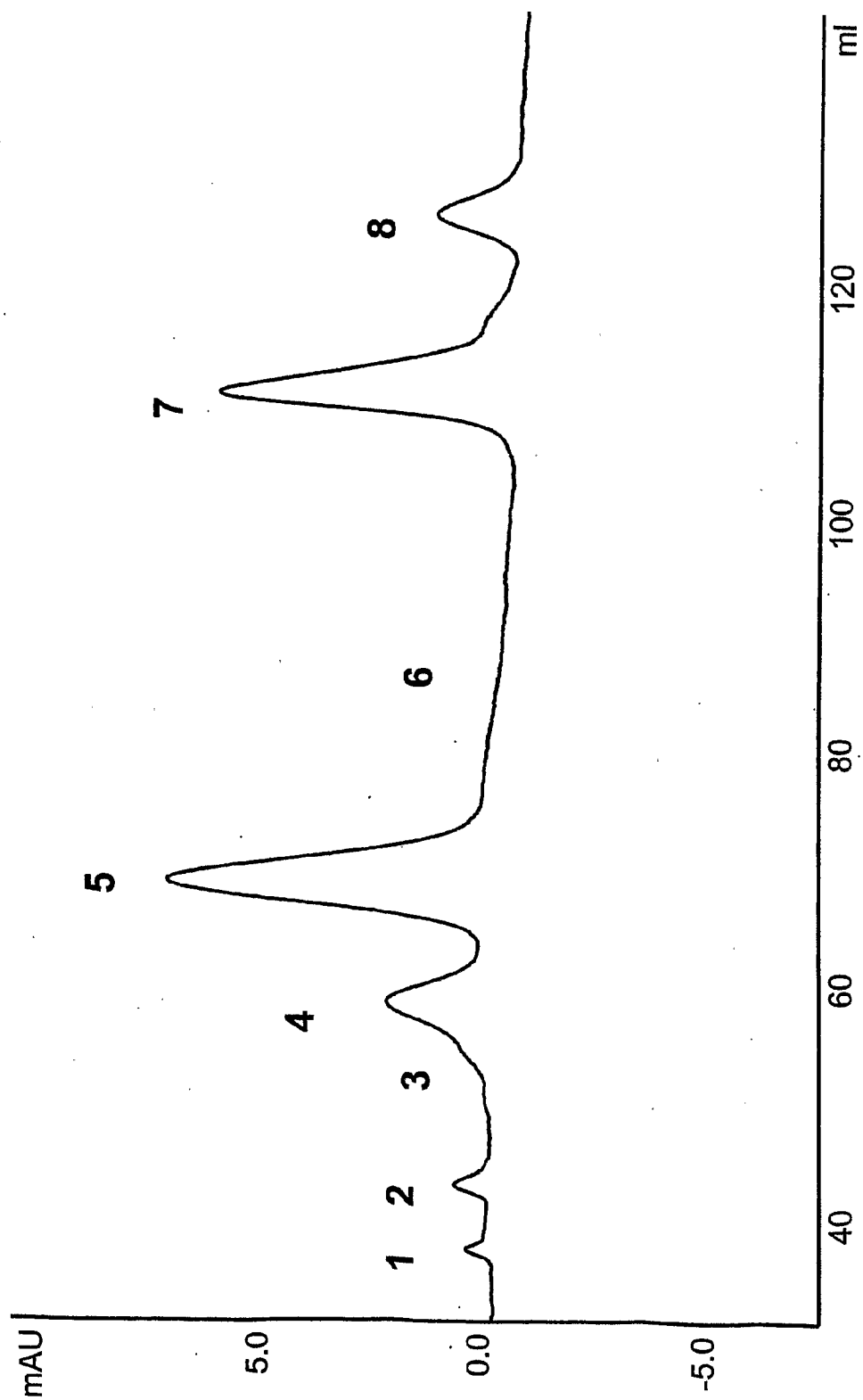


FIG. 177

481/498

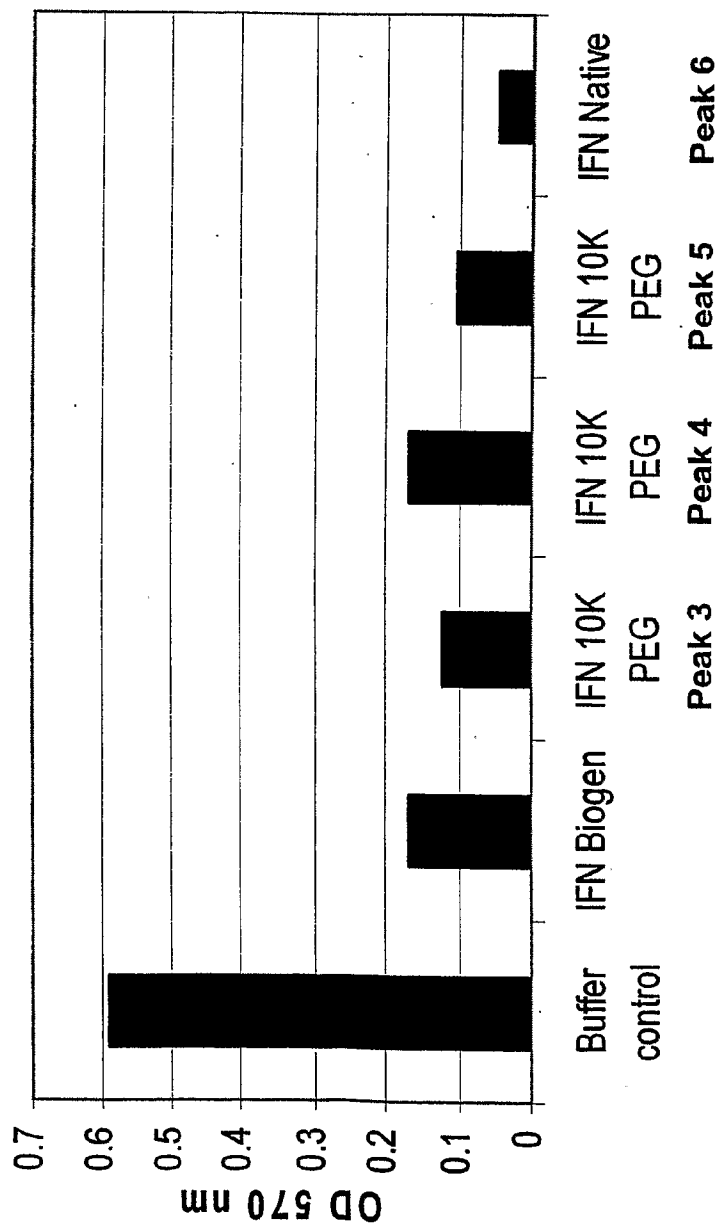


FIG. 178

482/498

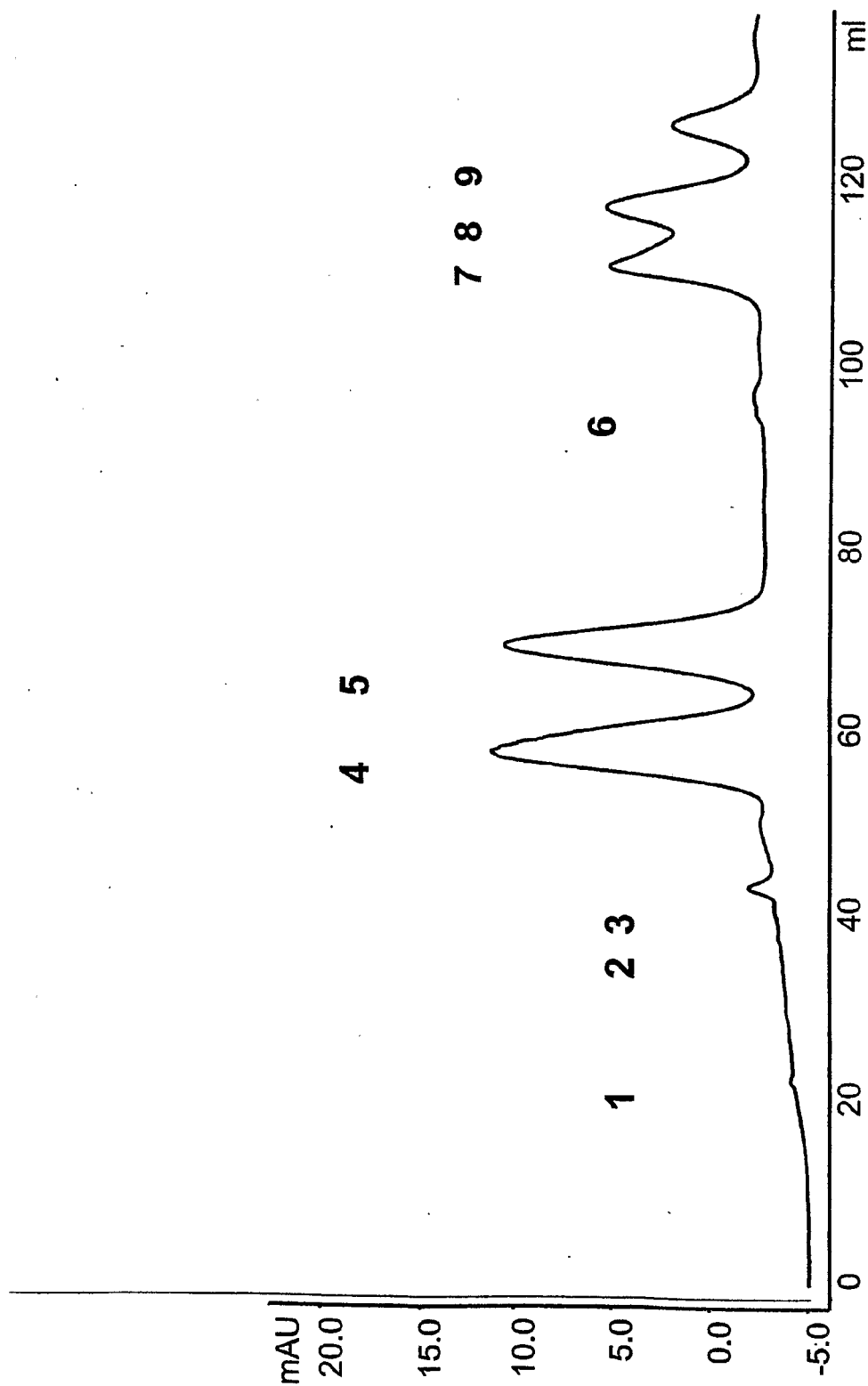


FIG. 179

483/498

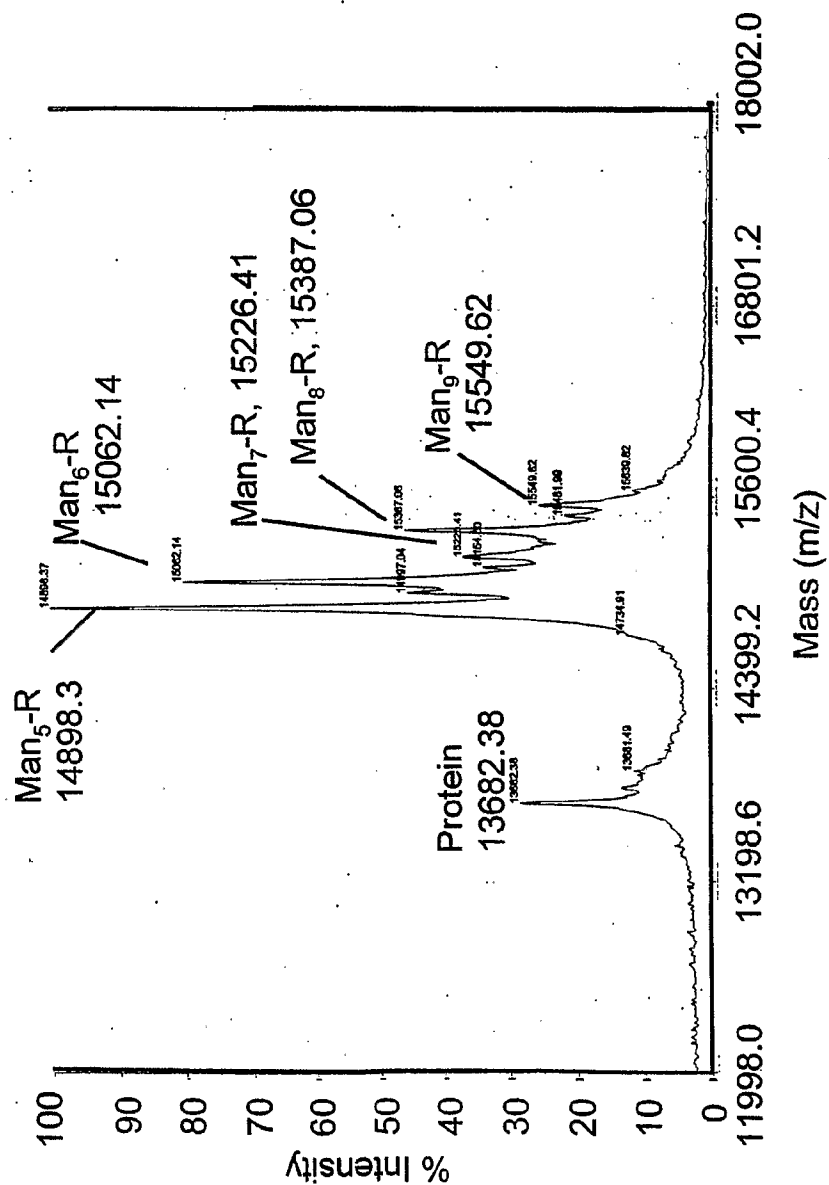


FIG. 180A

484/498

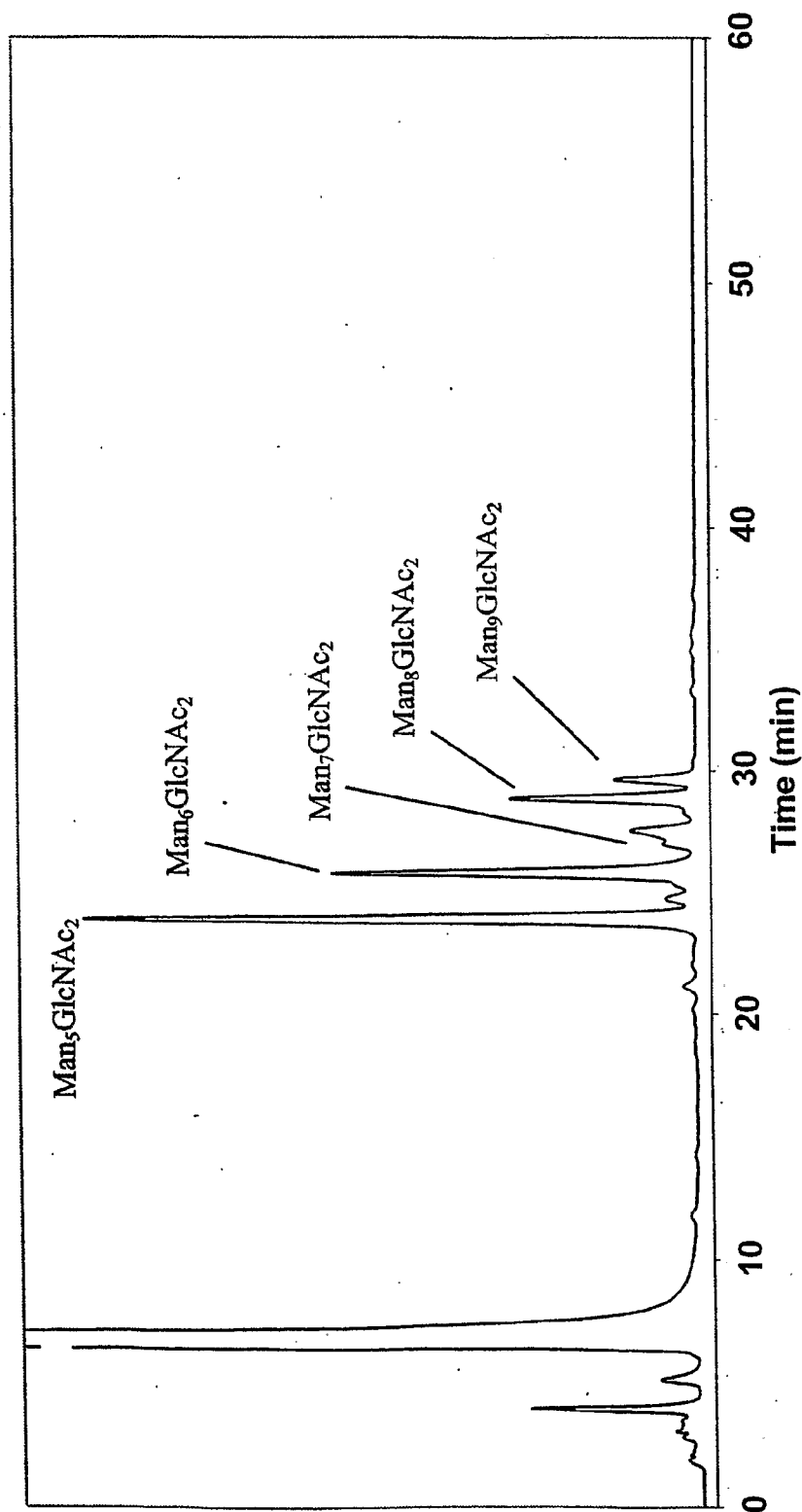


FIG. 180B

485/498

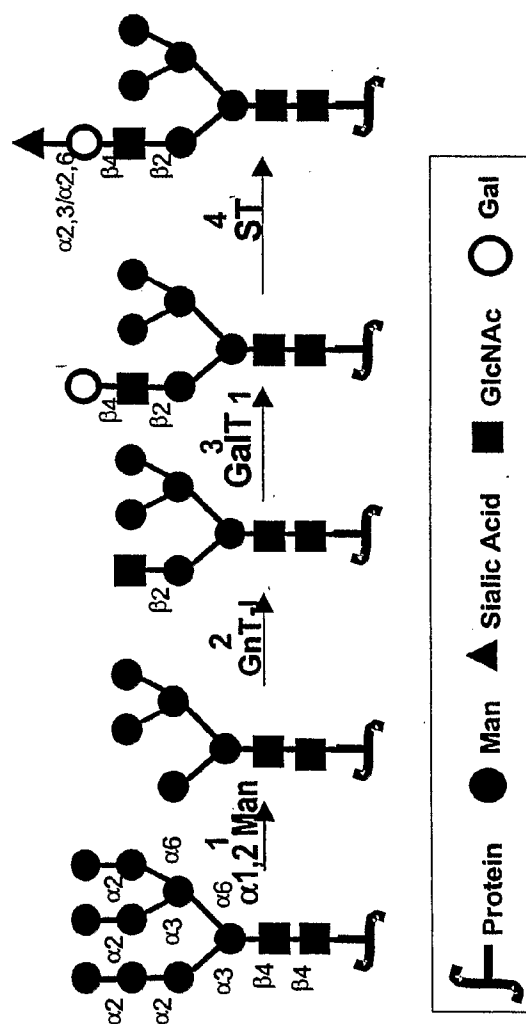


FIG. 181

486/498

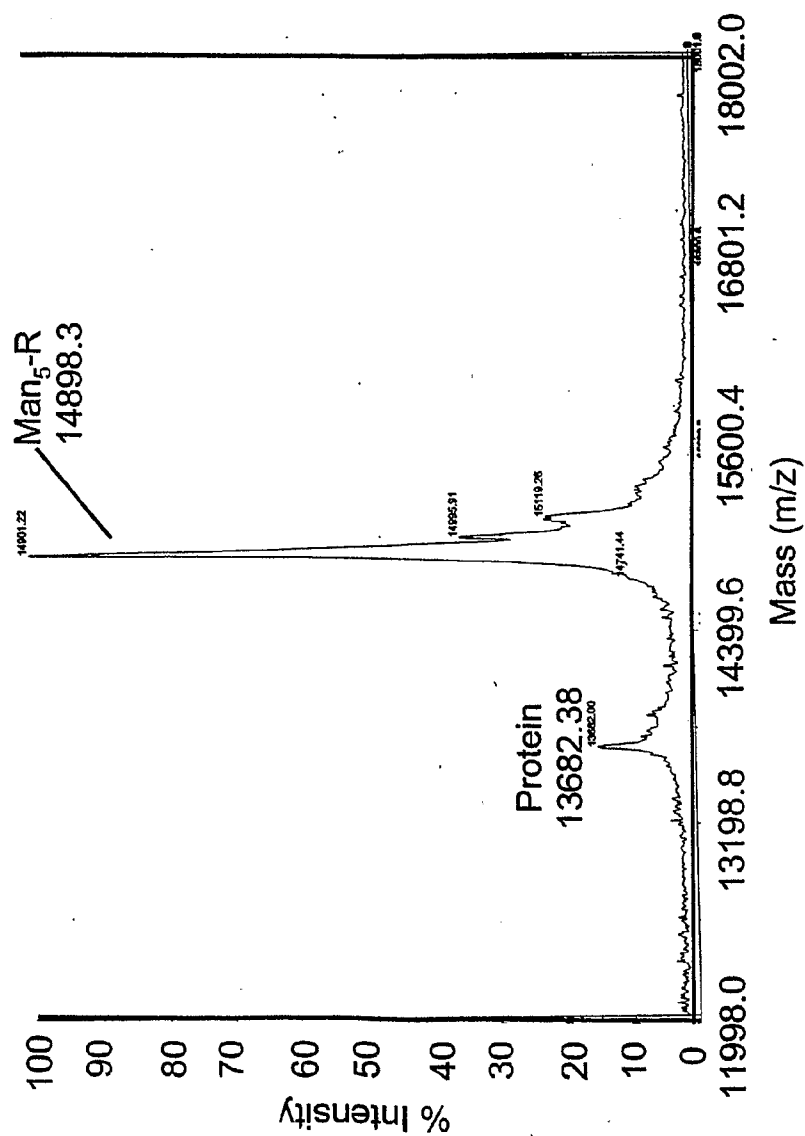


FIG. 182A

487/498

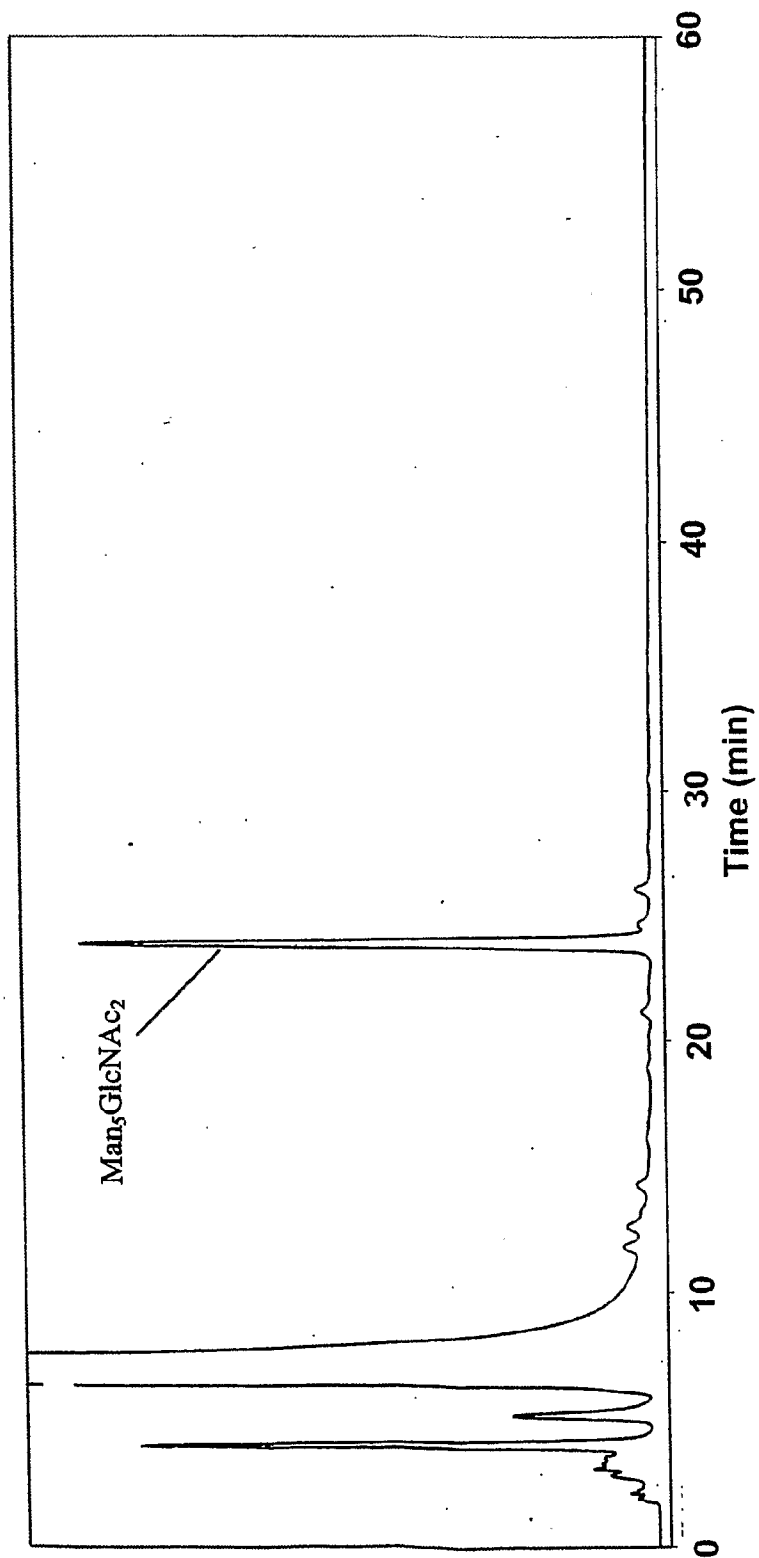


FIG. 182B

488/498

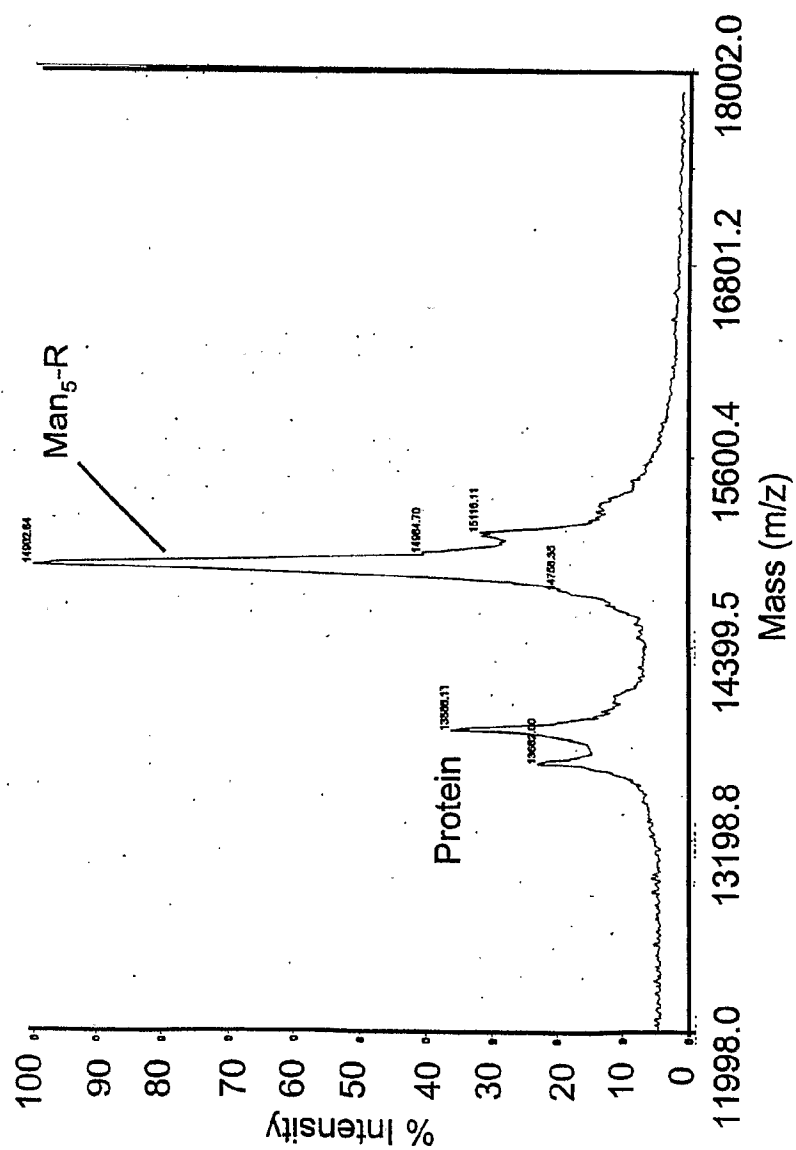


FIG. 183

489/498

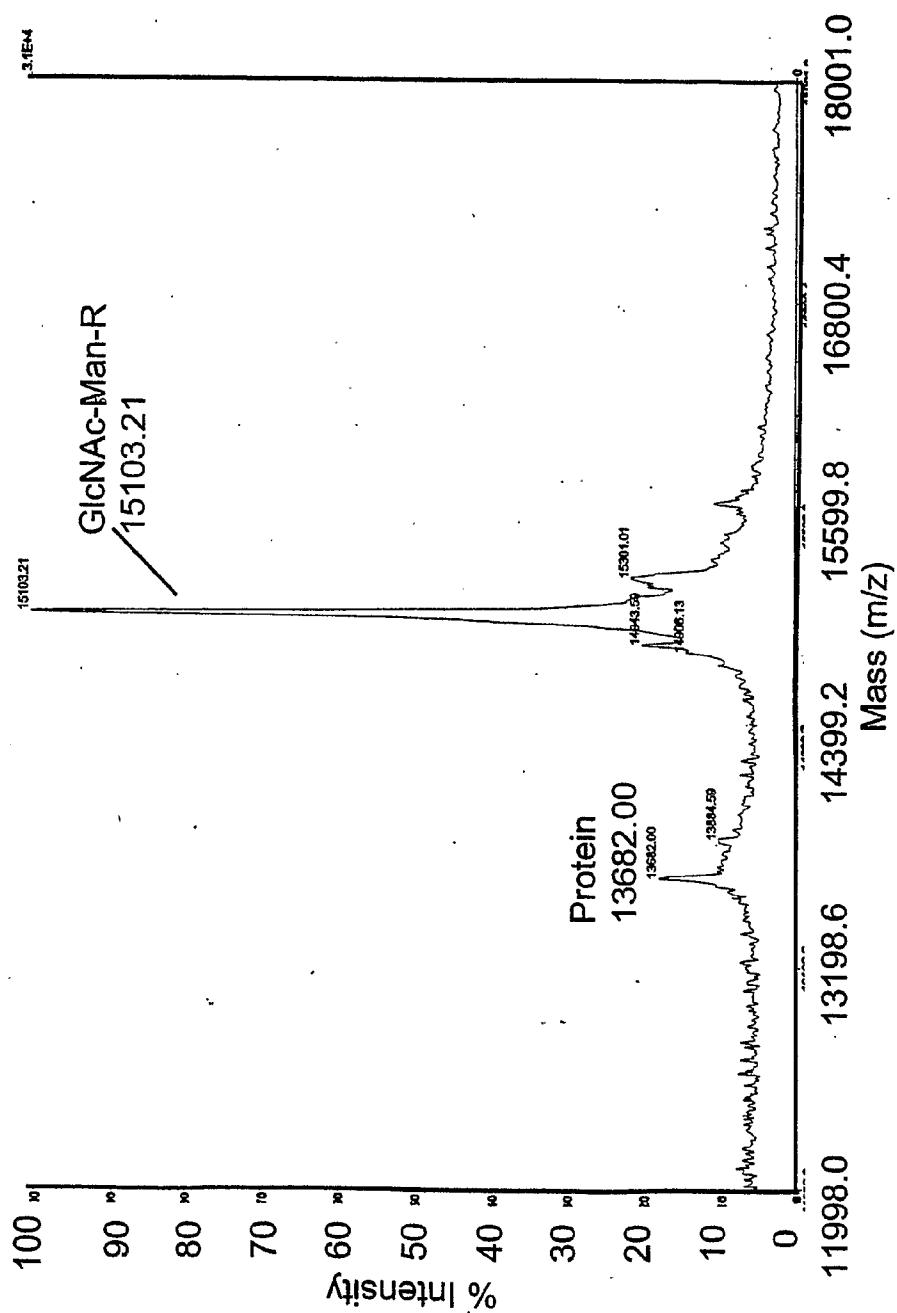


FIG. 184

490/498

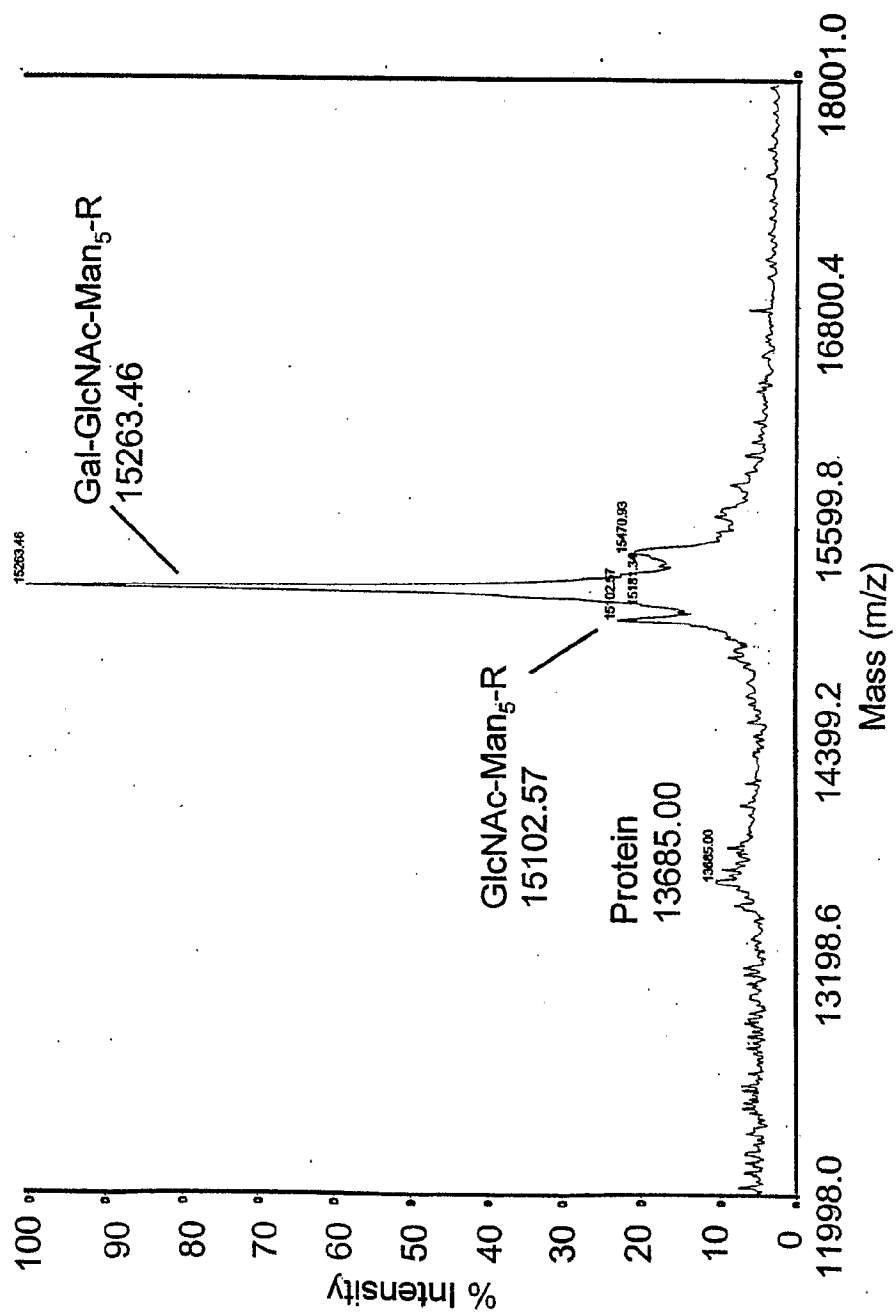


FIG. 185

491/498

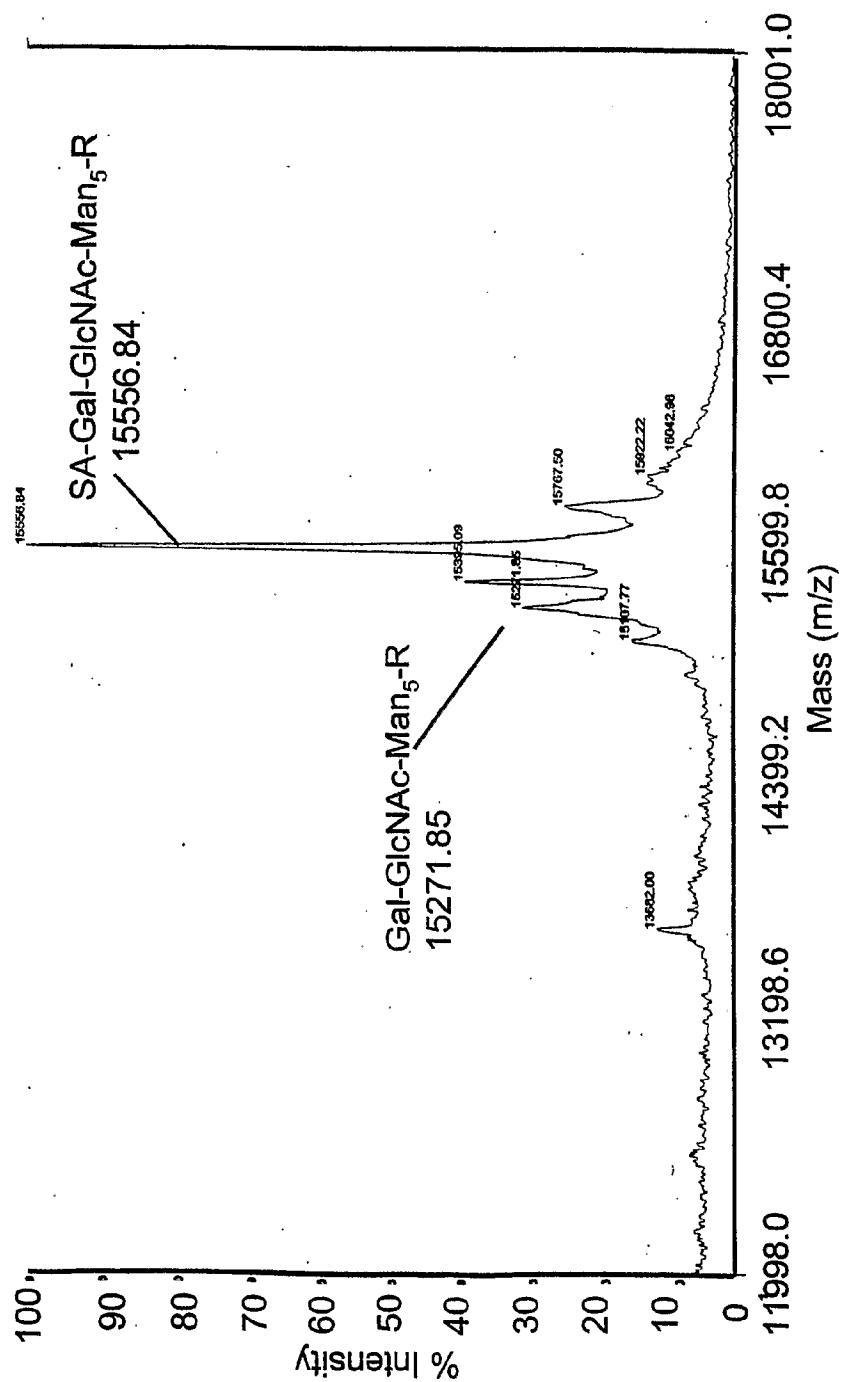


FIG. 186

[illegible]

FIG. 187A

493/498

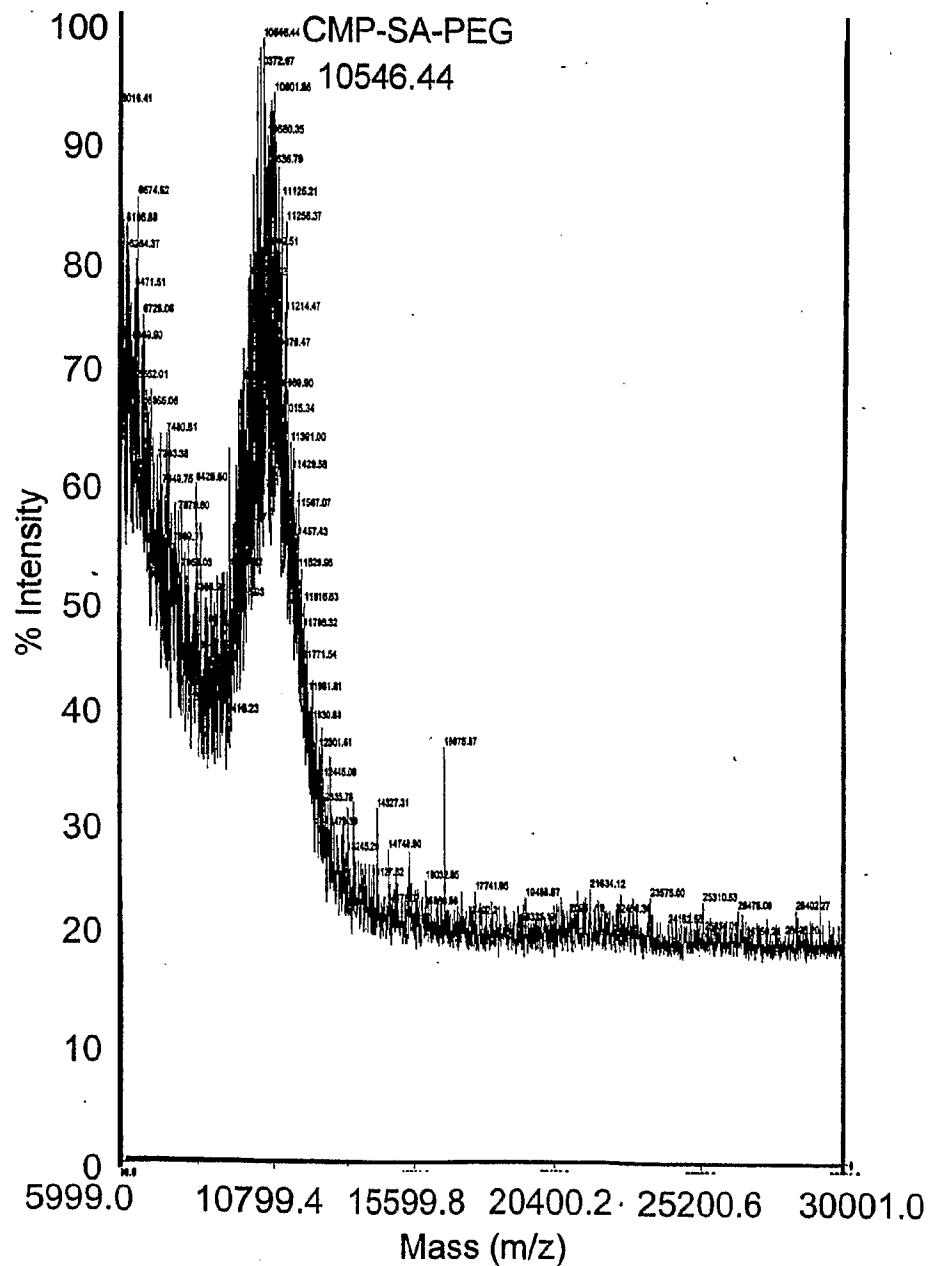


FIG. 187B

494/498

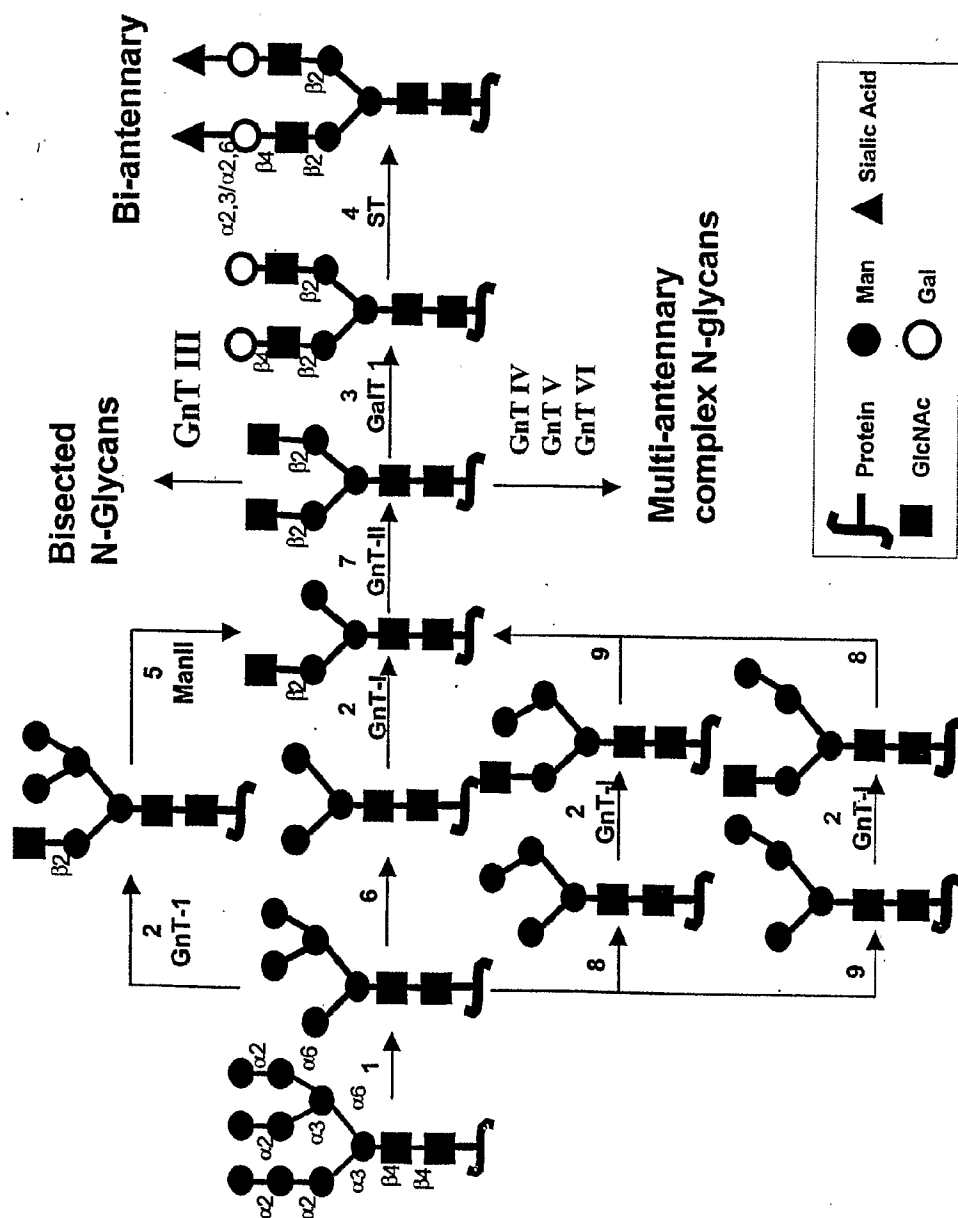


FIG. 188

495/498

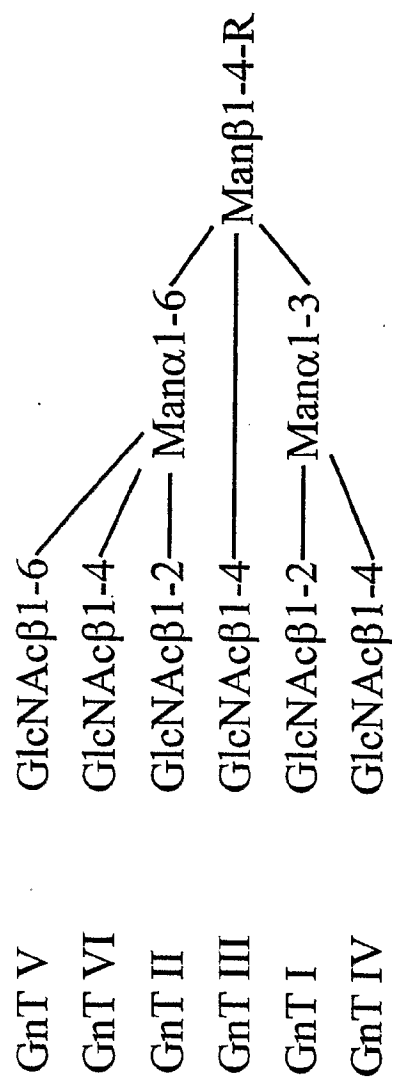


FIG. 189

496/498

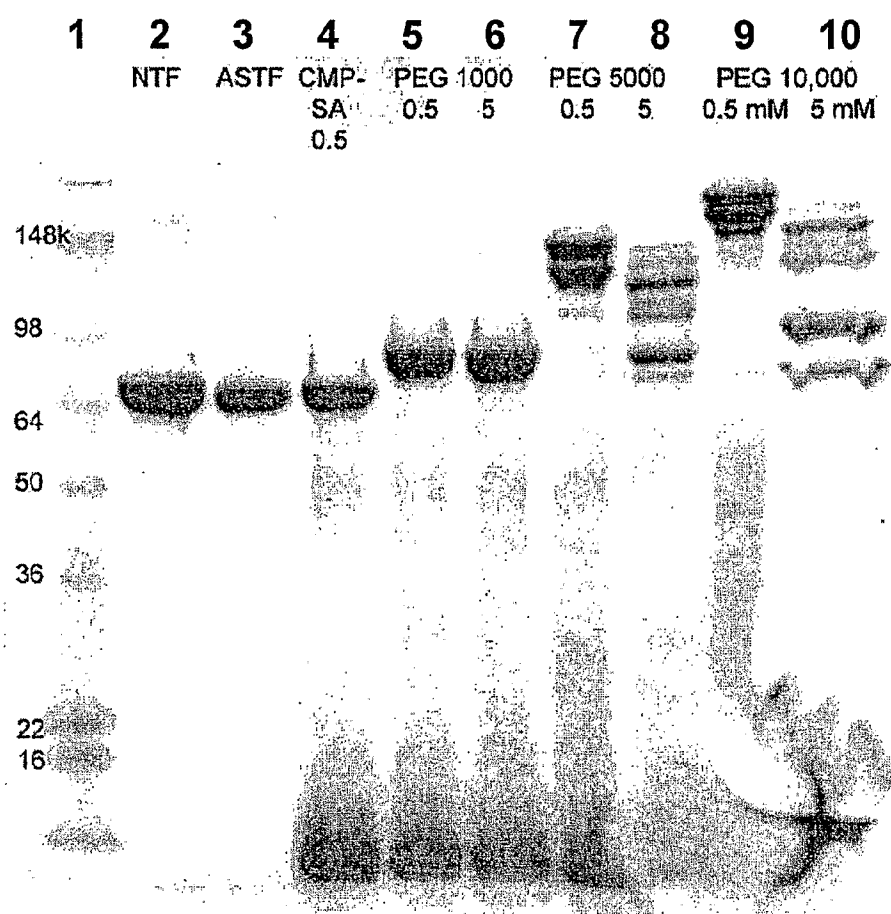


FIG. 190

497/498

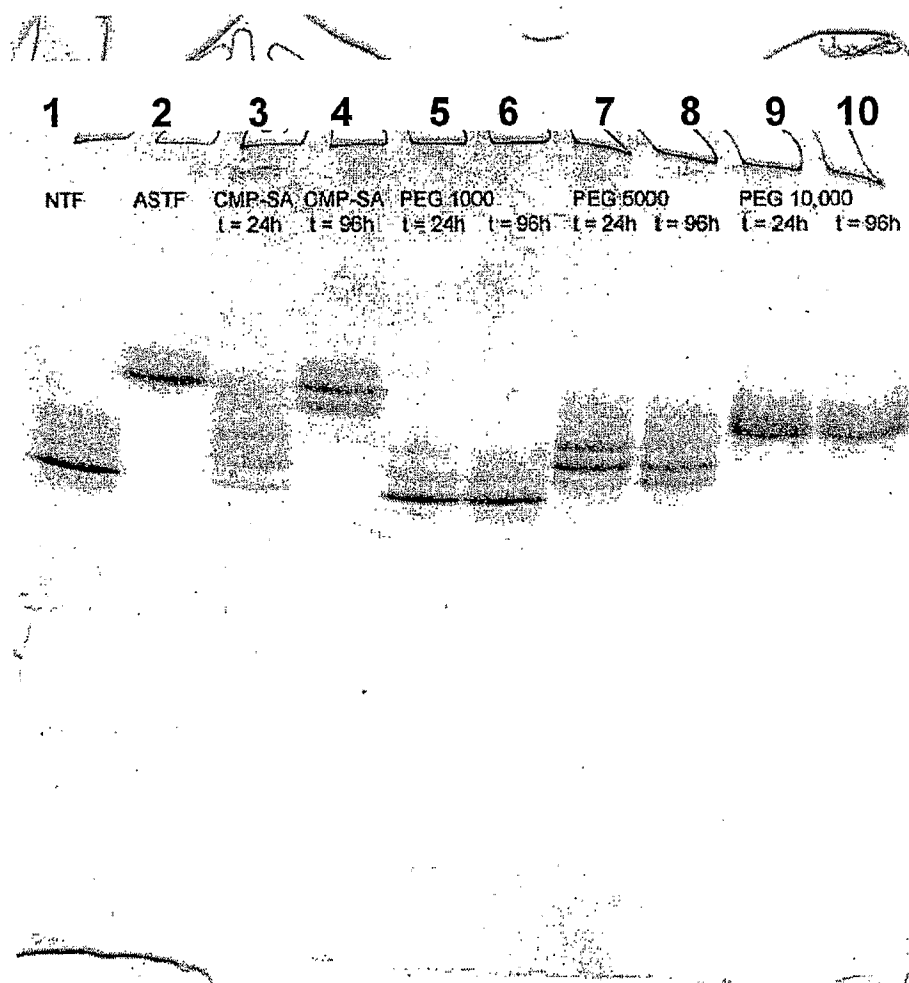
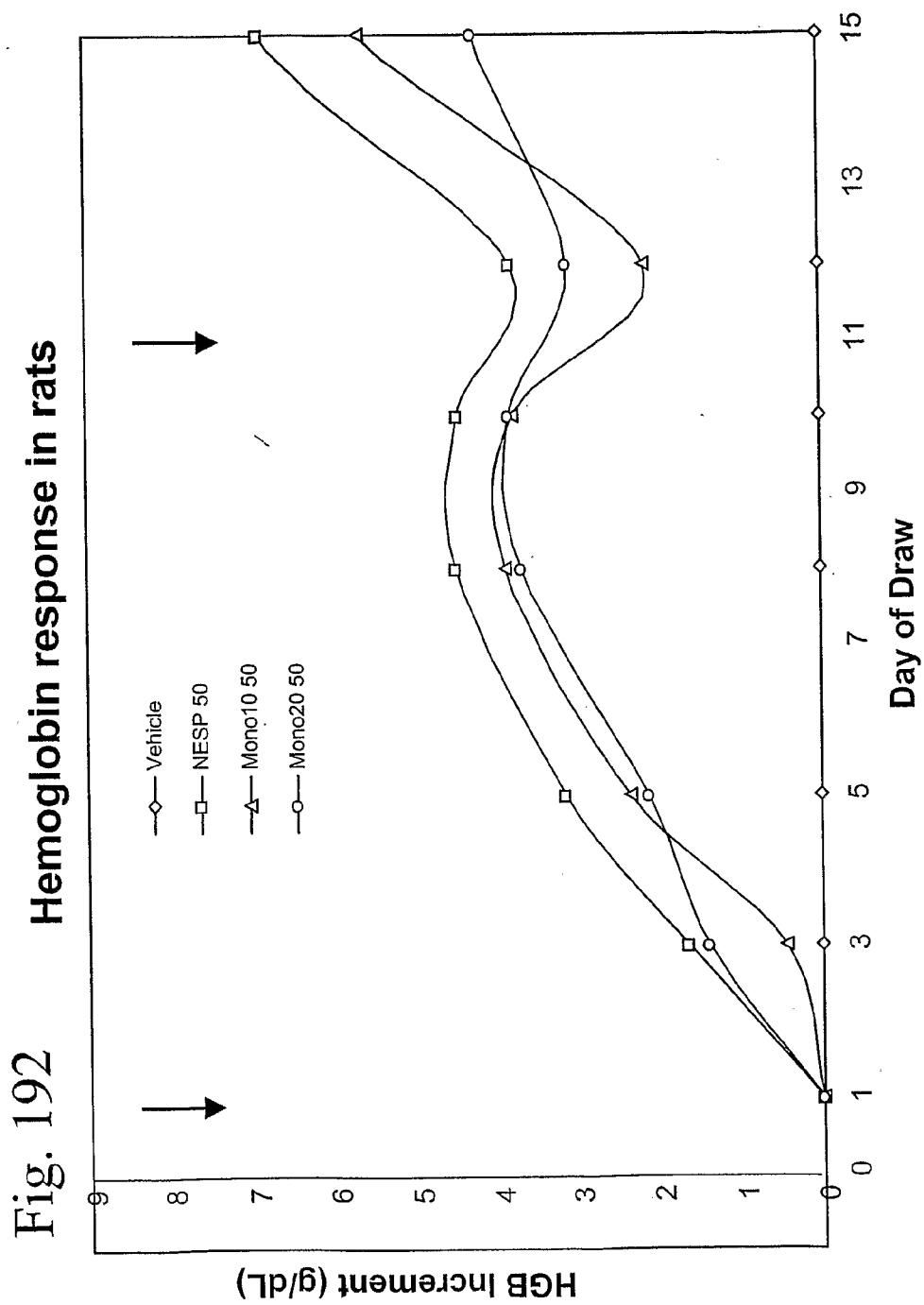


FIG. 191

498/498



SEQUENCE LISTING

<110> Neose Technologies, Inc.
 DeFrees, Shawn
 Zopf, David
 Bayer, Robert
 Hakes, David
 Chen, Xi
 Bowe, Caryne

<120> ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF
 ERYTHROPOIETIN

<130> 040853-01-5083WO

<150> PCT/US02/32263
 <151> 2002-10-09

<150> US 10/287,994
 <151> 2002-11-5

<150> US 10/360,770
 <151> 2003-01-06

<150> US 10/369,779
 <151> 2003-03-17

<150> US 10/410,945
 <151> 2003-04-09

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 ctgagcagct gcccagcca ggccctgcag ctggcaggct gcttgagcca actccatagc 240
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 gcctctgctt tccagcgccg ggcaggaggg gtcctgggtg cctccatct gcagagcttc 480
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 20 25 30
 Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 35 40 45
 Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 50 55 60
 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
 65 70 75 80
 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 85 90 95
 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 100 105 110
 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
 115 120 125
 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 130 135 140
 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
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 agtagaaagt aacacagggg catttgaaa atgtaaacga gtatgttccc tatttaaggc 420
 taggcacaaa gcaaggtctt cagagaacct ggagcctaag gtttaggctc acccatttca 480
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 35 40 45
 Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
 50 55 60
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 Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser

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 35 40 45
 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60
 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80
 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95
 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125
 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140
 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
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 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
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 gcgttccttg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc 180
 tccttcgagg aggccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240
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 gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag 360
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 Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
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 Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
 20 25 30
 Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
 35 40 45
 Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
 50 55 60
 Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65 70 75 80
 Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
 85 90 95
 Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
 100 105 110
 Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
 115 120 125
 Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
 130 135 140
 Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
 145 150 155 160
 Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
 165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
 180 185 190
 Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
 195 200 205
 Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
 210 215 220
 Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
 225 230 235 240
 Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
 245 250 255
 Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
 260 265 270
 Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 275 280 285
 Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300
 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415
 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
 420 425 430
 Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
 435 440

<210> 9
 <211> 1437
 <212> DNA
 <213> Homo sapiens

<400> 9
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ctgaatcggc caaagaggta taattcaggt aaattggaag agtttgttca agggaaacctt 180
 gagagagaat gtatggaaga aaagtgtagt tttgaagaac cacgagaagt ttttgaaaac 240
 actgaaaaga caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat 300
 ccatgtttta atggcggcag ttgcaaggat gacattaatt cctatgaatg ttgggtgtccc 360
 tttggatttg aaggaaaaga ctgtgaatta gatgtaacat gtaacattaa gaatggcaga 420
 tgcgagcagt tttgtaaaaa tagtgctgat aacaagggtg tttgctcctg tactgagggg 480
 tatcgacttg cagaaaacca gaagtcctgt gaaccagcag tgccatttcc atgtggaaga 540
 gtttctgttt cacaaacttc taagctcacc cgtgctgagg ctgtttttcc tgatgtggac 600
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 tttaatgact tcactcgggt tgttgggtgga gaagatgcca aaccagggtca attcccttgg 720
 cagggtgttt tgaatggtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa 780
 tggattgtaa ctgctgccc a ctgtgttgaa actggtgtta aaattacagt tgcgcaggt 840
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<210> 10

<211> 462

<212> PRT

<213> Homo sapiens

<400> 10

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Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
 20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
 35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys

| 50 | 55 | 60 |
|--|----|----|
| Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn 65 70 75 80 | | |
| Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln 85 90 95 | | |
| Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile 100 105 110 | | |
| Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys 115 120 125 | | |
| Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe 130 135 140 | | |
| Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly 145 150 155 160 | | |
| Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe 165 170 175 | | |
| Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala 180 185 190 | | |
| Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu 195 200 205 | | |
| Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe 210 215 220 | | |
| Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp 225 230 235 240 | | |
| Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile 245 250 255 | | |
| Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly 260 265 270 | | |
| Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu 275 280 285 | | |
| His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His 290 295 300 | | |
| Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu 305 310 315 320 | | |
| Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys 325 330 335 | | |
| Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly 340 345 350 | | |
| Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu 355 360 365 | | |
| Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu 370 375 380 | | |

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
 450 455 460

<210> 11
 <211> 603
 <212> DNA
 <213> Homo sapiens

<400> 11
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 ttcttctccc agcgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca 180
 tatcccactc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240
 tccacttgct gtgtagctaa atcatataac agggtcacag taatggggggg tttcaaagtg 300
 gagaaccaca cggcgtgcc aatgcagtact tgttattatc acaaatttta aatgttttac 360
 caagtgcctgt cttgatgact gctgattttc tggaatggaa aattaagttg tttagtgttt 420
 atggcctttgt gagataaaac tctccttttc cttaccatac cactttgaca cgcttcaagg 480
 atatactgca gctttactgc cttcctcctt atcctacagt acaatcagca gtctagttct 540
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 atc 603

<210> 12
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
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Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
 20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
 35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
100 105 110

Tyr His Lys Ser
115

<210> 13
<211> 390
<212> DNA
<213> Homo sapiens

<400> 13
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tgtgagctga ccaacatcac cattgcaata gagaaagaag aatgtcggtt ctgcataagc 120
atcaacacca cttggtgtgc tggctactgc tacaccaggg atctggtgta taaggaccca 180
gccaggccca aatccagaa aacatgtacc ttcaaggaac tggatatga aacagtgaga 240
gtgcccggct gtgctacca tgcagattcc ttgtatacat acccagtggc caccagtgt 300
cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggccagc 360
tactgctcct ttggtgaaat gaaagaataa 390

<210> 14
<211> 129
<212> PRT
<213> Homo sapiens

<400> 14
Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
1 5 10 15
Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30
Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45
Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60
Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80
Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95
Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
100 105 110
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys

115

120

125

Glu

<210> 15

<211> 1342

<212> DNA

<213> Homo sapiens

<400> 15

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gcccccggtg tggtcacccg gcgcgccccca ggctcgtgag ggaccccggc caggcgcgga      180
gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgtctcc      240
tctgggcctc ccagtcctgg gcgccccacc acgcctcctc tgtgacagcc gagtcctgga      300
gaggtacctc ttggaggcca aggaggccga gaatatcacg acgggctgtg ctgaacctg      360
cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag      420
gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc      480
tgtcctgcgg ggccaggccc tgttggtcaa ctcttcccag ccgtgggagc ccctgcagct      540
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agcccagaag gaagccatct cccctccaga tgcggcctca gctgctccac tccgaacaat      660
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ggtggcaaga gcccccttga cacoggggtg gtgggaacca tgaagacagg atgggggctg      1260
gcctctggct ctcatggggg ccaagttttg tgtattcttc aacctcattg acaagaactg      1320
aaaccaccaa aaaaaaaaaa aa                                             1342

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<210> 16

<211> 193

<212> PRT

<213> Homo sapiens

<400> 16

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Arg

<210> 17

<211> 435

<212> DNA

<213> Homo sapiens

<400> 17

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 cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcac 180
 tcagaaatgt ttgacctcca ggagccgacc tgctacaga cccgcctgga gctgtacaag 240
 cagggcctgc ggggcagcct caccaagctc aagggccct tgaccatgat ggccagccac 300
 tacaagcagc actgcctcc aaccccgaa acttcctgtg caaccagat tatcaccttt 360
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ccagtcagg agtga

435

<210> 18
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
 1 5 10 15
 Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
 20 25 30
 Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
 35 40 45
 Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
 50 55 60
 Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
 65 70 75 80
 Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
 85 90 95
 Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
 100 105 110
 Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
 115 120 125
 Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 130 135 140

<210> 19
 <211> 501
 <212> DNA
 <213> Homo sapiens

<400> 19
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 ggatcattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180
 gaggagagt acagaaaaat aatgcagagc caaattgtct ccttttactt caaacttttt 240
 aaaaacttta aagatgacca gagcatccaa aagagtgtgg agaccatcaa ggaagacatg 300
 aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360
 tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg 420
 gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480
 ggtcgaagag catcccagta a 501

<210> 20
 <211> 166

<212> PRT

<213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
 1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
 20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
 35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
 50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
 65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
 85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
 100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
 115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
 130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
 145 150 155 160

Gly Arg Arg Ala Ser Gln
 165

<210> 21

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 21

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 gacagatata tcccaccatg atcaggatca cccaaccttc aacaagatca ccccaacct 180
 ggctgagttc gccttcagcc tataccgcc gctggcacac cagtccaaca gcaccaatat 240
 cttcttctcc ccagttagca tcgtacagc ctttgcaatg ctctccctgg ggaccaaggc 300
 tgacactcac gatgaaatcc tggagggcct gaatttcaac ctcacggaga ttccggaggc 360
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 tgtcttctta atgattgaac aaaataccaa gtctcccctc ttcattggaa aagtggtgaa 1260
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 ccctggatga cattaaagaa gggttgagct gg 1352

<210> 22
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 22
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 20 25 30
 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 35 40 45
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 50 55 60
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 65 70 75 80
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 85 90 95
 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
 100 105 110
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 115 120 125
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 145 150 155 160
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 165 170 175
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 180 185 190
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 195 200 205
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 210 215 220
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
 225 230 235 240
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 245 250 255
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 260 265 270
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 275 280 285
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 290 295 300
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 305 310 315 320
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 325 330 335
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 340 345 350
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 355 360 365
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 370 375 380
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 385 390 395 400
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 405 410 415

Gln Lys

<210> 23

<211> 2004

<212> DNA

<213> Homo sapiens

<400> 23

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| ctctatcctt | cagagactct | ggaacccctg | tggtcttctc | ttcatctaat | gacctgagg | 120 |
| ggatggagtt | ttcaagtcct | tccagagagg | aatgtcccaa | gcctttgagt | agggtaagca | 180 |
| tcatggctgg | cagcctcaca | ggtttgcttc | tacttcaggc | agtgtcgtgg | gcatcaggtg | 240 |
| cccgccctg | catccctaaa | agcttcggct | acagctoggt | ggtgtgtgtc | tgcaatgcc | 300 |
| catactgtga | ctcctttgac | cccccgacct | ttcctgccct | tggtaccttc | agccgctatg | 360 |
| agagtacacg | cagtgggcga | cggatggagc | tgagtatggg | gcccattccag | gctaatacaca | 420 |
| cgggcacagg | cctgctactg | accctgcagc | cagaacagaa | gttccagaaa | gtgaagggat | 480 |
| ttggaggggc | catgacagat | gctgctgctc | tcaacatcct | tgccctgtca | ccccctgcc | 540 |
| aaaatttgct | acttaaactg | tacttctctg | aagaaggaat | cggatataac | atcatccggg | 600 |
| tacctatggc | cagctgtgac | ttctccatcc | gcacctacac | ctatgcagac | acctctgatg | 660 |
| atttcagtt | gcacaacttc | agcctcccag | aggaagatac | caagctcaag | ataccccga | 720 |
| ttcaccgagc | cctgcagttg | gccagcgtc | ccgtttcact | ccttgccagc | ccctggacat | 780 |
| caccacttg | gctcaagacc | aatggagcgg | tgaatgggaa | ggggtcactc | aagggaacagc | 840 |
| ccggagacat | ctaccaccag | acctgggcca | gatactttgt | gaagttcctg | gatgcctatg | 900 |
| ctgagcacia | gttacagttc | tgggcagtga | cagctgaaaa | tgagccttct | gctgggctgt | 960 |
| tgagtggata | ccccttccag | tgctgggct | tcacctga | acatcagcga | gacttcattg | 1020 |
| cccgtagcct | aggctctacc | ctcgccaaca | gtactacca | caatgtccgc | ctactcatgc | 1080 |
| tggatgacca | acgcttgctg | ctgccccact | gggcaaagg | ggtactgaca | gaccagaag | 1140 |
| cagctaaata | tgttcatggc | attgctgtac | attggtacct | ggactttctg | gctccagcca | 1200 |
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| ctgtctgtga | ctaaagaggg | cacagcaggg | ccagtgtgag | cttacagcga | cgtaagccca | 1860 |
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 Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
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 Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
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 Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
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 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
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 Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
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 Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
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 Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
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 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
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 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
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 Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
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 225 230 235 240
 Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
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 Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
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Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
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Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
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Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
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Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
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Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
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Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
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Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
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Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
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Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
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Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
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Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
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Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
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Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
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Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
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His Thr Tyr Leu Trp His Arg Gln
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<211> 1726

<212> DNA

<213> Homo sapiens

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| aaccagatc gagactcaaa gccctgggtg tacgtcttta aggcggggaa gtacagctca | 600 |
| gagttctgca gcacccctgc ctgctctgag ggaacagtg actgctactt tgggaatggg | 660 |
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| ctgggcaaac ataattactg ccggaatcct gatggggatg ccaagccctg gtgccacgtg | 840 |
| ctgaagaacc gcaggctgac gtgggagtac tgtgatgtgc cctcctgctc cacctgcggc | 900 |
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| gagcggctga aggaggctca tgtcagactg taccatcca gccgtgcac atcacaacat | 1440 |
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| ccccaggcaa acttgacga cgctgccag ggcgattcgg gaggccccct ggtgtgtctg | 1560 |
| aacgatggcc gcatgacttt ggtgggcata atcagctggg gcctgggctg tggacagaag | 1620 |
| gatgtcccg gtgtgtacac caaggttacc aactacctag actggattcg tgacaacatg | 1680 |
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 <212> PRT
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 Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
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 Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
 65 70 75 80
 Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
 85 90 95
 Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
 100 105 110
 Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
 115 120 125
 Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
 130 135 140
 Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
 145 150 155 160
 Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
 165 170 175
 Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
 180 185 190
 Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
 195 200 205
 Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
 210 215 220
 Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
 225 230 235 240
 Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
 245 250 255
 Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
 260 265 270
 Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
 275 280 285
 Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr
 290 295 300
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<212> DNA
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<212> PRT
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Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln
65 70 75 80
Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
85 90 95
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
100 105 110
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
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<212> DNA
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<400> 29

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Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
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Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
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Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
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His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
115 120 125
Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
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Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
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Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
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 Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
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 Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
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 Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
 245 250 255
 Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
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 Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
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 Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
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 Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
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 Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
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 Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
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 Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
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 His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys

| | | | | | | | | | | | | | | | | | | | |
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| | | 515 | | | | | 520 | | | | | 525 | | | | | | | |
| Lys | Tyr | Lys | Trp | Thr | Val | Thr | Val | Glu | Asp | Gly | Pro | Thr | Lys | Ser | Asp | | | | |
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| Pro | Arg | Cys | Leu | Thr | Arg | Tyr | Tyr | Ser | Ser | Phe | Val | Asn | Met | Glu | Arg | | | | |
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| | | | | 565 | | | | 570 | | | | | | 575 | | | | | |
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| | | | 580 | | | | | 585 | | | | | 590 | | | | | | |
| Ile | Leu | Phe | Ser | Val | Phe | Asp | Glu | Asn | Arg | Ser | Trp | Tyr | Leu | Thr | Glu | | | | |
| | 595 | | | | | | 600 | | | | | 605 | | | | | | | |
| Asn | Ile | Gln | Arg | Phe | Leu | Pro | Asn | Pro | Ala | Gly | Val | Gln | Leu | Glu | Asp | | | | |
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| Phe | Asp | Ser | Leu | Gln | Leu | Ser | Val | Cys | Leu | His | Glu | Val | Ala | Tyr | Trp | | | | |
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| Tyr | Ile | Leu | Ser | Ile | Gly | Ala | Gln | Thr | Asp | Phe | Leu | Ser | Val | Phe | Phe | | | | |
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| Ser | Gly | Tyr | Thr | Phe | Lys | His | Lys | Met | Val | Tyr | Glu | Asp | Thr | Leu | Thr | | | | |
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| Met | Thr | Ala | Leu | Leu | Lys | Val | Ser | Ser | Cys | Asp | Lys | Asn | Thr | Gly | Asp | | | | |
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| Asn | Asn | Ala | Ile | Glu | Pro | Arg | Ser | Phe | Ser | Gln | Asn | Ser | Arg | His | Arg | | | | |
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| Ser | Thr | Arg | Gln | Lys | Gln | Phe | Asn | Ala | Thr | Thr | Ile | Pro | Glu | Asn | Asp | | | | |
| | 770 | | | | | 775 | | | | | 780 | | | | | | | | |
| Ile | Glu | Lys | Thr | Asp | Pro | Trp | Phe | Ala | His | Arg | Thr | Pro | Met | Pro | Lys | | | | |
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| Ile | Gln | Asn | Val | Ser | Ser | Ser | Asp | Leu | Leu | Met | Leu | Leu | Arg | Gln | Ser | | | | |
| | | | | 805 | | | | | 810 | | | | | 815 | | | | | |
| Pro | Thr | Pro | His | Gly | Leu | Ser | Leu | Ser | Asp | Leu | Gln | Glu | Ala | Lys | Tyr | | | | |
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 Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
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 Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro
 1130 1135 1140

33

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| 1460 | 1465 | 1470 |
| Asp Gln Arg Glu Val Gly | Ser Leu Gly Thr Ser | Ala Thr Asn Ser |
| 1475 | 1480 | 1485 |
| Val Thr Tyr Lys Lys Val | Glu Asn Thr Val Leu | Pro Lys Pro Asp |
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| Leu Pro Lys Thr Ser Gly | Lys Val Glu Leu Leu | Pro Lys Val His |
| 1505 | 1510 | 1515 |
| Ile Tyr Gln Lys Asp Leu | Phe Pro Thr Glu Thr | Ser Asn Gly Ser |
| 1520 | 1525 | 1530 |
| Pro Gly His Leu Asp Leu | Val Glu Gly Ser Leu | Leu Gln Gly Thr |
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| Glu Gly Ala Ile Lys Trp | Asn Glu Ala Asn Arg | Pro Gly Lys Val |
| 1550 | 1555 | 1560 |
| Pro Phe Leu Arg Val Ala | Thr Glu Ser Ser Ala | Lys Thr Pro Ser |
| 1565 | 1570 | 1575 |
| Lys Leu Leu Asp Pro Leu | Ala Trp Asp Asn His | Tyr Gly Thr Gln |
| 1580 | 1585 | 1590 |
| Ile Pro Lys Glu Glu Trp | Lys Ser Gln Glu Lys | Ser Pro Glu Lys |
| 1595 | 1600 | 1605 |
| Thr Ala Phe Lys Lys Lys | Asp Thr Ile Leu Ser | Leu Asn Ala Cys |
| 1610 | 1615 | 1620 |
| Glu Ser Asn His Ala Ile | Ala Ala Ile Asn Glu | Gly Gln Asn Lys |
| 1625 | 1630 | 1635 |
| Pro Glu Ile Glu Val Thr | Trp Ala Lys Gln Gly | Arg Thr Glu Arg |
| 1640 | 1645 | 1650 |
| Leu Cys Ser Gln Asn Pro | Pro Val Leu Lys Arg | His Gln Arg Glu |
| 1655 | 1660 | 1665 |
| Ile Thr Arg Thr Thr Leu | Gln Ser Asp Gln Glu | Glu Ile Asp Tyr |
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| Asp Asp Thr Ile Ser Val | Glu Met Lys Lys Glu | Asp Phe Asp Ile |
| 1685 | 1690 | 1695 |
| Tyr Asp Glu Asp Glu Asn | Gln Ser Pro Arg Ser | Phe Gln Lys Lys |
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| Gly Met Ser Ser Ser Pro | His Val Leu Arg Asn | Arg Ala Gln Ser |
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| Gly Ser Val Pro Gln Phe | Lys Lys Val Val Phe | Gln Glu Phe Thr |
| 1745 | 1750 | 1755 |

| | | | | | | | | | | | | | | |
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| His | Leu | Gly | Leu | Leu | Gly | Pro | Tyr | Ile | Arg | Ala | Glu | Val | Glu | Asp |
| 1775 | | | | | | 1780 | | | | | 1785 | | | |
| Asn | Ile | Met | Val | Thr | Phe | Arg | Asn | Gln | Ala | Ser | Arg | Pro | Tyr | Ser |
| 1790 | | | | | | 1795 | | | | | 1800 | | | |
| Phe | Tyr | Ser | Ser | Leu | Ile | Ser | Tyr | Glu | Glu | Asp | Gln | Arg | Gln | Gly |
| 1805 | | | | | | 1810 | | | | | 1815 | | | |
| Ala | Glu | Pro | Arg | Lys | Asn | Phe | Val | Lys | Pro | Asn | Glu | Thr | Lys | Thr |
| 1820 | | | | | | 1825 | | | | | 1830 | | | |
| Tyr | Phe | Trp | Lys | Val | Gln | His | His | Met | Ala | Pro | Thr | Lys | Asp | Glu |
| 1835 | | | | | | 1840 | | | | | 1845 | | | |
| Phe | Asp | Cys | Lys | Ala | Trp | Ala | Tyr | Phe | Ser | Asp | Val | Asp | Leu | Glu |
| 1850 | | | | | | 1855 | | | | | 1860 | | | |
| Lys | Asp | Val | His | Ser | Gly | Leu | Ile | Gly | Pro | Leu | Leu | Val | Cys | His |
| 1865 | | | | | | 1870 | | | | | 1875 | | | |
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| 1880 | | | | | | 1885 | | | | | 1890 | | | |
| Glu | Phe | Ala | Leu | Phe | Phe | Thr | Ile | Phe | Asp | Glu | Thr | Lys | Ser | Trp |
| 1895 | | | | | | 1900 | | | | | 1905 | | | |
| Tyr | Phe | Thr | Glu | Asn | Met | Glu | Arg | Asn | Cys | Arg | Ala | Pro | Cys | Asn |
| 1910 | | | | | | 1915 | | | | | 1920 | | | |
| Ile | Gln | Met | Glu | Asp | Pro | Thr | Phe | Lys | Glu | Asn | Tyr | Arg | Phe | His |
| 1925 | | | | | | 1930 | | | | | 1935 | | | |
| Ala | Ile | Asn | Gly | Tyr | Ile | Met | Asp | Thr | Leu | Pro | Gly | Leu | Val | Met |
| 1940 | | | | | | 1945 | | | | | 1950 | | | |
| Ala | Gln | Asp | Gln | Arg | Ile | Arg | Trp | Tyr | Leu | Leu | Ser | Met | Gly | Ser |
| 1955 | | | | | | 1960 | | | | | 1965 | | | |
| Asn | Glu | Asn | Ile | His | Ser | Ile | His | Phe | Ser | Gly | His | Val | Phe | Thr |
| 1970 | | | | | | 1975 | | | | | 1980 | | | |
| Val | Arg | Lys | Lys | Glu | Glu | Tyr | Lys | Met | Ala | Leu | Tyr | Asn | Leu | Tyr |
| 1985 | | | | | | 1990 | | | | | 1995 | | | |
| Pro | Gly | Val | Phe | Glu | Thr | Val | Glu | Met | Leu | Pro | Ser | Lys | Ala | Gly |
| 2000 | | | | | | 2005 | | | | | 2010 | | | |
| Ile | Trp | Arg | Val | Glu | Cys | Leu | Ile | Gly | Glu | His | Leu | His | Ala | Gly |
| 2015 | | | | | | 2020 | | | | | 2025 | | | |
| Met | Ser | Thr | Leu | Phe | Leu | Val | Tyr | Ser | Asn | Lys | Cys | Gln | Thr | Pro |
| 2030 | | | | | | 2035 | | | | | 2040 | | | |
| Leu | Gly | Met | Ala | Ser | Gly | His | Ile | Arg | Asp | Phe | Gln | Ile | Thr | Ala |
| 2045 | | | | | | 2050 | | | | | 2055 | | | |

| | | | |
|---------|---------------------|---------------------|-----------------|
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| 2060 | 2065 | 2070 | |
| Tyr Ser | Gly Ser Ile Asn Ala | Trp Ser Thr Lys Glu | Pro Phe Ser |
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| Trp Ile | Lys Val Asp Leu Leu | Ala Pro Met Ile Ile | His Gly Ile |
| 2090 | 2095 | 2100 | |
| Lys Thr | Gln Gly Ala Arg Gln | Lys Phe Ser Ser Leu | Tyr Ile Ser |
| 2105 | 2110 | 2115 | |
| Gln Phe | Ile Ile Met Tyr Ser | Leu Asp Gly Lys Lys | Trp Gln Thr |
| 2120 | 2125 | 2130 | |
| Tyr Arg | Gly Asn Ser Thr Gly | Thr Leu Met Val Phe | Phe Gly Asn |
| 2135 | 2140 | 2145 | |
| Val Asp | Ser Ser Gly Ile Lys | His Asn Ile Phe Asn | Pro Pro Ile |
| 2150 | 2155 | 2160 | |
| Ile Ala | Arg Tyr Ile Arg Leu | His Pro Thr His Tyr | Ser Ile Arg |
| 2165 | 2170 | 2175 | |
| Ser Thr | Leu Arg Met Glu Leu | Met Gly Cys Asp Leu | Asn Ser Cys |
| 2180 | 2185 | 2190 | |
| Ser Met | Pro Leu Gly Met Glu | Ser Lys Ala Ile Ser | Asp Ala Gln |
| 2195 | 2200 | 2205 | |
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| Pro Ser | Lys Ala Arg Leu His | Leu Gln Gly Arg Ser | Asn Ala Trp |
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| Arg Pro | Gln Val Asn Asn Pro | Lys Glu Trp Leu Gln | Val Asp Phe |
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| Gln Lys | Thr Met Lys Val Thr | Gly Val Thr Thr Gln | Gly Val Lys |
| 2255 | 2260 | 2265 | |
| Ser Leu | Leu Thr Ser Met Tyr | Val Lys Glu Phe Leu | Ile Ser Ser |
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| 2285 | 2290 | 2295 | |
| Val Lys | Val Phe Gln Gly Asn | Gln Asp Ser Phe Thr | Pro Val Val |
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| Asn Ser | Leu Asp Pro Pro Leu | Leu Thr Arg Tyr Leu | Arg Ile His |
| 2315 | 2320 | 2325 | |
| Pro Gln | Ser Trp Val His Gln | Ile Ala Leu Arg Met | Glu Val Leu |
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<211> 461

<212> PRT

<213> Homo sapiens

<400> 32

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 1 5 10 15
 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30
 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 35 40 45
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220
 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240
 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255
 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285
 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser

| | | | | | |
|---|-----|--|-----|--|-----|
| | 325 | | 330 | | 335 |
| Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly | | | | | |
| | 340 | | 345 | | 350 |
| Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser | | | | | |
| | 355 | | 360 | | 365 |
| Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile | | | | | |
| | 370 | | 375 | | 380 |
| Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln | | | | | |
| | 385 | | 390 | | 395 |
| Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro | | | | | |
| | 405 | | 410 | | 415 |
| Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser | | | | | |
| | 420 | | 425 | | 430 |
| Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro | | | | | |
| | 435 | | 440 | | 445 |
| Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser | | | | | |
| | 450 | | 455 | | 460 |

<210> 33
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 33
 tccacctgtc cccgcagcgc cggctcgcgc cctcctgccg cagccaccga gccgccgtct 60
 agcgccccga cctcgccacc atgagagccc tgcctggcgc cctgcttctc tgcgtcctgg 120
 tcgtgagcga ctccaaaggc agcaatgaac ttcattcaagt tccatcgaac tgtgactgtc 180
 taaatggagg aacatgtgtg tccaacaagt acttctccaa cattcactgg tgcaactgcc 240
 caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300
 atggctactt ttaccgagga aaggccagca ctgacaccat gggccggccc tgccctgccct 360
 ggaactctgc cactgtcctt cagcaaactg accatgccc aagatctgat gctcttcagc 420
 tgggcctggg gaaacataat tactgcagga acccagacaa ccggaggcga ccctgggtgct 480
 atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcac ggtgcatgac tgcgcagatg 540
 gaaaaaagcc ctctctcct ccagaagaat taaaatttca gtgtggccaa aagactctga 600
 ggccccgctt taagattatt gggggagaat tcaccaccat cgagaaccag ccctgggttg 660
 cggccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca 720
 tcagcccttg ctgggtgatc agcgccacac actgcttcat tgattacca aagaaggagg 780
 actacatcgt ctacctgggt cgctcaaggc ttaactocaa cagcaaggg gagatgaagt 840
 ttgaggtgga aaacctcatc ctacacaagg actacagcgc tgacacgctt gctcaccaca 900

acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgcag ccatcccgga 960
 ctatacagac catctgcttg ccctcgatgt ataacgatcc ccagtttggc acaagctgtg 1020
 agatcactgg ctttggaaaa gagaattcta cagactatct ctatccggag cagctgaaga 1080
 tgactgttgt gaagctgatt tcccaccggg agtgtcagca gcccactac tacggctctg 1140
 aagtcaccac caaaatgctg tgtgctgctg acccacagtg gaaaacagat tcctgccagg 1200
 gagactcagg gggacccctc gtctgttccc tccaaggccg catgactttg actggaattg 1260
 tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac 1320
 acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggg 1380
 ccccagggag gaaacgggca ccaccgctt tcttgctggg tgcattttt gcagtagagt 1440
 catctccatc agctgtaaga agagactggg aagat 1475

<210> 34
 <211> 431
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
 1 5 10 15
 Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
 20 25 30
 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
 35 40 45
 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
 50 55 60
 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
 65 70 75 80
 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
 85 90 95
 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp

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<400> 35
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1          5          10          15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
          20          25          30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45

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Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 36
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 36
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30
 Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 37
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 37
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 38
 <211> 106
 <212> PRT
 <213> Mus musculus

<400> 38
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 39
 <211> 1039
 <212> DNA
 <213> Homo sapiens

<400> 39
 tcctgcacag gcagtgcctt gaagtgttc ttcagagacc tttcttcata gactactttt 60
 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120
 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg 180
 ggggcgctgc tggcactggc ggccctactg cagggggcgg tgtccctgaa gatcgcagcc 240
 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 300
 gtgcagatcc tgagccgcta tgacatcgcc ctgggtccagg aggtcagaga cageccacctg 360
 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420
 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480

cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg 540
 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgtt cacagaggtc 600
 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac 660
 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggga cgtcatgttg 720
 atggggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc 780
 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca 840
 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgcggtt 900
 gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg 960
 gcccagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc 1020
 cacaccagtt gaactgcag 1039

<210> 40

<211> 282

<212> PRT

<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
 195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
 210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
 225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
 245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
 260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys
 275 280

<210> 41
 <211> 678
 <212> DNA
 <213> Mus musculus

<400> 41
 gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60
 ttctcctgca gggccagtc gttcgttggc tcaagcatcc actggtatca gcaaagaaca 120
 aatggttctc caaggcttct cataaagtat gttcttgagt ctatgtctgg gatcccttcc 180
 aggttttagtg gcagtggatc agggacagat tttactotta gcatcaacac tgtggagtct 240
 gaagatatcg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggctcg 300
 gggacaaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa 360
 cctggaggat ccatgaaact ctctgtgtt gcctctggat tcattttcag taaccaactgg 420
 atgaactggg tccgccagtc tccagagaag gggcttgagt gggttgctga aattagatca 480
 aaatctatta attctgcaac acattatgcg gagtctgtga aaggagggtt caccatctca 540
 agagatgatt ccaaaagtgc tgtctacctg caaatgaccg acttaagaac tgaagacact 600
 ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggc 660
 accactctca cagtctcc 678

<210> 42
 <211> 226
 <212> PRT
 <213> Mus musculus

<400> 42
 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
 1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
 20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
 35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
 65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
 85 90 95

Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu
 100 105 110

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser
 115 120 125

Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val
 130 135 140

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser
 145 150 155 160

Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg
 165 170 175

Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met
 180 185 190

Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn
 195 200 205

Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
 210 215 220

Val Ser
 225

<210> 43
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 43
 gctgcatcag aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc 60
 gcctcctgcc cctgctggcg ctgctggccc tctggggacc tgaccagcc gcagcctttg 120
 tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaac 180
 gaggcttctt ctacacaccc aagaccgcc gggaggcaga ggacctgcag gtggggcagg 240
 tggagctggg cgggggccct ggtgcaggca gcctgcagcc cttggccctg gaggggtccc 300
 tgcaagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg 360
 agaactactg caactagacg cagcccgag gcagccccc acccgccgcc tctgcaccg 420
 agagagatgg aataaagccc ttgaaccago 450

<210> 44
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
 1 5 10 15
 Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
 20 25 30
 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
 35 40 45
 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
 50 55 60
 Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
 65 70 75 80
 Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
 85 90 95
 Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
 100 105 110

<210> 45
 <211> 1203
 <212> DNA
 <213> Hepatitis B virus

<400> 45
 atgggagggtt ggtcttccaa acctcgacaa ggcattgggga cgaatctttc tgttcccaat 60
 cctctgggat tctttccga tcaccagttg gacctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg acttcaacco caacaaggat cactggccag aggcaatcaa ggtaggagcg 180
 ggagacttgc ggccagggtt caccacacca caggcggtc ttttggggtg gagccctcag 240
 gctcagggca tattgacaac agtgccagca ggcctctc ctgtttccac caatggcag 300
 tcaggaagac agcctactcc catctctcca cctctaagag acagtcattc tcaggccatg 360
 cagtggaaact ccacaacatt ccaccaagct ctgctagatc ccagagttag ggcctatat 420
 tttcctgctg gtggctccag ttccggaaca gtaaaccctg ttccgactac tgtctcacc 480
 atatcgtcaa tcttctcgag gactggggac cctgcaccga acatggagag cacaacatca 540
 ggattcctag gacctgtgt cgtgttacag ggggggttt tcttggtgac aagaatcctc 600
 acaataccac agagtctaga ctggtggtg acttctctca attttctagg gggagcacc 660
 acgtgtcctg gccaaaattc gcagtcccca acctccaato actcaccaac ctcttgctct 720
 ccaatttgct ctggttatcg ctggatgtgt ctgcggtgt ttatcatatt cctcttcatt 780
 ctgctgctat gcctcatctt cttgttggtt cttctggact accaaggtat gttgcccggt 840

tgctctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt 900
 cctgctcaag gaacctctat gtttcctctet tgttgcgtga caaaccttc ggacggaaac 960
 tgcacttgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc 1020
 tcagtcogtt tctcctgggt cagtttacta gtgccatttg ttcagtgggt cgcagggtt 1080
 tccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac 1140
 aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt 1200
 tga 1203

<210> 46
 <211> 400
 <212> PRT
 <213> Hepatitis B virus

<400> 46
 Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
 1 5 10 15
 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30
 Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45
 Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60
 Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80
 Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95
 Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110
 Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125
 Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140
 Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160
 Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175
 Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190
 Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 225 230 235 240
 Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 245 250 255
 Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 260 265 270
 Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 275 280 285
 Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 290 295 300
 Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
 305 310 315 320
 Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
 325 330 335
 Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
 340 345 350
 Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
 355 360 365
 Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
 370 375 380
 Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 385 390 395 400

<210> 47
 <211> 799
 <212> DNA
 <213> Homo sapiens

<400> 47
 cgaaccactc agggctcctgt ggacagctca cctagctgca atggctacag gctcccggac 60
 gtccctgctc ctggcttttg gctgctctg cctgccctgg cttcaagagg gcagtgcctt 120
 cccaaccatt cccttatcca ggccttttga caacgctatg ctccgcgccc atcgtctgca 180
 ccagctggcc tttagacact accaggagtt tgaagaagcc tatatcccaa aggaacagaa 240
 gtattcattc ctgcagaacc ccagacctc cctctgtttc tcagagtcta ttccgacacc 300
 ctccaacagg gaggaacac aacagaaatc caacctagag ctgctccgca tctccctgct 360
 gctcatccag tcgtggctgg agcccgtag gttcctcagg agtgtcttcg ccaacagcct 420
 ggtgtacggc gcctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat 480
 ccaaacgctg atggggaggc tggaagatgg cagcccccg actgggcaga tcttcaagca 540
 gacctacagc aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg 600
 gctgctctac tgcttcagga aggacatgga caaggctogag acattcctgc gcacgtgca 660

gtgccgctct gtggagggca gctgtggctt ctagctgcc cgggtggcatc cctgtgaccc 720
 ctccccagtg cctctcctgg ccctggaagt tgccactcca gtgcccacca gccttgctct 780
 aataaaatta agttgcatc 799

<210> 48
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
 1 5 10 15
 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
 20 25 30
 Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
 35 40 45
 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
 50 55 60
 Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
 65 70 75 80
 Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
 85 90 95
 Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
 100 105 110
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
 115 120 125
 Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
 130 135 140
 Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
 145 150 155 160
 Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
 165 170 175
 His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
 180 185 190
 Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
 195 200 205
 Arg Ser Val Glu Gly Ser Cys Gly Phe
 210 215

<210> 49
 <211> 963
 <212> DNA
 <213> Homo sapiens

<400> 49

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 50 55 60
 Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
 65 70 75 80
 Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
 85 90 95
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
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Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
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 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
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 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
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 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 225 230 235 240
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
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 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
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 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
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 Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
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| 210 | 215 | 220 | |
| Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro | | | |
| 225 | 230 | 235 | 240 |
| Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser | | | |
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| Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp | | | |
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| Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn | | | |
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| Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val | | | |
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| Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu | | | |
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| Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys | | | |
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| Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr | | | |
| | 340 | 345 | 350 |
| Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr | | | |
| | 355 | 360 | 365 |
| Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu | | | |
| | 370 | 375 | 380 |
| Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu | | | |
| 385 | 390 | 395 | 400 |
| Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys | | | |
| | 405 | 410 | 415 |
| Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu | | | |
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| Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly | | | |
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<210> 64
 <211> 464
 <212> PRT
 <213> Homo sapiens

<400> 64
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 His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 35 40 45
 Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
 50 55 60
 Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
 65 70 75 80
 Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
 85 90 95
 His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
 100 105 110
 Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
 115 120 125
 Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
 130 135 140
 Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
 145 150 155 160
 Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
 165 170 175
 Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
 180 185 190
 Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys

| 195 | | | | | 200 | | | | | 205 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asn | Ala | Glu | Gln | Ser | Arg | Ala | Ala | Ile | Asn | Lys | Trp | Val | Ser | Asn |
| 210 | | | | | | 215 | | | | | 220 | | | | |
| Lys | Thr | Glu | Gly | Arg | Ile | Thr | Asp | Val | Ile | Pro | Ser | Glu | Ala | Ile | Asn |
| 225 | | | | | | 230 | | | | | 235 | | | | 240 |
| Glu | Leu | Thr | Val | Leu | Val | Leu | Val | Asn | Thr | Ile | Tyr | Phe | Lys | Gly | Leu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Trp | Lys | Ser | Lys | Phe | Ser | Pro | Glu | Asn | Thr | Arg | Lys | Glu | Leu | Phe | Tyr |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Lys | Ala | Asp | Gly | Glu | Ser | Cys | Ser | Ala | Ser | Met | Met | Tyr | Gln | Glu | Gly |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Lys | Phe | Arg | Tyr | Arg | Arg | Val | Ala | Glu | Gly | Thr | Gln | Val | Leu | Glu | Leu |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Pro | Phe | Lys | Gly | Asp | Asp | Ile | Thr | Met | Val | Leu | Ile | Leu | Pro | Lys | Pro |
| 305 | | | | | | 310 | | | | | 315 | | | | 320 |
| Glu | Lys | Ser | Leu | Ala | Lys | Val | Glu | Lys | Glu | Leu | Thr | Pro | Glu | Val | Leu |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Gln | Glu | Trp | Leu | Asp | Glu | Leu | Glu | Glu | Met | Met | Leu | Val | Val | His | Met |
| | | | 340 | | | | | | 345 | | | | | 350 | |
| Pro | Arg | Phe | Arg | Ile | Glu | Asp | Gly | Phe | Ser | Leu | Lys | Glu | Gln | Leu | Gln |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Asp | Met | Gly | Leu | Val | Asp | Leu | Phe | Ser | Pro | Glu | Lys | Ser | Lys | Leu | Pro |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Gly | Ile | Val | Ala | Glu | Gly | Arg | Asp | Asp | Leu | Tyr | Val | Ser | Asp | Ala | Phe |
| 385 | | | | | | 390 | | | | | 395 | | | | 400 |
| His | Lys | Ala | Phe | Leu | Glu | Val | Asn | Glu | Glu | Gly | Ser | Glu | Ala | Ala | Ala |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Ser | Thr | Ala | Val | Val | Ile | Ala | Gly | Arg | Ser | Leu | Asn | Pro | Asn | Arg | Val |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Thr | Phe | Lys | Ala | Asn | Arg | Pro | Phe | Leu | Val | Phe | Ile | Arg | Glu | Val | Pro |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Leu | Asn | Thr | Ile | Ile | Phe | Met | Gly | Arg | Val | Ala | Asn | Pro | Cys | Val | Lys |
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<210> 65
 <211> 1962
 <212> DNA
 <213> Homo sapiens

<400> 65
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<210> 66
 <211> 653
 <212> PRT
 <213> Homo sapiens

<400> 66

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Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
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Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
          20          25          30

Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
          35          40          45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
          50          55          60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65          70          75          80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
          85          90          95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
          100          105          110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
          115          120          125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
          130          135          140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145          150          155          160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
          165          170          175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
          180          185          190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
          195          200          205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
          210          215          220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225          230          235          240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
          245          250          255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
          260          265          270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
          275          280          285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val

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| 290 | | | | | 295 | | | | | 300 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Trp | Ser | Leu | Pro | Gln | Pro | Trp | Arg | Ala | Asp | Val | Thr | Tyr | Ala | Ala |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Met | Val | Val | Lys | Val | Ile | Ala | Gln | His | Gln | Asn | Leu | Leu | Leu | Ala | Asn |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Thr | Thr | Ser | Ala | Phe | Pro | Tyr | Ala | Leu | Leu | Ser | Asn | Asp | Asn | Ala | Phe |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Leu | Ser | Tyr | His | Pro | His | Pro | Phe | Ala | Gln | Arg | Thr | Leu | Thr | Ala | Arg |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Phe | Gln | Val | Asn | Asn | Thr | Arg | Pro | Pro | His | Val | Gln | Leu | Leu | Arg | Lys |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Pro | Val | Leu | Thr | Ala | Met | Gly | Leu | Leu | Ala | Leu | Leu | Asp | Glu | Glu | Gln |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Leu | Trp | Ala | Glu | Val | Ser | Gln | Ala | Gly | Thr | Val | Leu | Asp | Ser | Asn | His |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Thr | Val | Gly | Val | Leu | Ala | Ser | Ala | His | Arg | Pro | Gln | Gly | Pro | Ala | Asp |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Ala | Trp | Arg | Ala | Ala | Val | Leu | Ile | Tyr | Ala | Ser | Asp | Asp | Thr | Arg | Ala |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| His | Pro | Asn | Arg | Ser | Val | Ala | Val | Thr | Leu | Arg | Leu | Arg | Gly | Val | Pro |
| | | 450 | | | | 455 | | | | | 460 | | | | |
| Pro | Gly | Pro | Gly | Leu | Val | Tyr | Val | Thr | Arg | Tyr | Leu | Asp | Asn | Gly | Leu |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Cys | Ser | Pro | Asp | Gly | Glu | Trp | Arg | Arg | Leu | Gly | Arg | Pro | Val | Phe | Pro |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| Thr | Ala | Glu | Gln | Phe | Arg | Arg | Met | Arg | Ala | Ala | Glu | Asp | Pro | Val | Ala |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Ala | Ala | Pro | Arg | Pro | Leu | Pro | Ala | Gly | Gly | Arg | Leu | Thr | Leu | Arg | Pro |
| | | 515 | | | | | 520 | | | | | 525 | | | |
| Ala | Leu | Arg | Leu | Pro | Ser | Leu | Leu | Leu | Val | His | Val | Cys | Ala | Arg | Pro |
| | | 530 | | | | 535 | | | | | 540 | | | | |
| Glu | Lys | Pro | Pro | Gly | Gln | Val | Thr | Arg | Leu | Arg | Ala | Leu | Pro | Leu | Thr |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Gln | Gly | Gln | Leu | Val | Leu | Val | Trp | Ser | Asp | Glu | His | Val | Gly | Ser | Lys |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Cys | Leu | Trp | Thr | Tyr | Glu | Ile | Gln | Phe | Ser | Gln | Asp | Gly | Lys | Ala | Tyr |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Thr | Pro | Val | Ser | Arg | Lys | Pro | Ser | Thr | Phe | Asn | Leu | Phe | Val | Phe | Ser |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| Pro | Asp | Thr | Gly | Ala | Val | Ser | Gly | Ser | Tyr | Arg | Val | Arg | Ala | Leu | Asp |
| | 610 | | | | | 615 | | | | | 620 | | | | |

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
 625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
 645 650

<210> 67
 <211> 1290
 <212> DNA
 <213> Homo sapiens

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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
 gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctccagaaggc 240
 tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga 300
 gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta 360
 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420
 acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatgcca gacctttgct 480
 gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg 540
 gcagatgggt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
 tcctgtgagt ggctcttcta tatgtggccc tttaaaaagc ccaattatac agaaatccga 660
 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
 ggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa 840
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<210> 68
 <211> 429
 <212> PRT
 <213> Homo sapiens

<400> 68

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Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
          20           25           30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
          35           40           45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
          50           55           60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65           70           75           80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
          85           90           95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
          100          105          110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
          115          120          125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
130          135          140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
145          150          155          160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
          165          170          175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
          180          185          190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
          195          200          205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
210          215          220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
225          230          235          240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
          245          250          255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
          260          265          270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
          275          280          285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
          290          295          300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
305          310          315          320

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Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
 420 425

<210> 69
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 69
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 ttctttctccc agccgggtgc cccaatactt cagtgcattgg gctgctgctt ctctagagca 180
 tatccacttc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240
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<210> 70
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 70
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 20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
 35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
 65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
 85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
 100 105 110

Tyr His Lys Ser
 115

<210> 71
 <211> 498
 <212> DNA
 <213> Homo sapiens

<400> 71
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 gagggctgcc ccgtgtgcat caccgtcaac accaccatct gtgccggcta ctgccccacc 180
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<210> 72
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 72
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 20 25 30
 Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
 35 40 45
 Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val
 50 55 60
 Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
 65 70 75 80
 Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
 85 90 95
 Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
 100 105 110
 Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu

115 120 125
 Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro
 130 135 140
 Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
 145 150 155 160
 Pro Ile Leu Pro Gln
 165

<210> 73
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 73
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 20 25 30
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
 35 40 45
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
 50 55 60
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
 65 70 75 80
 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 85 90 95
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 100 105 110
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 115 120 125
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 130 135 140
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 145 150 155 160
 Cys Arg Thr Gly Asp
 165

<210> 74
 <211> 588
 <212> DNA
 <213> Homo sapiens

<400> 74
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 ctgcacaaa tgaggagaat ctccctttt ttgtgtotca aggacagaag agacttcagg 180

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ttccccagg agatggtaaa agggagccag ttgcagaagg cccatgtcat gtctgtcctc 240
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<212> PRT
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35 40 45
Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
50 55 60
Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65 70 75 80
His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95
Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110
His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140
Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160
Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
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Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190
Gly Ser Ser
195

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